









double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

ID AAF24290 standard; DNA; 21 BP.  
XX  
XX AC  
XX AAF24290;  
DT 03-APR-2001 (first entry)  
XX  
DE Complementary nucleic acid detection method related sequence #5.  
XX  
XX Complementary nucleic acid; gene analysis; polymorphism; variation;  
KW DNA chip; primer; ss.  
XX  
XX  
OS Unidentified.  
XX  
XX PN EP1065278-A2.  
XX  
XX PD 03-JAN-2001.  
XX  
XX PF 07-JUN-2000; 2000EP-00112235.  
XX  
XX PR 07-JUN-1999; 99JP-00159339.  
XX  
XX PA (FUJF ) FUJI PHOTO FILM CO LTD.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.

PF 31-DEC-1999; 99US-00475947.  
XX  
PR 31-DEC-1999; 99US-00475947.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Garner HR, Wren JD, Minna JD, Fondon JW;  
XX  
XX  
DR WPI; 2003-208818/20.  
XX  
XX Identifying a candidate polymorphic repeat within a coding sequence, for  
PT understanding or treating genetic disease, comprises detecting tandem  
PT repeats in a target coding sequence and scoring the repeats for  
PT polymorphic probability.  
XX  
XX Example; Col 495; 588pp; English.  
XX  
CC The invention discloses a method for identifying a candidate polymorphic  
CC repeat within a coding sequence (expressed sequence tag, EST), which  
CC comprises detecting tandem repeats in a target coding sequence, scoring  
CC the repeats for polymorphic probability and generating a dataset  
CC correlating the repeats with polymorphic probability to identify a  
CC candidate polymorphic repeat. The computational methods (polymorphic  
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
CC useful for identifying and detecting candidate polymorphic repeats in  
CC human genes, which can be used to understand, treat or eliminate genetic  
CC diseases, predispositions or adverse drug-treatment reactions. Examples  
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,  
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
CC the polymorphic repeats identified for a search of human ESTs  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 21;  
Best Local Similarity 95.2%; Pred. No. 6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21  
  
RESULT 705  
AAQ30431/c  
ID AAQ30431 standard; DNA; 23 BP.  
XX  
AC AAQ30431;  
XX  
XX 25-MAR-2003 (revised)  
DT 07-DEC-1992 (first entry)  
XX  
DE Oligomer IL6804 for forming triplex with HUMIL6 target duplex.  
XX  
XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
KW malignancy; hepatitis; inflammation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= N4 N4 ethanocytosine"  
FT 11. .12  
FT misc\_feature /\*tag= d  
FT /note= "o-xyloso dimer synthon linkage"  
FT 12. .23  
FT misc\_feature /\*tag= c  
FT /label= inverted\_polarity\_region  
FT /note= "see comments"  
FT modified\_base 23

FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
XX  
PN WO9209705-A1.  
XX  
PD 11-JUN-1992.  
XX  
PF 25-NOV-1991; 91WO-US008811.  
XX  
PR 23-NOV-1990; 90US-00617907.  
PR 18-JAN-1991; 91US-00643382.  
PR 08-APR-1991; 91US-00683420.  
PR 17-APR-1991; 91US-00686544.  
PR 17-APR-1991; 91US-00686546.  
PR 17-APR-1991; 91US-00686547.  
PR 27-SEP-1991; 91US-00766733.  
XX  
XX (GILE-) GILEAD SCI INC.  
XX  
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
PI  
XX WPI; 1992-217083/26.  
DR  
XX New oligomers contg. modified bases - which form a triplex with G-C  
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
XX herpes malignancy and inflammation.  
XX  
PS Claim 12; Page 71; 77pp; English.  
XX  
XX The synthetic oligomer is capable of forming a triplex at physiological  
XX pH with a purine rich target sequence by coupling into the major groove  
XX of the duplex. The specific target sequence of this oligomer is the human  
XX interleukin 6 gene untranslated sequence contg. a purine rich sequence  
XX concd. on one strand of the duplex. The oligomer, and others like it are  
XX useful in diagnosis and therapy of diseases characterised by specific DNA  
XX duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
XX tumours and inflammation. The triple helices form under mild conditions  
XX thus assays may be carried out without subjecting the test specimen to  
XX harsh conditions. The oligomer contains an inverted polarity region  
XX formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso  
XX (nucleotides have the 3'positions of xylose sugars linked via the o-  
XX xylene ring). Two nucleotides are coupled through a xylene residue to  
XX form the dimer synthon. This additional modifications may render the  
XX oligomer stable to nuclease activity. The oligomer is able to inhibit  
XX gene expression, as verified by in vitro systems. See also AAQ25452-25501  
XX and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 23;  
Best Local Similarity 95.2%; Pred. No. 7.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 23 TAAAAA AAAAAA AAAAAA AAAAAA 3  
  
RESULT 706  
AAQ30430/c  
ID AAQ30430 standard; DNA; 23 BP.  
XX  
AC AAQ30430;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-DEC-1992 (first entry)  
XX  
DE Oligomer IL6803 for forming triplex with HUMIL6 target duplex.  
XX  
KW Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;  
KW malignancy; hepatitis; inflammation; ss.  
XX



OS Synthetic.  
XX Key Location/Qualifiers  
FH modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
FT 11. .12  
FT /\*tag= d  
FT /note= "O-xyloso dimer synthon linkage"  
FT 12. .23  
FT /\*tag= c  
FT /label= inverted\_polarity\_region  
FT /note= "see comments"  
FT 23  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"  
XX WO9209705-A1.  
XX  
XX 11-JUN-1992.  
XX  
XX 25-NOV-1991; 91WO-US008811.  
XX  
XX 23-NOV-1990; 90US-00617907.  
XX 18-JAN-1991; 91US-00643382.  
XX 08-APR-1991; 91US-00683420.  
XX 17-APR-1991; 91US-00686544.  
XX 17-APR-1991; 91US-00686546.  
XX 17-APR-1991; 91US-00686547.  
XX 27-SEP-1991; 91US-00766733.  
XX  
XX (GILE-) GILEAD SCI INC.  
XX  
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
XX WPI; 1992-217083/26.  
XX  
XX New oligomers contg. modified bases - which form a triplex with G-C  
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
XX herpes malignancy and inflammation.  
XX  
XX Claim 12; Page 71; 77pp; English.  
XX  
XX The synthetic oligomer is capable of forming a triplex at physiological  
XX pH with a purine rich target sequence by coupling into the major groove  
XX of the duplex. The specific target sequence of this oligomer is the human  
XX interleukin 6 gene untranslated sequence contg. a purine rich sequence  
XX concd. on one strand of the duplex. The oligomer, and others like it are  
XX useful in diagnosis and therapy of diseases characterised by specific DNA  
XX duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant  
XX tumours and inflammation. The triple helices form under mild conditions  
XX thus assays may be carried out without subjecting the test specimen to  
XX harsh conditions. The oligomer contains an inverted polarity region  
XX formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso  
XX (nucleotides have the 3'positions of xylose sugars linked via the o-  
XX xylene ring). Two nucleotides are coupled through a xylene residue to  
XX form the dimer synthon. This additional modifications may render the  
XX oligomer stable to nuclease activity. The oligomer is able to inhibit  
XX gene expression, as verified by in vitro systems. See also AAQ25452-25501  
XX and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 23;  
Best Local Similarity 95.2%; Pred. No. 7.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAIAAAAAAAAAAAAAAAAAA 2804  
Db 23 TAAAAAAAAAAAAAAAAA 3

RESULT 707  
ABL01773  
ID ABL01773 standard; DNA; 23 BP.  
XX  
AC ABL01773;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.  
XX  
KW Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;  
XX hereditary non-polyposis colorectal cancer; ds.  
OS Homo sapiens.  
XX  
PN US2001044936-A1.  
XX  
PD 22-NOV-2001.  
XX  
PF 22-OCT-1999; 99US-00426548.  
XX  
PR 22-OCT-1998; 98US-0105180P.  
XX  
PA (ROBB/) ROBBINS D.  
PA (LING/) LIN-GOERKE J L.  
XX (LING/) LING J C.  
PI Robbins D, Lin-Goerke JL, Ling JC;  
XX WPI; 2002-105577/14.  
XX  
PT New variants of the human MLH1 and MSH2 genes for diagnosing or  
PT determining a predisposition for hereditary non-polyposis colorectal  
PT cancer.  
XX  
PS Disclosure; Page 4; 38pp; English.  
XX

CC The present invention describes a variant human MLH1 or MSH2 gene. Also  
CC described are: (1) a method for diagnosing or predicting susceptibility  
CC to hereditary non-polyposis colorectal cancer (HNPCC), comprising  
CC screening a DNA sample for the variant MLH1 or MSH2 gene where presence  
CC of the variant indicates presence of, or susceptibility to HNPCC; (2) a  
CC method of identifying mutants in splice donor or acceptor sites of a  
CC human MLH1 gene, comprising sequencing splice donor or acceptor sites of  
CC the gene with intronic primers for the human MLH1 gene and analysing the  
CC sequence to identify any mutants; (3) a method of identifying mutants in  
CC splice donor or acceptor sites of a human MSH2 gene, comprising  
CC sequencing splice donor or acceptor sites of the gene with intronic  
CC primers for the human MSH2 gene and analysing the sequence to identify  
CC any mutants; and (4) a transgenic model system for colorectal cancer  
CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and  
CC hMSH2 variants are used to diagnose or determine a patient's  
CC susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to  
CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene  
CC fragments from the present invention. ABL01832 to ABL01839 represent  
CC mutagenic primers used in the exemplification of the present invention  
XX  
SQ Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 23;  
Best Local Similarity 95.2%; Pred. No. 7.6e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAIAAAAAAAAAAAAAAAAAA 2804  
Db 2 TAAAAAAAAAAAAAAAAA 22

RESULT 708  
AAH24266  
ID AAH24266 standard; DNA; 24 BP.  
XX



XX This invention relates to the DNA and protein sequences of leukemia  
CC related protein 24.09. The invention also comprises methods for producing  
CC the protein using recombinant DNA technology and antagonists of the  
CC protein which may be used for inhibiting the action of the protein. The  
CC sequences of the invention may be used for treating several diseases such  
CC as leukaemia, lymphoma, other haemopathy and growth development  
CC disturbance disease. The present sequence represents a reverse  
CC transcription (RT) PCR primer used to isolate the leukaemia related  
CC protein cDNA 24.09 of the invention  
XX  
SQ Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 24;  
Best Local Similarity 95.2%; Pred. No. 8.5e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA 2801  
DB 22 AATTGAAAAA 2801  
  
RESULT 711  
ABZ23536  
ID ABZ23536 standard; DNA; 24 BP.  
XX  
AC ABZ23536;  
XX  
DT 07-APR-2003 (first entry)  
XX  
DE fragment of a plasmid used to detect somatic instability.  
XX  
KW Replication error; drug development; somatic instability; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 4 /\*tag= a  
FT /note= "this base represents an unspecified number of  
FT bases"  
FT 21  
FT misc\_feature /\*tag= b  
FT /note= "this base represents an unspecified number of  
FT bases"  
XX  
PN WO200295071-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 22-MAY-2002; 2002WO-NL000322.  
XX  
PR 22-MAY-2001; 2001EP-00201936.  
XX  
PA (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.  
PA (TIJS/) TIJSTERMAN M.  
XX  
PI Plasterk RHA, Tijsterman M;  
XX  
DR WPI; 2003-129440/12.  
XX  
PT Determining whether a product of a gene is involved in preventing a  
PT replication error in a cell comprises providing a specific inhibitor for  
PT the product and determining the level of expression of a marker gene.  
XX  
PS Example 1; Fig 3; 47pp; English.  
XX  
CC The specification describes a method for determining whether a product of  
CC a gene is involved in preventing a replication error in a cell. The  
CC method comprises providing the level of functional expression of a marker  
CC product and determining the level of expression of the marker gene is  
CC dependent on the occurrence of the replication error. The method is used  
CC gene in the cell, where the level of expression of the marker gene is  
CC dependent on the occurrence of the replication error. The method is used

CC for determining whether a product of a gene is involved in preventing a  
CC replication error in a cell. The identified genes are useful for  
CC developing diagnostic tools, or as targets for drug development to  
CC manipulate cells on the basis of the presence or absence of function of  
CC the gene. ABZ23535-36 represents fragments of plasmids used to detect  
CC somatic instability, in the course of the invention  
XX  
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 8.5e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAAA 2804  
DB 1 ATGNAAAAAA 2804  
  
RESULT 712  
ABZ23536/C  
ID ABZ23536 standard; DNA; 24 BP.  
XX  
AC ABZ23536;  
XX  
DT 07-APR-2003 (first entry)  
XX  
DE fragment of a plasmid used to detect somatic instability.  
XX  
KW Replication error; drug development; somatic instability; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 4 /\*tag= a  
FT /note= "this base represents an unspecified number of  
FT bases"  
FT 21  
FT misc\_feature /\*tag= b  
FT /note= "this base represents an unspecified number of  
FT bases"  
XX  
PN WO200295071-A2.  
XX  
PD 28-NOV-2002.  
XX  
PF 22-MAY-2002; 2002WO-NL000322.  
XX  
PR 22-MAY-2001; 2001EP-00201936.  
XX  
PA (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.  
PA (TIJS/) TIJSTERMAN M.  
XX  
PI Plasterk RHA, Tijsterman M;  
XX  
DR WPI; 2003-129440/12.  
XX  
PT Determining whether a product of a gene is involved in preventing a  
PT replication error in a cell comprises providing a specific inhibitor for  
PT the product and determining the level of expression of a marker gene.  
XX  
PS Example 1; Fig 3; 47pp; English.  
XX  
CC The specification describes a method for determining whether a product of  
CC a gene is involved in preventing a replication error in a cell. The  
CC method comprises providing the level of functional expression of a marker  
CC product and determining the level of expression of the marker gene is  
CC dependent on the occurrence of the replication error. The method is used  
CC gene in the cell, where the level of expression of the marker gene is  
CC dependent on the occurrence of the replication error. The method is used  
CC for determining whether a product of a gene is involved in preventing a  
CC replication error in a cell. The identified genes are useful for  
CC developing diagnostic tools, or as targets for drug development to  
CC manipulate cells on the basis of the presence or absence of function of

CC the gene. ABZ23535-36 represents fragments of plasmids used to detect  
CC somatic instability, in the course of the invention  
XX  
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 1 T; 0 U; 2 Other;  
Query Match 0.7%; Score 19.4; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 8.5e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2166 TTTTNTTTTNTTTTNTTTTNTTAA 2188  
Db 24 TTTNTTTTNTTTTNTTTTNTTINCA 2  
RESULT 713  
AAV42215/c  
ID AAV42215 standard; DNA; 25 BP.  
XX  
AC AAV42215;  
XX  
DT 16-OCT-1998 (first entry)  
XX  
DE Sequencing primer used to exemplify the invention.  
XX  
KW Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*note= "labelled with the donor carboxyfluoscein"  
FT modified\_base 7  
FT /\*tag= b  
FT /\*note= "optionally labelled with the acceptor 6-  
FT carboxyrhodamine"  
FT modified\_base 14  
FT /\*tag= b  
FT /\*note= "optionally labelled with the acceptor 6-  
FT carboxyrhodamine"  
FT modified\_base 17  
FT /\*tag= a  
FT /\*note= "optionally labelled with the donor  
FT carboxyfluoscein"  
FT modified\_base 17  
FT /\*tag= b  
FT /\*note= "optionally labelled with the acceptor 6-  
FT carboxyrhodamine"  
XX WO9831834-A1.  
XX  
PD 23-JUL-1998.  
XX  
PF 12-DEC-1997; 97WO-US022914.  
XX  
PR 15-JAN-1997; 97US-00784162.  
XX  
PA (INCY-) INCYTE PHARM INC.  
XX  
PI Ju J;  
XX  
DR WPI; 1998-414127/35.  
XX  
PT Set of energy-transfer fluorescent labels with donor and acceptor at  
PT different separations - useful for DNA sequencing allows use of fewer  
PT analysing wavelengths or an increased throughput.  
XX  
PS Example 1; Page 14; 30pp; English.  
XX  
CC The present sequence exemplified the primer of the invention, and is  
CC used to sequence Incyte clone 1 (AAV42737). The primer of the invention  
CC is labelled with a set of at least 2 different fluorescent labels. The  
CC set comprises an energy-transfer fluorescent label with at least 1 each

CC of a donor fluorophore and an acceptor fluorophore capable of energy  
CC transfer, and separated by a distance x, and a second similar fluorescent  
CC label in which the separation distance is y, x and y being sufficiently  
CC different for the two fluorescent labels to produce distinct fluorescent  
CC signals. Fluorescent labels are useful in multicomponent analyses, e.g.  
CC as probes for fluorescent in situ hybridisation or especially as primers  
CC for DNA sequencing  
XX  
SQ Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.4; DB 1; Length 25;  
Best Local Similarity 95.2%; Pred. No. 9.3e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAAAAAA 2804  
Db 24 TAAAAAAAAAAAAAAAAAAAAA 4  
RESULT 714  
AAX84259/c  
ID AAX84259 standard; DNA; 25 BP.  
XX  
AC AAX84259;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE PCR primer for human Nck associated protein 1 coding sequence.  
XX  
KW Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;  
KW therapy; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX WO9931239-A1.  
XX 24-JUN-1999.  
PF 14-DEC-1998; 98WO-JP005646.  
XX  
PR 15-DEC-1997; 97JP-00363183.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (SAKA/) SAKAKI Y.  
XX  
PI Sakaki Y;  
XX  
DR WPI; 1999-395181/33.  
XX  
PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of  
PT Alzheimer's disease.  
XX  
PS Disclosure; Page 76; 90pp; Japanese.  
XX  
CC This sequence represents a PCR primer used to isolate DNA encoding the  
CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits  
CC apoptosis. The protein can be used in the investigation, diagnosis and  
CC treatment (e.g. by gene therapy) of Alzheimer's disease  
XX  
SQ Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.4; DB 1; Length 25;  
Best Local Similarity 95.2%; Pred. No. 9.3e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAAAAAA 2804  
Db 25 TAAAAAAAAAAAAAAAAAAAAA 5  
RESULT 715  
ABZ23535



ID XX AC ABZ23535 standard; DNA; 25 BP.  
XX ABZ23535;  
DT C7-APR-2003 (first entry)  
XX fragment of a plasmid used to detect somatic instability.  
DE Replication error; drug development; somatic instability; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH misc\_feature 4  
FT /\*tag= a  
FT /note= "this base represents an unspecified number of  
FT bases"  
FT 22  
FT misc\_feature  
FT /\*tag= b  
FT /note= "this base represents an unspecified number of  
FT bases"  
XX  
PN WO200295071-A2.  
XX  
XX 28-NOV-2002.  
XX  
XX 22-MAY-2002; 2002WO-NL000322.  
XX  
XX 22-MAY-2001; 2001EP-00201936.  
XX  
XX (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.  
PA (TIJS/) TIJSTERMAN M.  
XX  
XX Plasterk RHA, Tijsterman M;  
PI  
XX WPI; 2003-129440/12.  
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PT replication error in a cell comprises providing a specific inhibitor for  
PT the product and determining the level of expression of a marker gene.  
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XX Example 1; Fig 3; 47pp; English.  
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XX The specification describes a method for determining whether a product of  
CC a gene is involved in preventing a replication error in a cell. The  
CC method comprises providing the cell with a specific inhibitor for the  
CC product and determining the level of functional expression of a marker  
CC gene in the cell, where the level of expression of the marker gene is  
CC dependent on the occurrence of the replication error. The method is used  
CC for determining whether a product of a gene is involved in preventing a  
CC replication error in a cell. The identified genes are useful for  
CC developing diagnostic tools, or as targets for drug development to  
CC manipulate cells on the basis of the presence or absence of function of  
CC the gene. ABZ23535-36 represents fragments of plasmids used to detect  
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Best Local Similarity 87.0%; Pred. No. 9.3e+02;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 ATGAAAAAAAAAAAAAAAAAAAAANA 23  
  
RESULT 716  
AAS20595/c  
ID AAS20595 standard; DNA; 26 BP.  
XX  
AC AAS20595;  
XX

DT 23-APR-2002 (first entry)  
XX Human zsig63 cDNA sequencing primer ZC7231.  
DE  
XX  
KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;  
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;  
KW gastrointestinal disease; urinary tract infection; vaginal infection;  
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;  
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;  
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.  
XX  
OS Homo sapiens.  
XX  
XX US6331413-B1.  
PN  
XX 18-DEC-2001.  
PD  
XX 17-MAR-2000; 2000US-00527345.  
PF  
XX 17-MAR-1999; 99US-0124820P.  
PR  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Adler DA, Sheppard PO;  
PI  
XX WPI; 2002-096707/13.  
DR  
XX Polynucleotides encoding salivary proteins useful as anti-microbial  
PT agents.  
PT  
XX  
PS Example 1; Col 53; 29pp; English.  
XX  
XX The invention relates to a polynucleotide derived from the 4q12-4q13  
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a  
CC secreted salivary protein with anti-microbial activity. Due to their  
CC microbial activity, the sequences can be used in the study of microbial  
CC infections, e.g. for recombinant production of anti-microbial proteins.  
CC The sequences can be used in the treatment of tooth decay, periodontal  
CC disease, thrush, gastrointestinal disease, urinary tract infections,  
CC vaginal infections, skin infections, epithelial wounds, chronic tissue  
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung  
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence  
CC represents a sequencing primer for cDNA encoding human zsig63  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1e+03;  
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804  
Db 26 BAAAAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 717  
ABS52637/c  
ID ABS52637 standard; DNA; 26 BP.  
XX  
AC ABS52637;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human secreted salivary protein zsig63 PCR primer ZC7321.  
XX  
KW Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;  
KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;  
KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;  
KW tooth decay; periodontal disease; thrush; gastrointestinal disease;  
KW urinary tract infection; vaginal infection; skin infection; microflora;  
KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;  
KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;  
KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;



RESULT 719  
AAD55692/c  
ID AAD55692 standard; DNA; 26 BP.  
XX  
AC AAD55692;  
XX  
DT 27-OCT-2003 (revised)  
DT 07-AUG-2003 (first entry)  
XX  
DE Bovine viral diarrhea virus gene 5' end amplifying PCR primer.  
XX  
KW Bovine Viral Diarrhea Virus; BVDV; infection; vaccine; prophylaxis;  
KW gene therapy; PCR; primer; ss.  
XX  
OS Pestivirus type 1.  
XX  
PN WO2003023041-A2.  
XX  
PD 20-MAR-2003.  
XX  
PF 05-SEP-2002; 2002WO-EP009925.  
XX  
PR 06-SEP-2001; 2001DE-01043813.  
XX  
PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
XX  
PI Elbers K, Meyer C, Von Freyburg M, Meyers G;  
XX  
DR WPI; 2003-333043/31.  
XX  
PT New DNA molecule useful for manufacturing a vaccine for the prophylaxis  
PT and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises  
PT a sequence complementary to a BVDV RNA.  
XX  
PS Example 1; Page 20; 73pp; English.  
XX  
CC The invention relates to a DNA molecule containing a sequence  
CC complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when  
CC introduced into susceptible host cells, induces the generation of  
CC infectious BVDV particles. The attenuated BVDV clone or strain is useful  
CC in the manufacture of a vaccine for the prophylaxis and treatment of BVDV  
CC infections. The invention is useful in gene therapy. The present sequence  
CC is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;  
Query Match 0.7%; Score 19.4; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1e+03;  
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2780 GAATTGAAAAA AAAAAAAAAA 2804  
Db :||| ||||| ||||| ||||| |||||  
26 BAAAAA AAAAAAAAAA AAAAAAAAAA 2  
RESULT 720  
ABX93598/c  
ID ABX93598 standard; DNA; 26 BP.  
XX  
AC ABX93598;  
XX  
DT 28-MAY-2003 (first entry)  
XX  
DE Human zsig63 PCR/sequencing primer ZC7231.  
XX  
KW ss; PCR; zsig63; adhesin; salivary gland; dental carries;  
KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;  
KW urinary tract infection; vaginal infection; skin infection; primer;  
KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;  
KW lung infection; cystic fibrosis; lung dysfunction; digestive;

KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;  
KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;  
KW cell culture media; gene therapy; human chromosome 4ql2-4ql3;  
KW dentinogenesis imperfecta; dentin dysplasia type II.  
XX  
OS Synthetic.  
XX  
PN US2002173027-A1.  
XX  
PD 21-NOV-2002.  
XX  
PF 03-AUG-2001; 2001US-00922469.  
XX  
PR 17-MAR-1999; 99US-0124820P.  
PR 17-MAR-2000; 2000US-00527345.  
XX  
PA (ADLE/) ADLER D A.  
PA (SHEP/) SHEPPARD P O.  
XX  
PI Adler DA, Sheppard PO;  
XX  
DR WPI; 2003-328428/31.  
XX  
PT Novel isolated zsig63 polypeptide, member of the adhesin family, useful  
PT for treating dental carries, periodontal disease, thrush,  
PT gastrointestinal disease, urinary tract infections, vaginal infections,  
PT skin infections.  
XX  
PS Example 1; Page 29; 32pp; English.  
XX  
CC The invention relates to an isolated zsig63 polypeptide comprising at  
CC least 90% identity to an amino acid sequence which comprises domain 1 of  
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also  
CC included are the polynucleotide encoding zsig63, a zsig63 expression  
CC vector, a cultured cell comprising the vector and expressing the protein,  
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-  
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a  
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing  
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is  
CC useful for detecting in a test sample, the presence of antagonist of  
CC zsig63 protein activity. Zsig63 has antimicrobial activity and since  
CC exhibits high expression in salivary gland, can be used for treating  
CC dental carries, periodontal disease, thrush, and gastrointestinal  
CC disease, urinary tract infections, vaginal infections, skin infections  
CC and other epithelial wounds. The polypeptides can be used to establish  
CC normal microflora and protect against pathogenic colonization and  
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity  
CC for treating chronic, tissue damage particularly in areas having limited  
CC or damaged vascular system, e.g. in diabetes, and for treating  
CC immunocompromised AIDS patients or in individuals that have undergone  
CC chemotherapy, radiation treatment, for treating lung infections e.g. in  
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high  
CC levels in the trachea may indicate that such polypeptides may serve as a  
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing  
CC conditions associated with salivary gland or lung dysfunction including  
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,  
CC chronic bronchitis, prostate dysfunctions such as prostate  
CC adenocarcinoma, aiding digestion, and as components of defined cell  
CC culture media and may be used to replace serum that is commonly used in  
CC culture. The DNA is useful in gene therapy applications to increase or  
CC inhibit zsig63 activity, and for detecting abnormalities on human  
CC chromosome 4 (e.g. 4ql2-4ql3, associated with dentinogenesis imperfecta,  
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The  
CC present sequence is a primer used to isolate and sequence nucleic acids  
CC encoding human zsig63  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;  
Query Match 0.7%; Score 19.4; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1e+03;  
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2780 GAATTGAAAAA AAAAAAAAAA 2804









XX PS Example 1; Fig 3; 90pp; English.

XX CC The present invention describes an isolated, purified nucleic acid, which

CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

CC residues 331-455 of the sequence comprising 455 nucleotides given in

CC AAF74905 where A in the wild type sequence at position 331 (corresponding

CC to position -125) is replaced with C. (I) has antiarthritic,

CC antirheumatic, immunosuppressive and antiinflammatory activities, and can

CC be used in gene therapy. (I) is useful in the study, diagnosis and

CC treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid

CC arthritis. The present sequence represents a CD40L poly-A tract sequence

CC which is used in an example from the present invention

XX SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 27;

Best Local Similarity 95.2%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTGTGTTTTTTTTTTT 2186

Db 22 TTTTGTGTTTTTTTTTTT 2

RESULT 726

AAF74932/c

ID AAF74932 standard; DNA; 27 BP.

XX AC AAF74932;

XX DT 23-MAY-2001 (first entry)

XX DE CD40L poly-A tract sequence SEQ ID NO:29.

Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;

diagnosis; antiarthritic; antirheumatic; immunosuppressive;

antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX PD 22-MAR-2001.

XX PF 13-SEP-2000; 2000WO-US024966.

XX PR 13-SEP-1999; 99US-0153625P.

(NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

Crow MK, Li Y;

WPI; 2001-244776/25.

New altered CD40L promoter for use in the study, diagnosis and treatment

of a variety of inflammatory disorders and autoimmune diseases, such as

rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

The present invention describes an isolated, purified nucleic acid, which

is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

residues 331-455 of the sequence comprising 455 nucleotides given in

AAF74905 where A in the wild type sequence at position 331 (corresponding

to position -125) is replaced with C. (I) has antiarthritic,

antirheumatic, immunosuppressive and antiinflammatory activities, and can

be used in gene therapy. (I) is useful in the study, diagnosis and

treatment of inflammatory and autoimmune diseases, as well as diseases in

which elevated expression of CD40L is a factor, e.g., rheumatoid

arthritis. The present sequence represents a CD40L poly-A tract sequence

which is used in an example from the present invention

XX SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 27;

Best Local Similarity 95.2%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTGTGTTTTTTTTTTT 2186

Db 22 TTTTGTGTTTTTTTTTTT 2

RESULT 727

AAF74931/c

ID AAF74931 standard; DNA; 27 BP.

XX AC AAF74931;

XX DT 23-MAY-2001 (first entry)

XX DE CD40L poly-A tract sequence SEQ ID NO:28.

Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;

diagnosis; antiarthritic; antirheumatic; immunosuppressive;

antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX PD 22-MAR-2001.

XX PF 13-SEP-2000; 2000WO-US024966.

XX PR 13-SEP-1999; 99US-0153625P.

(NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

Crow MK, Li Y;

WPI; 2001-244776/25.

New altered CD40L promoter for use in the study, diagnosis and treatment

of a variety of inflammatory disorders and autoimmune diseases, such as

rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

The present invention describes an isolated, purified nucleic acid, which

is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

residues 331-455 of the sequence comprising 455 nucleotides given in

AAF74905 where A in the wild type sequence at position 331 (corresponding

to position -125) is replaced with C. (I) has antiarthritic,

antirheumatic, immunosuppressive and antiinflammatory activities, and can

be used in gene therapy. (I) is useful in the study, diagnosis and

treatment of inflammatory and autoimmune diseases, as well as diseases in

which elevated expression of CD40L is a factor, e.g., rheumatoid

arthritis. The present sequence represents a CD40L poly-A tract sequence

which is used in an example from the present invention

XX SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 27;

Best Local Similarity 95.2%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTGTGTTTTTTTTTTT 2186

Db 22 TTTTGTGTTTTTTTTTTT 2

RESULT 728

AAF74934/c

ID AAF74934 standard; DNA; 27 BP.  
XX  
AC AAF74934;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:31.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 27;  
Best Local Similarity 95.2%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2166 TTTTGTGTTTTTTTTTTTTTTT 2186  
Db 22 TTTTGTGTTTTTTTTTTTTTTT 2  
  
RESULT 729  
AAT13977  
ID AAT13977 standard; DNA; 28 BP.  
XX  
AC AAT13977;  
XX  
DT 03-OCT-1996 (first entry)  
XX  
DE E. spinifera fumonisin esterase end-blocked polyT primer BamT17V.  
XX  
KW Fumonisin; esterase; transgenic plant; recombinant microorganism;  
KW expression; probiotic; feed inoculant; degradation; detoxification;  
KW maize seed; grain; animal feed; end blocked; polyT primer; nested;  
KW polymerase chain reaction; Exophiala spinifera; ss.  
XX  
OS Synthetic.

XX WO9606175-A2.  
PN  
XX  
PD 29-FEB-1996.  
XX  
PF 11-AUG-1995; 95WO-US010284.  
XX  
PR 12-AUG-1994; 94US-00289595.  
PR 07-JUN-1995; 95US-00484815.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Duvick J, Rood TA;  
XX  
DR WPI; 1996-151378/15.  
XX  
PT Detoxification of fumonisin and related mycotoxin cpds. in grains - using  
PT an enzyme esp. an esterase, from Exophiala spinifera, Rhinocladiella  
PT atrovirens or a bacterium.  
XX  
PS Example 8; Page 33; 54pp; English.  
XX  
CC The present sequence is a primer for the nested PCR amplification of the  
CC Exophiala spinifera (ATCC 74269), fumonisin esterase, cDNA, which was  
CC isolated from a maize seed. The esterase cDNA can be used to produce  
CC transgenic plants and genetically engineered microorganisms, capable of  
CC expressing the esterase. The microorganisms can be used as a probiotic or  
CC feed inoculant, along with the esterase to degrade fumonisins and related  
CC cpds., partic. for the detoxification of maize seed pre- or post-harvest  
CC (i.e. during the storage or processing of the harvested grain, or in the  
CC processed grain) prior to its use as an animal feed  
XX  
SQ Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 28;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2163 TCCGTTTTTTTTTTTTTTTTTT 2183  
Db 7 TCCGTTTTTTTTTTTTTTTTTT 27  
  
RESULT 730  
AAT70108  
ID AAT70108 standard; DNA; 28 BP.  
XX  
AC AAT70108;  
XX  
DT 24-SEP-1997 (first entry)  
XX  
DE PolyTV primer 3.  
XX  
KW primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640998-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US008582.  
XX  
PR 07-JUN-1995; 95US-00481687.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Wang X, Duvick JP, Briggs SP;  
XX  
DR WPI; 1997-087067/08.  
XX  
PT Method for prodn. of cDNA libraries with anchored ends - useful for

PT subtractive cloning of sequences of interest.  
XX  
PS Claim 1; Page 27; 56pp; English.  
XX  
CC The invention provides a PCR-based method for generating a full-length  
CC cDNA library with anchored ends. The method uses lock-docking primers  
CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
CC second primer, polyGH (H = A, C or T) locks onto the polyc tail added by  
CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-  
CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to  
CC amplify the first strand and produce a cDNA library with anchored ends.  
CC cDNA libraries produced may be used to identify new (unique) nucleotide  
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
CC method produces discreet sized PCR products which would not necessarily  
CC require further subcloning/screening. The method also produces full-  
CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 1 A; 5 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 28;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2163 TCCCTTTT TTTT TTTT TTTT TTTT 2183  
Db ||| ||||| ||||| ||||| |||||  
7 TCCGTTT TTTT TTTT TTTT TTTT 27  
  
RESULT 731  
AAT70106  
ID AAT70106 standard; DNA; 28 BP.  
XX  
AC AAT70106;  
XX  
DT 24-SEP-1997 (first entry)  
DE PolyTV primer 1.  
XX  
KW primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
XX Synthetic.  
XX WO9640998-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US008582.  
XX  
PR 07-JUN-1995; 95US-00481687.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Wang X, Duvick JP, Briggs SP;  
XX WPI; 1997-087067/08.  
XX  
PT Method for prodn. of cDNA libraries with anchored ends - useful for  
PT subtractive cloning of sequences of interest.  
XX  
PS Claim 1; Page 26; 56pp; English.  
XX  
CC The invention provides a PCR-based method for generating a full-length  
CC cDNA library with anchored ends. The method uses lock-docking primers  
CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
CC second primer, polyGH (H = A, C or T) locks onto the polyc tail added by  
CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-  
CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to

CC amplify the first strand and produce a cDNA library with anchored ends.  
CC cDNA libraries produced may be used to identify new (unique) nucleotide  
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
CC method produces discreet sized PCR products which would not necessarily  
CC require further subcloning/screening. The method also produces full-  
CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 2 A; 4 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.4; DB 1; Length 28;  
Best Local Similarity 95.2%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2163 TCCCTTTT TTTT TTTT TTTT TTTT 2183  
Db ||| ||||| ||||| ||||| |||||  
7 TCCGTTT TTTT TTTT TTTT TTTT 27  
  
RESULT 732  
AAT70107  
ID AAT70107 standard; DNA; 28 BP.  
XX  
AC AAT70107;  
XX  
DT 24-SEP-1997 (first entry)  
DE PolyTV primer 2.  
XX  
KW primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
XX Synthetic.  
XX WO9640998-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US008582.  
XX  
PR 07-JUN-1995; 95US-00481687.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Wang X, Duvick JP, Briggs SP;  
XX WPI; 1997-087067/08.  
XX  
PT Method for prodn. of cDNA libraries with anchored ends - useful for  
PT subtractive cloning of sequences of interest.  
XX  
PS Claim 1; Page 27; 56pp; English.  
XX  
CC The invention provides a PCR-based method for generating a full-length  
CC cDNA library with anchored ends. The method uses lock-docking primers  
CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
CC second primer, polyGH (H = A, C or T) locks onto the polyc tail added by  
CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-  
CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to  
CC amplify the first strand and produce a cDNA library with anchored ends.  
CC cDNA libraries produced may be used to identify new (unique) nucleotide  
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
CC method produces discreet sized PCR products which would not necessarily  
CC require further subcloning/screening. The method also produces full-  
CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 1 A; 4 C; 5 G; 18 T; 0 U; 0 Other;







PT rheumatoid arthritis.

XX

PS Example 1; Fig 3; 90pp; English.

XX

CC The present invention describes an isolated, purified nucleic acid, which

CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

CC residues 331-455 of the sequence comprising 455 nucleotides given in

CC AAF74905 where A in the wild type sequence at position 331 (corresponding

CC to position -125) is replaced with C. (I) has antiarthritic,

CC antirheumatic, immunosuppressive and antiinflammatory activities, and can

CC be used in gene therapy. (I) is useful in the study, diagnosis and

CC treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid

CC arthritis. The present sequence represents a CD40L poly-A tract sequence

CC which is used in an example from the present invention

XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;

Best Local Similarity 95.2%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2186

Db 23 TTTTGTGTTTTTTTTTTT 3

RESULT 738

AAF74927/c

ID AAF74927 standard; DNA; 28 BP.

XX

AC AAF74927;

XX

DT 23-MAY-2001 (first entry)

XX

DE CD40L poly-A tract sequence SEQ ID NO:24.

XX

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;

KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;

KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

XX

OS Homo sapiens.

XX

PN WO200119844-A1.

XX

PD 22-MAR-2001.

XX

PF 13-SEP-2000; 2000WO-US024966.

XX

PR 13-SEP-1999; 99US-0153625P.

XX

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX

PI Crow MK, Li Y;

XX

DR WPI; 2001-244776/25.

XX

PT New altered CD40L promoter for use in the study, diagnosis and treatment

PT of a variety of inflammatory disorders and autoimmune diseases, such as

PT rheumatoid arthritis.

XX

PS Example 1; Fig 3; 90pp; English.

XX

CC The present invention describes an isolated, purified nucleic acid, which

CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

CC residues 331-455 of the sequence comprising 455 nucleotides given in

CC AAF74905 where A in the wild type sequence at position 331 (corresponding

CC to position -125) is replaced with C. (I) has antiarthritic,

CC antirheumatic, immunosuppressive and antiinflammatory activities, and can

CC be used in gene therapy. (I) is useful in the study, diagnosis and

CC treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid

CC arthritis. The present sequence represents a CD40L poly-A tract sequence

CC which is used in an example from the present invention

XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;

Best Local Similarity 95.2%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2186

Db 23 TTTTGTGTTTTTTTTTTT 3

RESULT 739

AAF60450

ID AAF60450 standard; DNA; 28 BP.

XX

AC AAF60450;

XX

DT 27-APR-2001 (first entry)

XX

DE RNA oligonucleotide #7.

XX

KW Protein-RNA fusion; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT modified\_base 1 /\*tag= a

FT /mod\_base= OTHER

FT /note= "C6-psoralen-2-OMe-U"

FT modified\_base 28

FT /\*tag= b

FT /mod\_base= OTHER

FT /note= "A-TEG2"

XX

PN WO200107657-A1.

XX

PD 01-FEB-2001.

XX

PF 19-JUL-2000; 2000WO-US019653.

XX

PR 27-JUL-1999; 99US-0145834P.

XX

PA (PHYL-) PHYLLOS INC.

XX

PI Kurz M, Lohse P, Wagner R;

XX

DR WPI; 2001-182803/18.

XX

PT Affixing a peptide acceptor to an RNA molecule useful for producing

PT fusion proteins for isolating proteins or nucleic acids with desired

PT properties through attachment of a peptide acceptor to the 3' end of an

PT RNA molecule.

XX

PS Example 6; Page 29; 56pp; English.

XX

CC The present invention relates to a method for affixing a peptide acceptor

CC to an RNA molecule through the formation of a covalent bond, noncovalent

CC bond, or by chemical ligation. The method is useful for producing RNA-

CC protein fusions which can be used for the isolation of proteins or

CC nucleic acids with desired properties from large pools of partially or

CC completely random amino acid or nucleic acid sequences. The present

CC sequence is an RNA oligonucleotide used in the present invention

XX

SQ Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 28;

Best Local Similarity 90.5%; Pred. No. 1.2e+03;

Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2804







CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2186  
Db 24 TTTTGTGTTTTTTTTTTT 4

RESULT 745  
AAF74935/c  
ID AAF74935 standard; DNA; 29 BP.

XX AAF74935;

XX 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:32.

Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

PN 22-MAR-2001.

XX 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PA Crow MK, Li Y;

PI WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic.  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2186  
Db 24 TTTTGTGTTTTTTTTTTT 4

RESULT 746  
AAF74921/c  
ID AAF74921 standard; DNA; 29 BP.

XX AAF74921;

XX 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:18.

Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PA Crow MK, Li Y;

DR WPI; 2001-244776/25.

XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 95.2%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2186  
Db 24 TTTTGTGTTTTTTTTTTT 4

RESULT 747  
AAF74928/c  
ID AAF74928 standard; DNA; 29 BP.

XX AAF74928;

XX 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:25.



PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.

PS Disclosure; Page 14; 32pp; English.

CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data

XX  
SQ Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 79.3%; Pred. No. 1.3e+03;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2183  
Db 29 TTTTGGGAGATTTT 1

RESULT 750  
AAD33516/c  
ID AAD33516 standard; DNA; 29 BP.

XX  
AC AAD33516;

XX  
DT 01-JUL-2002 (first entry)

XX  
DE T7T18Apad\_PS18-29-0003 probe for calibration of molecular array data.

XX  
KW Molecular array; probe; ss.

XX  
OS Unidentified.

XX  
PN EP1186673-A2.

XX  
PD 13-MAR-2002.

XX  
PF 10-SEP-2001; 2001EP-00307665.

XX  
PR 11-SEP-2000; 2000US-00659173.

XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.

XX  
PI Wobler PK, Delenstarr GC;

XX  
DR WPI; 2002-282886/33.

XX  
PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.

PS Disclosure; Page 14; 32pp; English.

XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data

XX  
SQ Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 29;

Best Local Similarity 79.3%; Pred. No. 1.3e+03;  
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2155 TTTTCTCCTTTT 2183  
Db 29 TTTTGGGAGATTTT 1

RESULT 751  
ADC16682/c  
ID ADC16682 standard; DNA; 30 BP.

XX  
AC ADC16682;

XX  
DT 18-DEC-2003 (first entry)

XX  
DE Aminoacylation RNA molecule related DNA oligo, P3-2.

XX  
KW ribozyme; aminoacylate; tRNA; non-cognate; catalytic RNA molecule; cis;  
KW aminoacylation; trans; proteomic; ds.

XX  
OS Unidentified.

XX  
PN WO2003070740-A1.

XX  
PD 28-AUG-2003.

XX  
PF 18-FEB-2003; 2003WO-US005007.

XX  
PR 15-FEB-2002; 2002US-0357424P.

XX  
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.

XX  
PI Suga H, Murakami H, Saito H;

XX  
DR WPI; 2003-748198/70.

XX  
PT New polynucleotide, useful for preparing peptides containing non-cognate  
PT amino acids, encodes ribozyme that can aminoacylate tRNA with such amino  
PT acids.

XX  
PS Example 3; SEQ ID NO 42; 85pp; English.

XX  
CC The invention relates to a novel polynucleotide comprising a sequence  
CC encoding a ribozyme that can aminoacylate tRNA with a non-cognate amino  
CC acid. Ribozymes encoded by the polynucleotide of the invention are used  
CC to prepare polypeptides that contain non-cognate, including non-natural,  
CC amino acids. The invention more specifically provides catalytic RNA  
CC molecules having cis aminoacylation activity with a catalytic and  
CC aminoacylation domain, or an RNA molecule with trans aminoacylation  
CC activity with only a catalytic domain. The products of the invention are  
CC potentially useful for biomedical and therapeutic use, e.g. for probing  
CC the structure and function of proteins; preparation of peptide libraries  
CC and in proteomics. This polynucleotide sequence represents a DNA oligo  
CC relating to the RNA molecule with aminoacylation activity of the  
CC invention.

XX  
SQ Sequence 30 BP; 3 A; 5 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.4; DB 1; Length 30;  
Best Local Similarity 95.2%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAA 2804  
Db 21 TAAAAAAAAAAAAA 1

RESULT 752  
ACC42844

ID ACC42844 standard; DNA; 33 BP.

XX  
AC ACC42844;



XX 01-SEP-2003 (first entry)  
XX Nuclear transition protein I-9.57 PCR primer #4.  
XX Nuclear transition protein I-9.57; tumour; cytostatic; haemopathy; PCR;  
KW HIV infection; anti-HIV; immunological disease; inflammation; primer; ss.  
XX Unidentified.  
OS CN1380328-A.  
XX 20-NOV-2002.  
XX 10-APR-2001; 2001CN-00105924.  
XX 10-APR-2001; 2001CN-00105924.  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX Mao Y, Xie Y;  
PI WPI; 2003-222560/22.  
XX Polypeptide-nuclear transformation protein -9.57 and polynucleotide for  
PT coding this polypeptide.  
XX Example 5; Page 27; 29pp; Chinese.  
XX The present invention relates to nuclear transition protein I-9.57 and  
CC its coding sequence. The protein can be used for treating several  
CC diseases, such as malignant tumours, haemopathy, HIV infection,  
CC immunological disease and various inflammations. The present sequence is  
CC a PCR primer, which was used in an example from the invention. Note: The  
CC present sequence is SEQ ID 6 from the sequence listing. This sequence  
CC differs from the SEQ ID 6 shown in the disclosure (see ACC42932)  
XX Sequence 33 BP; 24 A; 4 C; 2 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19.4; DB 1; Length 33;  
Best Local Similarity 95.2%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAATAAAAAAAAAAAAAA 2804  
Db 11 TAAAAAATAAAAAAAAAAAAAA 31  
RESULT 753  
ACC48482  
ID ACC48482 standard; DNA; 21 BP.  
XX ACC48482;  
AC  
XX 11-AUG-2003 (first entry)  
XX Locked nucleic acid anchored oligo(I) primer ON12.  
DE  
XX Locked nucleic acid; LNA; gene therapy; primer; ss.  
KW  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 1 /tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 3 /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 5 /tag= c

FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
7 modified\_base /tag= d  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
9 modified\_base /tag= e  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
11 modified\_base /tag= f  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
13 modified\_base /tag= g  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
15 modified\_base /tag= h  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
17 modified\_base /tag= i  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
19 modified\_base /tag= j  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
21 modified\_base /tag= k  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
22 modified\_base /tag= l  
FT /mod\_base= OTHER  
FT /note= "OTHER= Compound 17d"  
XX WO2003020739-A2.  
XX 13-MAR-2003.  
XX 04-SEP-2002; 2002WO-IB003911.  
XX 04-SEP-2001; 2001US-0317034P.  
XX 22-SEP-2001; 2001US-0323967P.  
XX (EXIQ-) EXIQON AS.  
XX Wengel J, Kauppinen S;  
XX WPI; 2003-363021/34.  
XX Novel nucleic acid comprising a locked nucleic acid unit having a  
PT modified base that comprises an optionally substituted carbocyclic aryl  
PT moiety, or modified nucleobase or nucleosidic base other than  
PT oxazole/imidazole.  
XX Example 24a; Page 90; 119pp; English.  
XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
CC oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from  
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is  
CC one of a set of such primers (see also ACC48483-85) that were used in an  
CC example from the invention to demonstrate improved reverse transcription  
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
CC were observed: efficient priming on mRNAs with short poly(A) tails;  
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T  
CC units resulting in an improved T20-VN anchor primer and thus avoiding  
CC reverse transcription of long poly(A) tracts; and improved reverse  
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts

CC due to increased specificity. The invention relates to modified LNA units  
CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
CC base substitutions can mediate universal hybridisation when incorporated  
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
CC and in diagnostics  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 6.6e+02;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2168 TTTTTTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 754  
ACC48482/c  
ID ACC48482 standard; DNA; 21 BP.

AC ACC48482;

DT 11-AUG-2003 (first entry)  
XX Locked nucleic acid anchored oligo(I) primer ON12.  
DE Locked nucleic acid; LNA; gene therapy; primer; ss.  
KW  
XX  
OS Synthetic.

FH Key Location/Qualifiers  
FT modified\_base 1 /tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 3 /tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 5 /tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 7 /tag= d  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 9 /tag= e  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 11 /tag= f  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 13 /tag= g  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 15 /tag= h  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 17 /tag= i  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 19 /tag= j  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"

FT modified\_base 21 /tag= k  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 22 /tag= 1  
FT /mod\_base= OTHER  
FT /note= "OTHER= Compound 17d"

XX WO2003020739-A2.

XX 13-MAR-2003.

XX 04-SEP-2002; 2002WO-IB003911.

XX 04-SEP-2001; 2001US-0317034P.

PR 22-SEP-2001; 2001US-0323967P.

XX (EXIQ-) EXIQON AS.

XX Wengel J, Kauppinen S;

XX WPI; 2003-363021/34.

XX Novel nucleic acid comprising a locked nucleic acid unit having a  
PT modified base that comprises an optionally substituted carbocyclic aryl  
PT moiety, or modified nucleobase or nucleosidic base other than  
PT oxazole/imidazole.

XX Example 24a; Page 90; 119pp; English.

XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
CC oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from  
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is  
CC one of a set of such primers (see also ACC48483-85) that were used in an  
CC example from the invention to demonstrate improved reverse transcription  
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
CC were observed: efficient priming on mRNAs with short poly(A) tails;  
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T  
CC units resulting in an improved T20-VN anchor primer and thus avoiding  
CC reverse transcription of long poly(A) tracts; and improved reverse  
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts  
CC due to increased specificity. The invention relates to modified LNA units  
CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
CC base substitutions can mediate universal hybridisation when incorporated  
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
CC and in diagnostics

XX Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 6.6e+02;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804

Db 20 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 755

ACC99729

ID ACC99729 standard; DNA; 21 BP.

XX ACC99729;

AC ACC99729;

XX 02-SEP-2003 (first entry)

XX Oligonucleotide.

KW Multiplex real-time quantitative PCR; PCR primer; copy number;  
KW Alzheimer's disease; ss.







FT /\*tag= j  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 21  
FT /\*tag= k  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 22  
FT /\*tag= l  
FT /mod\_base= OTHER  
FT /note= "OTHER= Compound 17d"

XX WO2003020739-A2.  
XX 13-MAR-2003.  
XX 04-SEP-2002; 2002WO-IB003911.  
XX 04-SEP-2001; 2001US-0317034P.  
XX 22-SEP-2001; 2001US-0323967P.

XX (EXIQ-) EXIQON AS.

XX Wengel J, Kauppinen S;

XX WPI; 2003-363021/34.

XX Novel nucleic acid comprising a locked nucleic acid unit having a  
PT modified base that comprises an optionally substituted carbocyclic aryl  
PT moiety, or modified nucleobase or nucleosidic base other than  
PT oxazole/imidazole.

PS Example 24a; Page 90; 119pp; English.

XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
CC oligo(dT) primer ON14, which was used in first-strand cDNA synthesis from  
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is  
CC one of a set of such primers (see also ACC48482-85) that were used in an  
CC example from the invention to demonstrate improved reverse transcription  
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
CC were observed: efficient priming on mRNAs with short poly(A) tails;  
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T  
CC units resulting in an improved T20-VN anchor primer and thus avoiding  
CC reverse transcription of long poly(A) tracts; and improved reverse  
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts  
CC due to increased specificity. The invention relates to modified LNA units  
CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
CC base substitutions can mediate universal hybridisation when incorporated  
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
CC and in diagnostics

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 22;  
Best Local Similarity 95.0%; Pred. No. 7.4e+02;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804  
Db :|||||  
21 BAAAAAAAAAAAAAAAAAAAA 2

RESULT 760  
ACC48485/c  
ID ACC48485 standard; DNA; 22 BP.

XX ACC48485;

XX 11-AUG-2003 (first entry)

DE Locked nucleic acid anchored oligo(I) primer ON15.

XX Locked nucleic acid; LNA; gene therapy; primer; ss.  
KW Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 21 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 22 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= Compound 17d"

XX WO2003020739-A2.

XX 13-MAR-2003.

XX 04-SEP-2002; 2002WO-IB003911.

XX 04-SEP-2001; 2001US-0317034P.

XX 22-SEP-2001; 2001US-0323967P.

XX (EXIQ-) EXIQON AS.

XX Wengel J, Kauppinen S;

XX WPI; 2003-363021/34.

XX Novel nucleic acid comprising a locked nucleic acid unit having a  
PT modified base that comprises an optionally substituted carbocyclic aryl  
PT moiety, or modified nucleobase or nucleosidic base other than  
PT oxazole/imidazole.

PS Example 24a; Page 90; 119pp; English.

XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
CC oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from  
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is  
CC one of a set of such primers (see also ACC48482-84) that were used in an  
CC example from the invention to demonstrate improved reverse transcription  
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
CC were observed: efficient priming on mRNAs with short poly(A) tails;  
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T  
CC units resulting in an improved T20-VN anchor primer and thus avoiding  
CC reverse transcription of long poly(A) tracts; and improved reverse  
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts  
CC due to increased specificity. The invention relates to modified LNA units  
CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
CC base substitutions can mediate universal hybridisation when incorporated  
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
CC and in diagnostics

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 22;  
Best Local Similarity 95.0%; Pred. No. 7.4e+02;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804  
Db :|||||  
21 BAAAAAAAAAAAAAAAAAAAA 2

RESULT 761  
ACC48483/c  
ID ACC48483 standard; DNA; 22 BP.

XX ACC48483;

XX

DT 11-AUG-2003 (first entry)  
XX Locked nucleic acid anchored oligo(I) primer ON13.  
DE Locked nucleic acid; LNA; gene therapy; primer; ss.  
KW Synthetic.  
XX  
OS  
XX  
FH  
FT Location/Qualifiers  
FT modified\_base 2 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 5 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 8 /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 11 /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 14 /\*tag= e  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 17 /\*tag= f  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 21 /\*tag= g  
FT /mod\_base= OTHER  
FT /note= "OTHER= locked nucleic acid"  
FT modified\_base 22 /\*tag= h  
FT /mod\_base= OTHER  
FT /note= "OTHER= Compound 17d"  
XX  
PN WO2003020739-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 04-SEP-2002; 2002WO-IB003911.  
XX  
PR 04-SEP-2001; 2001US-0317034P.  
PR 22-SEP-2001; 2001US-0323967P.  
XX  
PA (EXIQ-) EXIQON AS.  
XX  
PI Wengel J, Kauppinen S;  
XX  
DR WPI; 2003-363021/34.  
XX  
PS Example 24a; Page 90; 119pp; English.  
XX  
PT Novel nucleic acid comprising a locked nucleic acid unit having a  
PT modified base that comprises an optionally substituted carbocyclic aryl  
PT moiety, or modified nucleobase or nucleosidic base other than  
PT oxazole/imidazole.  
XX  
PS Example 24a; Page 90; 119pp; English.  
XX  
CC The present sequence is that of pyrene-anchored locked nucleic acid (LNA)  
CC oligo(dT) primer ON13, which was used in first-strand cDNA synthesis from  
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based  
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is  
CC one of a set of such primers (see also ACC48482-85) that were used in an  
CC example from the invention to demonstrate improved reverse transcription  
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results  
CC were observed: efficient priming on mRNAs with short poly(A) tails;  
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T

CC units resulting in an improved T20-VN anchor primer and thus avoiding  
CC reverse transcription of long poly(A) tracts; and improved reverse  
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts  
CC due to increased specificity. The invention relates to modified LNA units  
CC that comprise unique base groups. Desirable nucleobase and nucleosidic  
CC base substitutions can mediate universal hybridisation when incorporated  
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as  
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,  
CC and in diagnostics  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 22;  
Best Local Similarity 95.0%; Pred. No. 7.4e+02;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804  
Db :|||||  
21 BAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 762  
AAD51324/C  
ID AAD51324 standard; DNA; 22 BP.  
XX  
AC AAD51324;  
XX  
DT 16-APR-2003 (first entry)  
DE Anchored oligo dT primer used to illustrate the method of the invention.  
XX  
KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;  
KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;  
KW musculoskeletal damage; ss.  
XX  
OS Unidentified.  
XX WO200290579-A1.  
PN 14-NOV-2002.  
XX  
PD 03-MAY-2002; 2002WO-AU0000553.  
PF 04-MAY-2001; 2001AU-00004809.  
XX 29-JUN-2001; 2001US-00896941.  
XX  
PA (GENO-) GENOMICS RES PARTNERS PTY LTD.  
XX  
PI Brandon RB;  
XX  
DR WPI; 2003-120558/11.  
XX  
PT Assessing condition e.g. athletic ability, stage of disease, presence of  
PT drugs, response to exercise, response to vaccines, therapies, nutritional  
PT states, of performance animal involves analyzing nucleic acid expression.  
XX  
PS Disclosure; Page 46; 87pp; English.  
XX  
CC The invention relates to a method for assessing a condition of a  
CC performance animal. The method involves determining in sample abundance  
CC of expressed target nucleic acid; transmitting digital sample signal to  
CC remote diagnostic server; processing digital sample signal at remotely  
CC located database to correlate digital signal with digital information and  
CC returning report of particular condition of animal. The method is useful  
CC for assessing a condition of a performance animal preferably human, dog  
CC or camel. The condition can be an athletic ability and a condition that  
CC enhances, hinders, impedes or does not change an expected ability of the  
CC performance animal; and also normal, pre-clinical, overt progress and/or  
CC stage of disease, undiagnosed of unclassified conditions, presence of  
CC drugs, response to exercise, response to vaccines, therapies, nutritional  
CC states and response to environmental conditions. Diseases assessed by the  
CC invention include laminitis, lameness, viral or bacterial disease,  
CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,

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CC musculoskeletal damage or disorders and joint diseases. The present
CC sequence is a primer used to illustrate the method of the invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match          0.7%; Score 19.2; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 7.4e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804
Db 21 BAAAAAAAAAAAAAAAAAAAA 2

RESULT 763
ABK13916/c
ID ABK13916 standard; DNA; 23 BP.
XX
AC ABK13916;
XX
DT 21-MAY-2002 (first entry)
XX
DE 3'-PCR primer used in method of identifying transcribed genes.
XX
KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200208461-A2.
XX
PD 31-JAN-2002.
XX
PF 23-JUL-2001; 2001WO-IB001539.
XX
PR 21-JUL-2000; 2000GB-00018016.
PR 21-JUL-2000; 2000US-0219925P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G;
XX
DR WPI; 2002-217065/27.
XX
PT Providing mRNA profile, by generating two independent patterns
PT characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
PS Example 2; Page 45; 67pp; English.
XX
CC The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the methods of the present invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;

Query Match          0.7%; Score 19.2; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 8.3e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804
Db 21 BAAAAAAAAAAAAAAAAAAAA 2
```

```
Db 21 BAAAAAAAAAAAAAAAAAAAA 2

RESULT 764
ABK48140/c
ID ABK48140 standard; DNA; 24 BP.
XX
AC ABK48140;
XX
DT 18-JUN-2002 (first entry)
XX
DE Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX
KW Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
KW baked product; cheese; poly-T; reverse transcriptase PCR.
XX
OS Synthetic.
XX
PN WO200216618-A1.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-EP009925.
XX
PR 23-AUG-2000; 2000EP-00202995.
XX
PA (STAM ) DSM NV.
XX
PI Basten D, Dekker PJT, Schuurhuizen PW, Schaap PJ, Visser J;
XX
DR WPI; 2002-257917/30.
XX
PT An isolated polypeptide with aminopeptidase activity, for preparing food
PT compositions, such as bread and cheese, with enhanced flavoring.
XX
PS Example 5; Page 40; 94pp; English.
XX
CC The invention relates to an isolated polypeptide with aminopeptidase
CC activity and the gene encoding it (including sequences complementary to
CC the gene and which hybridise to it at high stringency), from Aspergillus
CC niger. Also included are a nucleic acid construct comprising the above
CC polynucleotide operably linked to one or more control sequences that
CC direct the production of the polypeptide in a suitable expression host, a
CC recombinant expression vector comprising the above nucleic acid
CC construct, a recombinant host cell comprising the above construct or
CC vector, and producing the protein comprising cultivating an above strain/
CC recombinant host cell to produce a supernatant and/or cells comprising
CC the polypeptide and recovering the polypeptide. The aminopeptidase is
CC used to prepare a food composition such as dough to enhance the flavour
CC of a baked product from the dough and for preparing a cheese to enhance
CC the flavour. The invention provides a bacterial enzyme for protein
CC hydrolysis i.e. with aminopeptidase activity, to produce flavouring
CC agents, and the enzyme has been isolated and characterised, compared to a
CC previously observed weak aminopeptidase activity which was detected in an
CC Aspergillus niger culture filtrate but the source was never isolated or
CC identified. The use of enzymes to produce flavouring agents from
CC proteinaceous material is better than use of strong acids which can
CC severely degrade the amino acids obtained. The present sequence is a
CC reverse transcriptase (RT)-PCR primer used to investigate the intron-exon
CC structure of the aminopeptidase gene
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other;

Query Match          0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 9.2e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804
Db 24 BAAAAAAAAAAAAAAAAAAAA 5

RESULT 765
```

```

AAT99286
ID AAT99286 standard; DNA; 24 BP.
XX
AC AAT99286;
XX
DT 15-APR-1998 (first entry)
XX
DE POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; probe; hybridisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5672479-A.
XX
PD 30-SEP-1997.
XX
PF 07-JUN-1995; 95US-00486421.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
WPI; 1997-488859/45.
DR
XX
PT Assays for PUR protein ligands or modulators - using immobilised PUR
PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS Example; Col 33; 64pp; English.
XX
CC The oligonucleotides AAT99279-T99286 were used as competitor
CC oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence
CC can be used to identify chemical or biological compounds that bind to PUR
CC or binding fragments of PUR. Inhibitors of PUR activity may be used to
CC treat hyperproliferative diseases such as cancer
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 766
AAV31743
ID AAV31743 standard; DNA; 24 BP.
XX
AC AAV31743;
XX
DT 24-SEP-1998 (first entry)
XX
DE Nucleotide sequence of the oligonucleotide POLYA.
XX
KW PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
KW hyperproliferative disease; ss.
XX
OS Synthetic.
XX
PN US5756684-A.
XX
PD 26-MAY-1998.
XX
PF 06-JUN-1995; 95US-00470911.

AAT99286
ID AAT99286 standard; DNA; 24 BP.
XX
AC AAT99286;
XX
DT 15-APR-1998 (first entry)
XX
DE POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW cancer; probe; hybridisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5672479-A.
XX
PD 30-SEP-1997.
XX
PF 07-JUN-1995; 95US-00486421.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
WPI; 1997-488859/45.
DR
XX
PT Assays for PUR protein ligands or modulators - using immobilised PUR
PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS Example; Col 33; 64pp; English.
XX
CC The oligonucleotides AAT99279-T99286 were used as competitor
CC oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence
CC can be used to identify chemical or biological compounds that bind to PUR
CC or binding fragments of PUR. Inhibitors of PUR activity may be used to
CC treat hyperproliferative diseases such as cancer
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 767
AAX04086
ID AAX04086 standard; DNA; 24 BP.
XX
AC AAX04086;
XX
DT 12-APR-1999 (first entry)
XX
DE Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW monoclonal antibody; identification; characterisation; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5869622-A.
XX
PD 09-FEB-1999.
XX
PF 07-JUN-1995; 95US-00486809.
XX
PR 28-AUG-1992; 92US-00938189.
PR 02-FEB-1993; 93US-00014943.
PR 06-JUN-1995; 95US-00470911.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Bergemann AD, Johnson EM;
XX
WPI; 1999-152881/13.
DR
XX
PT Monoclonal antibody specific for PUR protein - useful for treating
PT cancer.
XX
PS Example; Col 33; 64pp; English.
XX
CC The present invention describes a monoclonal antibody that specifically
CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC protein and neutralise PUR activity may be used to treat
```









CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAA 1

RESULT 775  
ABS77949/C  
ID ABS77949 standard; DNA; 24 BP.

AC ABS77949;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #433.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 27; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAA 1

RESULT 776  
ABS78478  
ID ABS78478 standard; DNA; 24 BP.

AC ABS78478;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #962.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 36; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;



Best Local Similarity	87.5%;	Pred. No.	9.2e+02;
Matches	21; Conservative	0; Mismatches	3; Indels
			0; Gaps
			0;

**Qy** 2781 AATTGAAAAAAAAAAAAAAAAAAAAA 2804  
||| ||| ||| ||| ||| ||| ||| |||  
**Db** 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 777  
ABL39405/C  
ID ABL39405 standard; DNA; 24 BP.  
XX  
XX AC ABL39405;  
XX  
XX  
DT 16-APR-2002 (first entry)  
XX  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 841.  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
XX  
OS Synthetic.

Key	Location/Qualifiers
modified_base	1..24
	/*tag= a
	/mod_base= OTHER
	/note="phosphorothioate backbone"

WO200197843-A2.  
XX  
PN PD 27-DEC-2001.  
XX  
XX  
PF 22-JUN-2001; 2001WO-US020154.  
XX  
PR 22-JUN-2000; 2000US-0213346P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX  
XX WPI; 2002-154611/20.  
DR

Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of developing cancer.

PS Disclosure; Page 309; 312pp; English.

The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other; ;  
SQ

Query Match	0.7%	Score 19.2;	DB 1;	Length 24;
Best Local Similarity	87.5%;	Pred. No. 9.2e+02;		
Matches 21;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY 2781 AATTGAAATAAAAAAAAAAAAAA 2804

```

Db      24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 778
ABA98840
ID      ABA98840 standard; DNA; 24 BP.
XX
XX
XX      AC      ABA98840;
XX
DT      01-JUL-2002 (first entry)
XX
DE      A24 oligonucleotide for the creation of Pc-A24.
XX
KW      Component detection; clinical diagnosis; cell detection; drug detection;
KW      metabolite detection; pesticide detection; ligand detection; ss.
XX
XX      Synthetic.
OS
OS
FH      Key      Location/Qualifiers
FT      modified_base 24
FT      /*tag= a
FT      /label= OTHER
FT      /note= "modified by PO2OCH2CH2CH2SSCH2CH2CH2OH"

```

WO200184157-A2.

08-NOV-2001.

03-MAY-2001: 2001WO-US014528.

04-MAY-2000: 2000US-00564230.

(DADE-) DADE BEHRING INC.

Pease JS, Cromer R, Patel R, Kurn N, De Keczzer S;

WPI; 2002-164078/21.

Detection of multiple analytes, e.g. ligands, receptors, polynucleotides and pollutants, involves adding a combination of sensitizer reagents and reactive reagent. Actuatable by a product of the sensitizer reagents.

Example; Page 58; 87pp; English.

The invention relates to the detection of multiple components in a medium, comprising combining the medium with at least two sensitizer reagents, and at least one reactive reagent activated by a product generated by the sensitizer reagents when activated; and differentially activating the sensitizer reagents. The combination of sensitizer reagents and reactive reagent(s) allows differential detection of the components. Methods of the invention may be used for the detection of ligands, receptors and polynucleotides, and also for the detection of e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated biphenyls, phosphate esters, thiophosphates, carbamates and polyhalogenated sulfenamides) and pollutants. Methods of the invention allow the detection of multiple analytes in a single test medium. An application of the methods of the present invention would be in the field of clinical diagnostics. The current sequence represents A24 oligonucleotide for the creation of oligonucleotide coated phthalocyanine sensitizer particles (PC-A24)

SQ Sequence 24 BP: 24 A: 0 C: 0 G: 0 T: 0 U: 0 Other: 0

```
Query Match          0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 2781 AATTGAAAAA 2804  
|||  
Db 1 AAAAAA 24

RESULT 779

AAS17869  
ID AAS17869 standard; DNA; 24 BP.  
XX  
AC AAS17869;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE A24 oligonucleotide used to create dopTAR chemiluminescer particles.  
XX  
KW Polymorphism detection; sequence detection; mutation detection; A24;  
KW probe; non-dissociative termolecular complex; dopTAR sensitizer particle;  
KW single nucleotide polymorphism; SNP; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 24  
FT /\*tag= a  
FT /note= "A is covalently linked to a  
FT PO2OCH2CH2CH2CH2SSCH2CH2CH2OH moiety"  
XX  
PN WO200190399-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 17-MAY-2001; 2001WO-US016089.  
XX  
PR 19-MAY-2000; 2000US-00574596.  
XX  
PA (DADE-) DADE BEHRING INC.  
XX  
PI Patel RD;  
XX  
DR WPI; 2002-097664/13.  
XX  
PT Detecting presence of polynucleotide, differences between polynucleotide  
PT sequences, useful for detecting single nucleotide polymorphism and  
PT alleles of polynucleotide sequence involves use of three competitive  
PT probes.  
XX  
PS Example; Page 47; 75pp; English.  
XX  
CC This invention represents a method for detecting the presence of a  
CC polynucleotide sequence, differences in polynucleotide sequences or  
CC mutations in genomic DNA. The method involves contacting 3  
CC oligonucleotide probes with a sample containing a polynucleotide. The  
CC first probe hybridises to a region of the polynucleotide sequence and the  
CC second and third probes can bind a second region of the polynucleotide  
CC sequence. The second and third probes are identical except for the  
CC presence or difference of one or more nucleotides. The reaction medium is  
CC then subjected to conditions for forming substantially non-dissociative  
CC termolecular complexes, which can be at least one of, the polynucleotide  
CC sequence with the first and second probes or the polynucleotide sequence  
CC with the first and third probes. The oligonucleotide probes have labels  
CC non-covalently bound to allow for their detection upon binding. The  
CC method of the invention is useful for detecting the presence of a single  
CC nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method  
CC can be used for the direct detection of nucleic acid in very small  
CC quantities without amplification. In addition, the method may be carried  
CC out with amplification of the target and reference sequences. This  
CC sequence represents an oligonucleotide probe A24 used to create dopTAR  
CC chemiluminescer sensitizer particles in the method of the invention.  
CC Binding the nucleic acid to a suspendable particle acts as a support and  
CC provides a means of segregating the bound polynucleotide target from the  
CC bulk solution  
XX  
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 24  
RESULT 780  
ABK15639/c  
ID ABK15639 standard; DNA; 24 BP.  
XX  
AC ABK15639;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE RNA-PCR procedure primer poly(dT)24.  
XX  
KW RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;  
KW mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;  
KW high throughput screening; D-RNAi; DNA-RNA interference; RdRp;  
KW RNA dependent RNA polymerase; posttranscriptional gene silencing.  
XX  
OS Synthetic.  
XX  
PN WO200210374-A2.  
XX  
PD 07-FEB-2002.  
XX  
PF 02-AUG-2001; 2001WO-US024412.  
XX  
PR 02-AUG-2000; 2000US-0222479P.  
XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
XX  
PI Lin S, Chuong C, Widelitz RB;  
XX  
DR WPI; 2002-188740/24.  
XX  
PT Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or  
PT treating or preventing microbe related genes, comprises thermocycling  
PT steps of promoter-linked double-stranded cDNA or RNA synthesis.  
XX  
PS Example 5; Page 26; 53pp; English.  
XX  
CC The invention relates to generating mRNA-cDNA hybrids, comprising (a)  
CC providing a solution containing a nucleic acid template, one or more  
CC primers complementary to the sense conformation of the nucleic acid  
CC template, and one or more promoter-linked primers complementary to the  
CC antisense conformation of the nucleic acid template, and with an RNA  
CC promoter, (b) treating the nucleic acid template with the one of more  
CC primers to synthesise a first cDNA strand, (c) treating the first cDNA  
CC strand with one or more promoter-linked primers to synthesise a promoter-  
CC linked double-stranded nucleic acid, (d) treating the promoter-linked  
CC double-stranded nucleic acid to synthesise amplified mRNA fragments and  
CC (e) treating the mRNA fragments with one or more primers to synthesise  
CC mRNA-cDNA hybrids by reverse transcription of the amplified mRNA  
CC fragments. The method is useful for preparing high amounts of pure and  
CC specific mRNA-cDNA hybrids for transducing biological effects of interest  
CC in vitro as well as in vivo, for inhibiting gene function in prokaryotes  
CC and eukaryotes in vivo and in vitro, for suppressing cancer-related  
CC genes, in treating or preventing microbe related genes, in studying  
CC candidate molecular pathways with systematic knock out of involved  
CC molecules, in high throughput screening of gene functions based on  
CC microarray analysis, and as a tool in studying gene function in  
CC physiological conditions. The mRNA-cDNA hybrids may be used to screen for  
CC special gene functions, for manipulating gene expression in vitro, and  
CC for designing therapy for genetic diseases in vivo. The cDNA part of a D-  
CC RNAi (DNA-RNA interference) can be modified by nucleotide analogue  
CC incorporation to increase the stability and effectiveness of transfected  
CC probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may  
CC provide higher affinity of the mRNA template of a D-RNAi compared to ds-  
CC RNA due to lower binding interaction between DNA-RNA duplexes than RNA-  
CC RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene  
CC knockout activity in addition to the posttranscriptional gene silencing  
CC (PTGS) mechanisms of the sense-RNA template, resulting in multiple  
CC specific gene interference effects with one probe. The present sequence

CC is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to  
CC reverse transcribe mRNA into first strand cDNA in the method of the  
CC invention

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2781 AATTGAAAAA 2804  
||| |||||  
Db 24 AAAAAA 1

RESULT 781  
ACA58802/c  
ID ACA58802 standard; DNA; 24 BP.

XX ACA58802;

DT 10-JUN-2003 (first entry)

XX Gastric ulcer treatment immunostimulatory nucleic acid #148.

DE Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;  
KW Helicobacter pylori.

XX Synthetic.

XX US2002198165-A1.

XX 26-DEC-2002.

XX 01-AUG-2001; 2001US-00920313.

XX 01-AUG-2000; 2000US-0222248P.

XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.

XX Bratzler RL, Petersen DM;

XX WPI; 2003-370798/35.

XX Prevention or treatment of gastric ulcer involves administering nucleic acid.

XX Disclosure; Page 14; 45pp; English.

CC The invention relates to a method of prevention or treatment of gastric  
CC ulcer comprising administering a nucleic acid to a subject in need for  
CC treatment of gastric ulcer. A nucleic acid sample comprising  
CC oligonucleotide 2006 was administered to a mouse model by an oral route  
CC or a vehicle control. Colonisation of mice by Helicobacter pylori was  
CC assessed at time points from 1 day to 1 month after treatment. The  
CC ability of the nucleic acid to reduce H. pylori colonisation was  
CC assessed. The method is useful for preventing or treating a gastric ulcer  
CC on a subject e.g. human or non-human vertebrate animal including dog,  
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,  
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively  
CC treats or prevents gastric ulcers. The present sequence represents an  
CC immunostimulatory nucleic acid for the treatment of gastric ulcers

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2781 AATTGAAAAA 2804  
||| |||||  
Db 24 AAAAAA 1

RESULT 782

ABZ80181/c

ID ABZ80181 standard; DNA; 24 BP.

XX ABZ80181;

DT 23-MAY-2003 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO:53.

XX Immunostimulation; immune response; natural killer cell; interferon;  
KW type 1 interferon; IFN; cancer; infectious disease; allergic disorder;  
KW immune related disorder; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..24

FT /tag= a

FT /mod\_base= OTHER

FT /note= "optionally phosphorothioate backbone"

XX WO2003015711-A2.

XX 27-FEB-2003.

XX 19-AUG-2002; 2002WO-US026468.

XX 17-AUG-2001; 2001US-0313273P.

XX 03-JUL-2002; 2002US-0393952P.

XX (COLE-) COLEY PHARM GROUP INC.  
PA (COLE-) COLEY PHARM GMBH.  
PA (IOWA ) UNIV IOWA RES FOUND.

XX Krieg AM, Vollmer J, Uhlman E;

XX WPI; 2003-268241/26.

XX New immunostimulatory nucleic acid, useful for preparing a composition  
XX for treating an allergic condition.

XX Example 1; Page 44; 115pp; English.

CC The present invention describes immunostimulatory nucleic acids of 14-100  
CC nucleotides in length comprising the formula 5' X1DCGHX2 3' (I), where X1  
CC or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other  
CC than C; C = cytosine; G = guanine; H = nucleotide other than G. The  
CC immunostimulatory nucleic acid further comprises a sequence consisting of  
CC P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell  
CC neutralising sequence, where N begins with a CGG trinucleotide and is at  
CC least 10 nucleotides long and P is GC-rich palindrome containing sequence  
CC at least 10 nucleotides long. Also described: (1) a pharmaceutical  
CC composition comprising the immunostimulatory nucleic acid and a carrier;  
CC and (2) treating an allergic condition. (I) has anti-allergic activity and  
CC can be used in gene therapy. (I) can be used for preparing a composition  
CC for treating a variety of immune related disorders such as cancer,  
CC infectious diseases and allergic disorders. (I) also stimulates the  
CC activation of natural killer cells and the production of type 1  
CC interferon (IFN). The present sequence represents an immunostimulatory  
CC oligonucleotide, which is used in an example from the present invention

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2781 AATTGAAAAA 2804  
||| |||||  
Db 24 AAAAAA 1



RESULT 783  
ACA62284/c  
ID ACA62284 standard; DNA; 24 BP.  
XX  
AC ACA62284;  
XX  
DT 12-AUG-2003 (first entry)  
XX  
DE Oligo (dT)24 RT-PCR primer.  
XX  
SS; PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy;  
KW mRNA expression profile; promoter containing primer.  
XX  
OS Synthetic.  
XX  
PN US2003022318-A1.  
PD 30-JAN-2003.  
XX  
PF 07-SEP-2001; 2001US-00949305.  
XX  
PR 25-JAN-2000; 2000US-00494212.  
XX  
PA (EPIC-) EPICLONE INC.  
XX  
PI Lin S, Ying S;  
XX  
DR WPI; 2003-479488/45.  
XX  
PT Improved polymerase thermocycling reaction for nucleic acid  
PT amplification, by thermal cycling of promoter-linked nucleic acid  
PT template synthesis and in vitro transcriptional amplification of nucleic  
PT acid sequences.  
XX  
PS Example 7; Page 14; 28pp; English.  
XX  
CC The invention relates to an improved polymerase thermocycling reaction  
CC (M1) for linear amplification of nucleic acid sequences, involves  
CC denaturing a number of nucleic acid templates (I), combining the  
CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a  
CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,  
CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA  
CC polymerase, contacting P1 with (I) to generate a number of promoter-  
CC containing templates, denaturing the promoter-containing templates,  
CC contacting P2 with the denatured promoter-containing templates to  
CC generate a number of promoter-containing double-stranded DNA templates,  
CC where the double-stranded nucleic acid templates are flanked by P1 in one  
CC end and P2 in the other end of the other orientation, transcribing the  
CC promoter-containing double-stranded DNA templates to form a number of  
CC amplified RNA sequences, including the primer region of the promoter-  
CC containing double-stranded DNA templates, contacting the amplified RNA  
CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA  
CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method  
CC is useful for improved polymerase thermocycling reaction for linear  
CC amplification of nucleic acid sequences, and thus for producing mRNA  
CC expression profile of a cell by M1 to generate multiple copies of the  
CC mRNA. M1 is also useful for determining aberrant protein production of  
CC cells in a diseased state, by generating an expression profile by the  
CC above method, of cells in both normal and diseased states, comparing the  
CC expression profile of the cells in the normal and diseased states,  
CC determining the differences in mRNA composition of the cell(s) in the  
CC diseased state, isolating the mRNA sequences of cell(s) in the diseased  
CC state that differ from mRNA in cell(s) in non-diseased state, amplifying  
CC the isolated mRNA by M1, and determining aberrant protein function of the  
CC protein coded for by the isolated mRNA. M1 is also useful for treating a  
CC cell in a diseased state caused by aberrant protein production, by  
CC determining protein expression of a cell in a diseased state, determining  
CC the mRNA sequence for the aberrant proteins, synthesising an antisense  
CC sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and  
CC delivering a pharmaceutically effective dosage of a composition  
CC comprising the anti-sense mRNA and a compatible lipid based biological

CC carrier. M1 is also useful for predicting the efficacy of a proposed drug  
CC targeted against an aberrant protein, by determining aberrant protein  
CC production of cell in a diseased state by the above method, amplifying  
CC the aberrant protein by M1 and using recombinant techniques to determine  
CC the effect of proposed drug on the aberrant protein. M1 is also useful  
CC for differential screening of tissue-specific gene expression at a  
CC cellular level, for preparing labeled RNA/DNA probes for a gene chip  
CC technology, and for determining the efficacy of a drug regimen against a  
CC gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse  
CC transcriptase) PCR primer used to produce first strand cDNA in the method  
CC of the invention  
XX

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 9.2e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2781 AATTGAAAAA AAAAAAAAAA 2804

Db 24 AAAAAAAAAA AAAAAAAAAA 1

RESULT 784

ACD99729/c

ID ACD99729 standard; DNA; 24 BP.

XX

AC ACD99729;

XX

DT 25-SEP-2003 (first entry)

XX

DE Immunostimulatory nucleic acid #415.

XX

KW Immunostimulatory; antiinflammatory; dermatologic; antipsoriatic;

KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX

OS Synthetic.

XX

PN US2003050268-A1.

XX

PD 13-MAR-2003.

XX

PF 29-MAR-2002; 2002US-00112653.

XX

PR 29-MAR-2001; 2001US-0279642P.

XX

PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX

PI Krieg AM, Berg DJ;

XX

DR WPI; 2003-521815/49.

XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.

XX

PS Disclosure; Page 20; 229pp; English.

XX

CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid

SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match

0.7%; Score 19.2; DB 1; Length 24;



Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAA 1

RESULT 785  
ACH03285  
ID ACH03285 standard; DNA; 24 BP.  
XX AC ACH03285;  
XX DT 25-SEP-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #920.  
XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR Immunostimulatory nucleic acid #920.  
XX PA Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX PS Disclosure; Page 34; 229pp; English.  
XX CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 1 AAAAAA 24

RESULT 786  
ACH03284/c  
ID ACH03284 standard; DNA; 24 BP.  
XX AC ACH03284;  
XX DT 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #919.  
DE XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX PS Disclosure; Page 34; 229pp; English.  
XX CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAA 1

RESULT 787  
ADA66379  
ID ADA66379 standard; mRNA; 24 BP.  
XX AC ADA66379;  
XX DT 20-NOV-2003 (first entry)  
XX mRNA poly A.  
XX ss; nucleic acid amplification; multiple step elimination;  
KW varying reaction condition elimination; poly A tract.  
XX OS Unidentified.  
XX FT Key primer\_bind Location/Qualifiers  
FT 1..24 /tag= a  
FT /note= "Binds to nucleotides 42-19 of the 1st strand cDNA  
FT synthesis primer"  
XX PN US6582938-B1.



Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAAAAAA 1

RESULT 790  
ADB37259  
ID ADB37259 standard; DNA; 24 BP.  
XX AC ADB37259;  
XX DT 04-DEC-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #873.  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX OS Synthetic.  
XX PN US2003087848-A1.  
XX PD 08-MAY-2003.  
XX PF 02-FEB-2001; 2001US-00776479.  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX PA (BRAT/) BRATZLER R L.  
XX PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
XX PI Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX DR Treating and/or preventing allergy or asthma using an immunostimulatory  
XX PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX PS Disclosure; Page 18; 221pp; English.  
XX CC The invention relates to a method of treating or preventing allergy or  
XX CC asthma which comprises administering to a subject a poly-G nucleic acid  
XX CC in an aerosol formulation. The methods and compositions of the present  
XX CC invention are useful for diagnosing and/or treating asthma and allergy  
XX CC especially in a hypo-responsive subject. The present sequence represents  
XX CC an immunostimulatory nucleic acid of the invention.  
XX SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 1 AAAAAAAAAA 24

RESULT 791  
ADD31867/c  
ID ADD31867 standard; DNA; 24 BP.  
XX AC ADD31867;  
XX DT 15-JAN-2004 (first entry)  
XX DE Butterfly biliverdin binding protein BBP-B1X oligonucleotide SEQ ID:106.  
XX KW recombination product; synthetic gene technology; butterfly;

biliverdin binding protein; ss.  
OS synthetic.  
XX WO2003064611-A2.  
XX PD 07-AUG-2003.  
XX PF 29-JAN-2003; 2003WO-US002612.  
XX PR 30-JAN-2002; 2002US-00062188.  
XX PA (EGEA-) EGEA BIOSCIENCES INC.  
XX EVANS GA;  
XX WPI; 2003-663477/62.  
XX PT Creating recombination products between two distinct nucleotide  
XX PT sequences, useful in the field of synthetic gene technology, and in  
XX PT assembling a library, or a population or a collection of polypeptide  
XX PT variants.  
XX PS Example 3; SEQ ID NO 106; 132pp; English.  
XX CC The present invention describes a method for creating a collection of  
XX CC recombination products between two nucleotide sequences. The method  
XX CC comprises combining an initial set of oligonucleotides corresponding to a  
XX CC first nucleotide sequence with a subsequent set of oligonucleotides  
XX CC corresponding to a distinct nucleotide sequence and further combining the  
XX CC initial and subsequent sets of combination oligonucleotides having a  
XX CC sequence region corresponding to the initial nucleotide sequence and a  
XX CC sequence region corresponding to the second oligonucleotide sequence.  
XX CC Also described is a method of creating a collection of recombination  
XX CC products between two genes. The methods and compositions of the present  
XX CC invention are useful in the field of synthetic gene technology, and more  
XX CC specifically, to generating a collection of recombination products  
XX CC between distinct nucleotide sequences. They can also be used in  
XX CC assembling a library, or a population or a collection of polypeptide  
XX CC variants that correspond to single or multiple polynucleotide  
XX CC recombination products. The present sequence is used in the  
XX CC exemplification of the present invention.  
XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.2; DB 1; Length 24;  
Best Local Similarity 87.5%; Pred. No. 9.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 24 AAAAAAAAAA 1

RESULT 792  
ADE25524/c  
ID ADE25524 standard; DNA; 24 BP.  
XX AC ADE25524;  
XX DT 29-JAN-2004 (first entry)  
XX DE Rolling circle amplification related probe control oigo POS1/2.  
XX KW RCA; rolling circle amplification; genotyping;  
XX KW single-nucleotide polymorphism; single base extension; SBE;  
XX KW immuno-hybridisation; probe; ss.  
XX OS Synthetic.  
XX FH Key modified\_base 24 Location/Qualifiers  
XX FT /\*tag= a











XX 18-DEC-2003 (first entry)  
XX Oligonucleotide of the invention SEQ ID NO:4.  
XX ss; probe carrier; discharge.  
XX Synthetic.  
OS  
OS JP2003035711-A.  
PN  
XX  
XX 07-FEB-2003.  
PD  
XX 28-MAR-2002; 2002JP-00093023.  
PF  
XX 28-MAR-2001; 2001JP-00094400.  
PR  
XX (CANO ) CANON KK.  
PA  
XX WPI; 2003-535999/51.  
DR  
XX Probe carrier manufacturing method for inkjet system, involves scanning  
XX liquid discharge head in direction orthogonal to scanning direction, at  
XX angle satisfying predetermined relation.  
XX  
XX Example 2; SEQ ID NO 4; 17pp; Japanese.  
XX The invention relates to a novel probe carrier and the method for  
XX manufacturing the carrier. The invention enables stable discharge of  
XX solution, and removes liquid droplets adhering to discharge nozzle. The  
XX present sequence is used in the exemplification of the invention.  
XX  
XX Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804  
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 803  
ADC54008  
ID ADC54008 standard; DNA; 25 BP.  
XX  
AC ADC54008;  
XX  
XX 18-DEC-2003 (first entry)  
XX Oligonucleotide of the invention SEQ ID NO:3.  
DE ss; probe carrier; discharge.  
XX  
XX Synthetic.  
OS  
PN JP2003035711-A.  
XX  
PD 07-FEB-2003.  
XX  
PF 28-MAR-2002; 2002JP-00093023.  
XX  
PR 28-MAR-2001; 2001JP-00094400.  
XX  
PA (CANO ) CANON KK.  
XX WPI; 2003-535999/51.  
DR Probe carrier manufacturing method for inkjet system, involves scanning  
XX liquid discharge head in direction orthogonal to scanning direction, at  
XX angle satisfying predetermined relation.  
XX

PS Example 2; SEQ ID NO 3; 17pp; Japanese.  
XX The invention relates to a novel probe carrier and the method for  
CC manufacturing the carrier. The invention enables stable discharge of  
CC solution, and removes liquid droplets adhering to discharge nozzle. The  
CC present sequence is used in the exemplification of the invention.  
XX  
SQ Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 1e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24  
RESULT 804  
ABK86170/C  
ID ABK86170 standard; DNA; 25 BP.  
XX  
AC ABK86170;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Oligo dT primer #3 used in method to study gene expression.  
XX  
KW Oligo dT primer; gene expression analysis; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200236828-A2.  
XX  
PD 10-MAY-2002.  
XX  
PF 01-NOV-2001; 2001WO-US045401.  
XX  
PR 01-NOV-2000; 2000US-0244933P.  
XX  
PA (GENO-) GENOMIC SOLUTIONS INC.  
XX  
PI Kane MD, Dombkowski AA, Nagel AC;  
XX WPI; 2002-508123/54.  
DR  
XX  
PT Identifying and characterizing gene expression in samples, for  
PT identifying mRNAs expressed at different levels, comprises employing an  
PT identifier having a oligo-dT primer of a specific sequence and a  
PT detectable marker at its 5' end.  
XX  
PS Example 2; Page 21; 45pp; English.  
XX The invention relates to systems for identification and characterisation  
CC of gene expression in one or more samples, comprising an identifier having  
CC a specific oligo-dT primer sequence, where the identifier comprises a  
CC detectable marker at its 5' end. The system is useful for identifying any  
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well  
CC as the relative differences in mRNA between 2 or more samples, where  
CC desired, for supporting discovery of new genes, and for identifying mRNAs  
CC that are expressed at different levels between 2 or more samples. The new  
CC system or method addresses limitations of prior methods by comprising  
CC compositions and systems that incorporate new strategies where molecular  
CC or biochemical assay compositions and systems are linked to DNA or RNA  
CC sequence databases for optimal resource efficiency in assaying gene  
CC expression. The system has the following advantages over existing  
CC methods: (a) prior sequence information or clone library construction is  
CC not needed to enable the assay; (b) provides immediate sequence  
CC information in addition to information concerning changes or differences  
CC in mRNA level, to determine mRNA expression level and mRNA identification  
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the  
CC sample for subsequent investigation by common molecular biology  
CC techniques; and (d) does not require prior knowledge of the sequence of





XX BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST; ss.  
KW Synthetic.  
KW WO9859049-A1.  
XX 30-DEC-1998.  
XX 19-JUN-1998; 98WO-US012862.  
XX 20-JUN-1997; 97US-00879354.  
XX (ABBO ) ABBOTT LAB.  
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Russell JC;  
PI Scheffel CP, Stroupe SD, Yu H;  
XX WPI; 1999-105623/09.  
DR New isolated BS124 polynucleotides and polypeptides - used for detecting,  
PT diagnosing, preventing or treating diseases or conditions of the breast,  
PT such as breast cancer.  
XX Disclosure; Page 97; 125pp; English.  
XX The sequence is that of an oligonucleotide used in the isolation of a  
CC BS124-specific EST clone. It is useful for detecting, diagnosing,  
CC staging, preventing or treating, or determining predisposition to  
CC diseases or conditions of the breast, such as breast cancer  
XX Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 19.2; DB 1; Length 26;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAA AAAAAAAAAA 2804  
Db 25 AAAAAAAAAA AAAAAAAAAA 2  
RESULT 808  
AAX78723/c  
ID AAX78723 standard; DNA; 26 BP.  
XX AAX78723;  
XX 03-SEP-1999 (first entry)  
DT Human pancreatic PA153 EST-specific clone primer 12.  
XX Pancreatic disease; PA153; human; cytostatic; detection; antigen;  
KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;  
KW gene therapy; EST; expressed sequence tag; primer; ss.  
XX Synthetic.  
OS Homo sapiens.  
XX WO9931274-A2.  
XX 24-JUN-1999.  
PD 11-DEC-1998; 98WO-US026441.  
XX 15-DEC-1997; 97US-00990568.  
XX (ABBO ) ABBOTT LAB.  
PA Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;

PI Russell JC, Stroupe SD;  
XX WPI; 1999-405041/34.  
XX PA153 cDNA transcribed from pancreatic tissue.  
XX Example 2; Page 121; 123pp; English.  
PS This invention describes novel contiguous and partially overlapping cDNA  
XX sequences and their encoded polypeptides, designated PA153, transcribed  
CC from human pancreatic tissue and which have cytostatic activity. The  
CC PA153 polynucleotides, proteins and antibodies are all useful in methods  
CC of detection. Detection of PA153 polynucleotide, antigens or anti-PA153  
CC antibodies in a sample is indicative of pancreatic disease. PA153  
CC antibodies (antagonists) can also be used in vivo for therapeutic use,  
CC e.g. treatment of pancreatic disease, tumours or metastases. Antisense  
CC PA153 polynucleotides can be used in gene therapy of pancreatic diseases.  
CC AAX78712-X78725 represent primers used in the method of the invention  
XX Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 19.2; DB 1; Length 26;  
Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAA AAAAAAAAAA 2804  
Db 25 AAAAAAAAAA AAAAAAAAAA 2  
RESULT 809  
AAV71936/c  
ID AAV71936 standard; DNA; 27 BP.  
XX AAV71936;  
AC 18-FEB-1999 (first entry)  
DT Anchored poly T RT-PCR primer.  
XX Normalised; cDNA library; mRNA cloning; reverse transcription;  
KW immobilise; screening; hybridisation; nucleic acid amplification;  
KW expression pattern; drug development; PCR primer; RT-PCR; ss.  
XX Synthetic.  
OS WO9851789-A2.  
XX 19-NOV-1998.  
PD 13-MAY-1998; 98WO-DK000186.  
XX 13-MAY-1997; 97DK-00000547.  
PR 19-MAY-1997; 97US-00871030.  
PR 27-MAR-1998; 98DK-00000432.  
XX (DISP-) DISPLAY SYSTEMS BIOTECH APS.  
XX Warthoe PR;  
PI WPI; 1999-009772/01.  
XX Preparation of normalised, subdivided cDNA libraries from mRNA - by  
PT reverse transcription and amplification, used to screen for new genes and  
PT interacting proteins, potential drugs, and for diagnosis.  
XX Example 1; Page 29; 71pp; English.  
PS The invention relates to preparation of a normalised, subdivided library  
XX of amplified cDNA from the coding regions of mRNA in a sample. The method  
CC involves reverse transcription, with at least one cDNA primer of formula  
CC 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence  
CC of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3 and n4

CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand  
CC cDNA synthesis using the first strand as template and a second cDNA  
CC primer of a similar formula, in the presence of DNA polymerase I (or its  
CC Klenow fragment) and amplification of double-stranded cDNA with a set of  
CC amplification primers. Comparison of cDNA in the prepared library with a  
CC database (a computer-generated list of molecular weights of restricted  
CC DNA fragments of known sequence) is used to determine presence of an  
CC expressed protein in a cell, also to detect changes in such expression  
CC (particularly for diagnosis of disease). Surfaces (chip) having amplified  
CC cDNA stably immobilised on it, obtained by a similar method, are used to  
CC screen for genes of a particular family, by hybridisation with nucleic  
CC acid from the family (to identify new genes) and to detect differences in  
CC expression patterns between cells. The polypeptides expressed by the  
CC libraries can be used for drug development. Sequences AAV71935 to  
CC AAV71946 represent primers used to exemplify the method of the invention  
XX  
SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.2; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAAAAAAAA AAAAAA 2804  
||| ||||| ||||| ||||| |||||  
Db 25 AAAAAAAAAA AAAAAAAAAA AAAAAA 2  
  
RESULT 810  
ABS53863/C  
ID ABS53863 standard; DNA; 27 BP.  
XX  
AC ABS53863;  
XX  
XX 25-NOV-2002 (first entry)  
DT Human androgen receptor complex-associated protein 5'RACE PCR primer #1.  
XX  
DE Human; androgen receptor complex-associated protein; ARCAP; primer; ss;  
XX androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE.  
KW Homo sapiens.  
XX  
OS BP1227150-A2.  
XX  
PN 31-JUL-2002.  
XX  
PD 16-JAN-2002; 2002EP-00250305.  
XX  
PF 17-JAN-2001; 2001US-0262312P.  
PR 12-FEB-2001; 2001US-00781693.  
XX  
XX (VETE-) VETERANS GEN HOSPITAL.  
PA Tai-Jay C;  
XX  
PI WPI; 2002-676576/73.  
XX  
DR Novel substantially pure androgen receptor (AR) complex-associated  
XX protein which binds to AR and increases ability of AR to transactivate  
XX androgen-responsive gene, useful as drug target for treating liver  
XX cancer.  
XX  
PS Example; Page 11; 26pp; English.  
XX  
PS The invention relates to an androgen receptor complex-associated protein  
XX (ARCAP) sequence and the cDNA encoding it. The protein is useful for  
XX screening a compound that decreases AR-mediated (androgen receptor  
XX mediated) transactivation which involves contacting the ARCAP protein  
XX with a protein complex comprising an AR in the presence of a candidate  
XX compound, measuring the extent of binding between the polypeptide, and  
XX determining if the extent of binding is less than the extent of binding  
XX between the polypeptide and the protein complex in the absence of the  
XX candidate compound. The ARCAP DNA is useful for determining if a sample

CC contains cancerous cells which involves providing a sample from a human  
CC patient and detecting ARCAP expression in the sample. The sequences are  
CC useful for determining whether a sample contains liver tumour cells. This  
CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA  
XX  
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
  
Query Match 0.7%; Score 19.2; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAAAAAAAA AAAAAA 2804  
||| ||||| ||||| ||||| |||||  
Db 25 AAAAAAAAAA AAAAAAAAAA AAAAAA 2  
  
RESULT 811  
ABS54324/C  
ID ABS54324 standard; DNA; 27 BP.  
XX  
AC ABS54324;  
XX  
DT 10-DEC-2002 (first entry)  
XX  
DE Human ARCAP associated 5'RACE PCR primer.  
XX  
KW Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002262871-A.  
XX  
PD 17-SEP-2002.  
XX  
XX 28-FEB-2001; 2001JP-00055192.  
PF 12-FEB-2001; 2001US-00781693.  
PR (VETE-) VETERANS GEN HOSPITAL.  
XX  
PA Tai-Jay C;  
XX  
PI WPI; 2002-676576/73.  
XX  
DR Novel substantially pure androgen receptor (AR) complex-associated  
XX protein which binds to AR and increases ability of AR to transactivate  
XX androgen-responsive gene, useful as drug target for treating liver  
XX cancer.  
XX  
PS Example; Page 15; 18pp; Japanese.  
XX  
PS The present invention relates to the isolation of human androgen receptor  
XX complex-coupled protein (ARCAP), and the polynucleotide sequence encoding  
XX it. The ARCAP polypeptide complexes with an androgen receptor to increase  
XX the activity of the androgen receptor, transactivating the androgen the  
XX responding gene. The invention also describes a vector containing the  
XX ARCAP polynucleotide sequence, and a host cell containing the ARCAP  
XX polynucleotide sequence. The ARCAP polypeptide can be used as a treating  
XX agent. The present sequence represents a PCR primer used in the example  
XX of the present invention  
XX  
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;  
  
Query Match 0.7%; Score 19.2; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAAAAAAAA AAAAAA 2804  
||| ||||| ||||| ||||| |||||  
Db 25 AAAAAAAAAA AAAAAAAAAA AAAAAA 2  
  
RESULT 812

AAAL47309  
ID AAL47309 standard; DNA; 27 BP.  
XX  
AC AAL47309;  
XX  
DT 30-AUG-2002 (first entry)  
XX  
DE Intracellular target molecule property modulation method oligo #1.  
XX  
DE Intracellular target; cellular component; property modulation;  
KW antimicrobial; immunomodulatory; nootropic; neuroprotective; metabolic;  
KW neuroleptic; cytostatic; cardiant; infection; ds; immunological disorder;  
KW neurological disorder; metabolic disorder; psychiatric disorder;  
KW myopathy; cancer; cardiovascular disorder.  
XX  
OS Synthetic.  
XX  
PN EP1205191-A1.  
XX  
PD 15-MAY-2002.  
XX  
PF 13-NOV-2000; 2000EP-00403156.  
XX  
PR 13-NOV-2000; 2000EP-00403156.  
XX  
PA (CNRS ) CENT NAT RECH SCI.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
PA (MOLE-) MOLECULAR SCI INST.  
XX  
PI Colas P, Brent R, Cohen BA;  
XX  
DR WPI; 2002-418829/45.  
XX  
XX  
PT Process for specifically modulating the properties of an intracellular  
target molecule used for the treatment of various disorders.  
XX  
PS Example 4; Page 16; 33pp; English.  
XX  
CC The present invention relates to a process for specifically modulating  
the properties of an intracellular target molecule T, and/or of a  
cellular component C which interacts directly or indirectly in a cell  
with the target. The process involves the introduction into the cell of a  
chimeric molecule known as a targeted effector, comprising a recognition  
moiety capable of recognising T and an effector moiety. The chimeric  
protein or nucleic acid can be used in the preparation of a medicament  
for the treatment of microbial infections, immunological disorders,  
neurological disorders, metabolic disorders, psychiatric disorders,  
myopathies, genetic disorders, cancer, cardiovascular disorders and  
dental disorders. The present sequence is an oligonucleotide used in the  
construction of a fusion protein in the exemplification of the invention  
XX  
SQ Sequence 27 BP; 19 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 1.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAATAAAAAAAAAAAAAA 2804  
Db 1 AATTGAAGAAGAAAAAAGAAAA 24  
RESULT 813  
AAA40362/c  
ID AAA40362 standard; DNA; 28 BP.  
XX  
AC AAA40362;  
XX  
DT 10-NOV-2000 (first entry)  
XX  
DE pBluescriptSK+ phagemid primer SEQ ID NO: 12.  
XX  
KW Primer; cloning; ligation; ss.

XX  
OS Synthetic.  
XX  
PN WO200036088-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 17-DEC-1999; 99WO-US030277.  
XX  
PR 17-DEC-1998; 98US-00213834.  
PA (ROMA/) ROMANTCHIKOV Y.  
XX  
PI Romantchikov Y;  
XX  
DR WPI; 2000-442381/38.  
XX  
PT Inserting a nucleic acid into a circular vector comprising joining their  
ends, melting, and reannealing ends at two different concentrations,  
PT useful for cloning small amounts of nucleic acids and forming genomic  
PT libraries.  
XX  
PS Example 4; Page 68; 71pp; English.  
XX  
CC This invention describes a novel method (M1) for inserting a nucleic acid  
(N1) into a circular vector (V1) comprising joining ends of N1 and V1  
under a first nucleic acid concentration, melting hybridized cohesive  
circularization ends, and reannealing the ends at a second concentration.  
CC The methods are useful for the cloning small amounts of nucleic acids and  
forming genomic libraries of complex populations of DNA or cDNA. The  
methods allow the cloning of minute amounts of nucleic acids efficiently  
and avoids the size selection problems of prior art systems. Larger  
nucleic acid fragments are just as easily cloned, allowing highly  
representative libraries to be made. Vector to vector ligation is avoided  
using the methods. AAA40351-A40366 represents primers used to illustrate  
the method of the invention  
XX  
SQ Sequence 28 BP; 0 A; 2 C; 2 G; 24 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 28;  
Best Local Similarity 87.5%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAATAAAAAAAAAAAAAA 2804  
Db 28 AAAAAAAAAAAAAAAAAAAAAA 5  
RESULT 814  
AAA40358/c  
ID AAA40358 standard; DNA; 28 BP.  
XX  
AC AAA40358;  
XX  
DT 10-NOV-2000 (first entry)  
XX  
DE pBluescriptSK+ phagemid primer SEQ ID NO: 8.  
XX  
KW Primer; cloning; ligation; ss.  
XX  
OS Synthetic.  
XX  
PN WO200036088-A1.  
XX  
PD 22-JUN-2000.  
XX  
PF 17-DEC-1999; 99WO-US030277.  
XX  
PR 17-DEC-1998; 98US-00213834.  
PA (ROMA/) ROMANTCHIKOV Y.  
XX  
PI Romantchikov Y;





QY 2781 AATTGAAAAA 2804  
Db 2 AAAAAA 25

RESULT 817  
AAL44903/C  
ID AAL44903 standard; DNA; 29 BP.  
XX AC AAL44903;  
XX DT 05-AUG-2002 (first entry)  
XX DE Triplex forming oligonucleotide #4.  
XX KW Cancer; cytostatic; gene therapy; triplex forming oligonucleotide; ds.  
XX OS Unidentified.  
XX PN KR2001086830-A.  
XX PD 15-SEP-2001.  
XX PF 03-MAR-2000; 2000KR-00010744.  
XX PR 03-MAR-2000; 2000KR-00010744.  
XX PA (KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.  
XX PI Choi JG, Lee DH, Lee GY, Park GH, Park MG, Son JW;  
XX DR WPI; 2002-233771/29.  
XX PT Novel triplex forming synthetic oligonucleotide, useful for gene therapy of tumor.  
XX PS Claim 4; Page 11; 13pp; Korean.  
XX CC The present invention relates to a triplex forming oligonucleotide which specifically binds to a specific gene. This is useful for the gene therapy of cancer by binding itself to Auger electron emitters. The present sequence is a triplex forming oligonucleotide of the invention

QY 2781 AATTGAAAAA 2804  
Db 27 AAAAAA 4

RESULT 818  
AAA71176  
ID AAA71176 standard; DNA; 29 BP.  
XX AC AAA71176;  
XX DT 27-APR-2001 (first entry)  
XX DE Molecular interaction site DNA #157.  
XX KW Modulator; identification; molecular interaction; virtual library; ss.  
XX OS Canis familiaris.  
XX PN WO9958947-A2.  
XX PD 18-NOV-1999.  
XX PF 12-MAY-1999; 99WO-US010361.

Query Match 0.7%; Score 19.2; DB 1; Length 29;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2801  
Db 4 TAGACCTAAAAA 27

RESULT 819  
AAA71193  
ID AAA71193 standard; RNA; 29 BP.  
XX AC AAA71193;  
XX DT 27-APR-2001 (first entry)  
XX DE Molecular interaction site RNA #230.  
XX KW Modulator; identification; molecular interaction; virtual library; ss.  
XX OS Canis familiaris.  
XX PN WO9958947-A2.  
XX PD 18-NOV-1999.  
XX PF 12-MAY-1999; 99WO-US010361.

Query Match 0.7%; Score 19.2; DB 1; Length 29;  
Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 12-MAY-1998; 98US-00076404.  
PR 12-MAY-1998; 98US-0085092P.  
XX (ISIS-) ISIS PHARM INC.  
PA Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, Mcneil J;  
XX WPI; 2000-086439/07.  
XX Identifying compounds which modulate activity of target biomolecules, used to provide compounds which can be used as pharmacological, agricultural and industrial compounds.  
PS Example 8; Fig 134; 405pp; English.  
XX This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating in silico a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first double stranded (ds) region; (b) 2 nucleotides forming a first side of an internal loop region; (c) 4 nucleotides forming a first side of a second ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUAACAUAUUCUAGUUUACAGAAAAUC (II). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds

SQ Sequence 29 BP; 21 A; 2 C; 1 G; 3 T; 0 U; 2 Other;







Db 32 AAAAAAAAAAAAAAAAAAAAAA 9

RESULT 824  
AAL44170/C  
ID AAL44170 standard; DNA; 33 BP.  
XX  
AC AAL44170;  
XX  
DT 03-OCT-2002 (first entry)  
XX  
DE Porphyra yezoensis cytochrome C - related PCR primer, SEQ ID NO 4.  
XX  
KW Cytochrome C; ss; maturation protein; nitrogen oxide trapping;  
KW polluted atmosphere purification; PCR; primer.  
XX  
OS Porphyra yezoensis.  
XX  
PN WO200259339-A1.  
XX  
PD C1-AUG-2002.  
XX  
PF 23-JAN-2002; 2002WO-JP0000467.  
XX  
PR 23-JAN-2001; 2001JP-00014510.  
XX  
PA (UYNI-) UNIV NIPPON.  
XX  
PI Oku T, Nishio T, Satoh T;  
XX  
DR WPI; 2002-557951/59.  
XX  
PT Production of cytochrome c by culturing prokaryote transformed with  
PT vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome  
PT c maturation protein for use in reagents and drugs for trapping nitrogen  
PT oxide.  
XX  
PS Example 1; Page 7-8; 27pp; Japanese.  
XX  
CC The invention comprises a method for the production of cytochrome C. The  
CC method involves culturing a prokaryote that has been transformed with a  
CC vector encoding a signal peptide and a cytochrome C maturation protein.  
CC The method of the invention is useful for producing cytochrome C.  
CC Cytochrome C produced by the method of the invention is used in reagents  
CC and drugs for trapping nitrogen oxide (e.g. in purifying polluted  
CC atmosphere by trapping nitrogen oxide). The present DNA sequence  
CC represents a Porphyra yezoensis cytochrome C - related PCR primer  
XX  
SQ Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 33;  
Best Local Similarity 87.5%; Pred. No. 1.8e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAAAAAAAAAAAAAAAAA 2804  
Db 33 AAAAAAAAAAAAAAAAAAAAAA 10

RESULT 825  
ABQ80396  
ID ABQ80396 standard; DNA; 35 BP.  
XX  
AC ABQ80396;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Probe APC 2.  
XX  
KW Probe; target; nanoparticle; detection; DNA sequencing; pathogen;  
KW infection; screening; colour change; ss.  
XX  
OS Homo sapiens.

XX  
FH Key modified\_base 1 Location/Qualifiers  
FT /\*tag= a  
FT /note= "Gold-S'-A"  
XX  
PN WO2003048769-A1.  
XX  
PD 12-JUN-2003.  
XX  
PF 27-NOV-2002; 2002WO-US038069.  
XX  
PR 30-NOV-2001; 2001US-0334644P.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Storhoff JJ, Fritz BM, Herrmann M;  
XX  
DR WPI; 2003-617993/58.  
XX  
PT Detecting target polynucleotide in a sample, by amplifying target,  
PT hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle  
PT detection system, and determining amount of signal generated due to  
PT binding.  
XX  
PS Example 1; Page 35; 74pp; English.  
XX  
CC The sequences given in ABQ80394-99 represent probes and targets which  
CC were used in the method of the invention for detecting a target  
CC polynucleotide in a sample. The method comprises amplifying the target,  
CC hybridizing the target to oligonucleotides bound to nanoparticles in a  
CC nanoparticle detection system, determining the amount of signal generated  
CC as a result of binding, optionally repeating the above steps, and  
CC detecting the presence of the target oligonucleotide by analysing for the  
CC amount of signal produced after at least one amplification cycle. The  
CC method is useful for detecting target polynucleotide in a sample, and for  
CC determining the quantity of target polynucleotide in a sample. The method  
CC is useful in research and analytical laboratories in DNA sequencing, in  
CC the field to detect the presence of specific pathogens, in the doctor's  
CC office for quick identification of an infection to assist in prescribing  
CC a drug for treatment, and in homes and health centres for inexpensive  
CC first-line screening. The method is based on observing colour change with  
CC the naked eye, hence the method is cheap, fast, simple, robust, do not  
CC require specialized or expensive equipment, and little or no  
CC instrumentation is required  
XX  
SQ Sequence 35 BP; 28 A; 1 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19.2; DB 1; Length 35;  
Best Local Similarity 87.5%; Pred. No. 2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 826  
AAF85682/C  
ID AAF85682 standard; DNA; 37 BP.  
XX  
AC AAF85682;  
XX  
DT 25-JUN-2001 (first entry)  
XX  
DE Pea blight resistance protein related oligonucleotide #1.  
XX  
KW Pea; blight resistance; nucleotide triphosphate decomposition; ds.  
XX  
OS Unidentified.  
XX  
PN JP2001017176-A.  
XX

PD 23-JAN-2001.  
XX  
PF 02-JUL-1999; 99JP-00189129.  
XX  
PR 02-JUL-1999; 99JP-00189129.  
XX  
PA (KYOU ) UNIV KYOTO.  
XX  
XX WPI; 2001-320697/34.  
DR  
XX  
XX  
PT New blight-resistant polypeptide useful for giving blight resistance to a  
PT plant.  
XX  
PS Example; Page 6; 20pp; Japanese.  
XX  
CC The present invention provides the protein and coding sequences of a pea  
CC protein with nucleotide triphosphate decomposing activity. The gene can  
CC be used for conferring blight resistance on a plant  
XX  
SQ Sequence 37 BP; 2 A; 3 C; 3 G; 29 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.2; DB 1; Length 37;  
Best Local Similarity 87.5%; Pred. No. 2.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA 2804  
Db 37 AAAAAA 14  
  
RESULT 827  
AAQ75552  
ID AAQ75552 standard; DNA; 19 BP.  
AC AAQ75552;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
CC  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

PD 23-JAN-2001.  
XX  
PF 02-JUL-1999; 99JP-00189129.  
XX  
PR 02-JUL-1999; 99JP-00189129.  
XX  
PA (KYOU ) UNIV KYOTO.  
XX  
XX WPI; 2001-320697/34.  
DR  
XX  
XX  
PT New blight-resistant polypeptide useful for giving blight resistance to a  
PT plant.  
XX  
PS Example; Page 6; 20pp; Japanese.  
XX  
CC The present invention provides the protein and coding sequences of a pea  
CC protein with nucleotide triphosphate decomposing activity. The gene can  
CC be used for conferring blight resistance on a plant  
XX  
SQ Sequence 37 BP; 2 A; 3 C; 3 G; 29 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19.2; DB 1; Length 37;  
Best Local Similarity 87.5%; Pred. No. 2.2e+03;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA 2804  
Db 37 AAAAAA 14  
  
RESULT 827  
AAQ75552  
ID AAQ75552 standard; DNA; 19 BP.  
AC AAQ75552;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
CC  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2170 TTTTTTTTTTTTTTTTAA 2188  
Db 1 TTTTTTTTTTTTTTTTAA 19  
  
RESULT 828  
AAQ75556/c  
ID AAQ75556 standard; DNA; 19 BP.  
XX  
AC AAQ75556;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
CC  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2784 TGAATAAAAAAAAAA 2802  
Db 19 TGAATAAAAAAAAAA 1  
  
RESULT 829  
AAT10757  
ID AAT10757 standard; RNA; 19 BP.  
XX  
AC AAT10757;  
XX  
DT 09-SEP-1996 (first entry)  
XX  
DE Oligonucleotide probe, T-2.  
XX  
KW Electronically self-addressable device; ED; electrode; current source;  
KW attachment layer; permeable; counterion; genetic typing; probe;







CC P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific  
CC example of an oligonucleotide so prepared  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT 19  
  
RESULT 834  
AAV06820/c  
ID AAV06820 standard; DNA; 19 BP.  
XX  
AC AAV06820;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE Oligonucleotide containing modified internucleotide linkage.  
XX  
DE oligonucleotide; ss.  
KW  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16. .18  
FT /\*tag= a  
FT /note= "these T residues are formed as part of a  
FT conventional phosphoramidite oligonucleotide synthesis  
FT process but using as the reactant a thymosine nucleoside  
FT having at the 3'-position a group of formula -CH2-  
FT P(OCH2CH2CN)-N(iPr)2"  
XX  
PN WO9747636-A2.  
XX  
XX  
PD 18-DEC-1997.  
XX  
PF 03-JUN-1997; 97WO-GB001490.  
XX  
PR 13-JUN-1996; 96GB-00012600.  
XX  
PA (NOVS ) NOVARTIS AG.  
XX  
XX Collingwood SP, Moser HE, Altmann K, Douglas ME;  
PI  
XX WPI; 1998-052233/05.  
DR  
XX New tetra:hydro:furan derivatives - useful in the synthesis of  
XX oligo:nucleotide(s).  
PT  
PT  
XX  
PS Example 12; Page 29; 37pp; English.  
XX  
CC The invention relates, inter alia, to a method of preparing an  
CC oligonucleotide by coupling (1) a new nucleoside having a protected 5'-  
CC hydroxy group and at the 3'-position a group of formula -CH2-P(OR3)-  
CC NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy  
CC group, to give (3) a precursor having an internucleoside linkage of  
CC formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-  
CC P(OR3)(=X)-O- (where X = S or O). The present sequence is a specific  
CC example of an oligonucleotide so prepared  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 TTTT TTTT TTTT TTTT TTTT 19

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 835  
AAX81316  
ID AAX81316 standard; DNA; 19 BP.  
XX  
AC AAX81316;  
XX  
DT 20-AUG-1999 (first entry)  
XX  
DE 5' amino oligonucleotide probe T-2.  
XX  
KW Microelectronic device; multi-step reaction; microscopic format;  
KW ion-permeable permeation layer; electrode; electrical control; transport;  
KW attachment; binding; DNA/RNA hybrid; probe; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= a  
FT /note= "amino group attached at 5' terminal"  
XX  
PN WO9929711-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 01-DEC-1998; 98WO-US025475.  
XX  
PR 05-DEC-1997; 97US-00986065.  
XX  
PA (NANO-) NANOGEN INC.  
XX  
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;  
XX WPI; 1999-385567/32.  
DR  
XX New microelectronic device designed to carry out and control multi-step  
XX and multiplex molecular biological reactions in microscopic format.  
PT  
PT  
XX  
PS Example 1; Page 90; 179pp; English.  
XX  
CC The specification describes a self-addressable, self-assembling  
CC microelectronic device which is designed to actively carry out and  
CC control multi-step and multiplex molecular biological reactions in  
CC microscopic formats. A key aspect of this inventions is played by the ion  
CC -permeable permeation layer which overlies the electrode. This permeation  
CC layer allows attachment of nucleic acids to permit immobilization but  
CC also separates the attached oligonucleotides and hybridized target DNA  
CC sequences from the highly reactive electrochemical environment generated  
CC immediately at the electrode surface. The microelectronic device is  
CC designed and fabricated to actively carry out and control reactions such  
CC as nucleic acid hybridizations, antibody/antigen reactions, sample  
CC preparation, diagnostics and biopolymer synthesis. The device can  
CC electronically control the transport and attachment of specific binding  
CC entities, such as nucleic acids and polypeptides, to specific micro-  
CC locations. The device can subsequently control the transport and reaction  
CC of analytes or reactants at the addressed specific micro-locations. The  
CC device is able to concentrate analytes and reactants, remove non-  
CC specifically bound molecules, provide stringency control for DNA  
CC hybridization reactions and improve the detection of analytes. The  
CC present sequence represents a probe used to exemplify the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 836  
AAX81316/c  
ID AAX81316 standard; DNA; 19 BP.  
XX  
AC AAX81316;  
XX  
DT 20-AUG-1999 (first entry)  
XX  
DE 5' amino oligonucleotide probe T-2.  
XX  
KW Microelectronic device; multi-step reaction; microscopic format;  
KW ion-permeable permeation layer; electrode; electrical control; transport;  
KW attachment; binding; DNA/RNA hybrid; probe; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /tag= a  
FT /note= "amino group attached at 5' terminal"  
XX  
PN WO9929711-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 01-DEC-1998; 98WO-US025475.  
XX  
PR 05-DEC-1997; 97US-00986065.  
XX  
PA (NANO-) NANOGEN INC.  
XX  
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;  
XX WPI; 1999-385567/32.  
XX  
PT New microelectronic device designed to carry out and control multi-step  
PT and multiplex molecular biological reactions in microscopic format.  
XX  
PS Example 1; Page 90; 179pp; English.  
XX  
CC The specification describes a self-addressable, self-assembling  
CC microelectronic device which is designed to actively carry out and  
CC control multi-step and multiplex molecular biological reactions in  
CC microscopic formats. A key aspect of this inventions is played by the ion  
CC -permeable permeation layer which overlies the electrode. This permeation  
CC layer allows attachment of nucleic acids to permit immobilization but  
CC also separates the attached oligonucleotides and hybridized target DNA  
CC sequences from the highly reactive electrochemical environment generated  
CC immediately at the electrode surface. The microelectronic device is  
CC designed and fabricated to actively carry out and control reactions such  
CC as nucleic acid hybridizations, antibody/antigen reactions, sample  
CC preparation, diagnostics and biopolymer synthesis. The device can  
CC electronically control the transport and attachment of specific binding  
CC entities, such as nucleic acids and polypeptides, to specific micro-  
CC locations. The device can subsequently control the transport and reaction  
CC of analytes or reactants at the addressed specific micro-locations. The  
CC device is able to concentrate analytes and reactants, remove non-  
CC specifically bound molecules, provide stringency control for DNA  
CC hybridization reactions and improve the detection of analytes. The  
CC present sequence represents a probe used to exemplify the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 837  
AAX81927  
ID AAX81927 standard; DNA; 19 BP.  
XX  
AC AAX81927;  
XX  
DT 07-SEP-1999 (first entry)  
XX  
DE Polynucleotide strand with amino groups.  
XX  
KW Enzyme-specific cleavable polynucleotide substrate;  
KW quenched fluorescent moiety; biological assay; detection; identification;  
KW microorganism; sterilization assurance; nuclease; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 7  
FT /tag= a  
FT /note= "amine-modified C6 derivative of deoxythymidine  
FT (dT)"  
FT modified\_base 9  
FT /tag= b  
FT /note= "amine-modified C6 derivative of deoxythymidine  
FT (dT)"  
FT modified\_base 11  
FT /tag= c  
FT /note= "amine-modified C6 derivative of deoxythymidine  
FT (dT)"  
FT modified\_base 13  
FT /tag= d  
FT /note= "amine-modified C6 derivative of deoxythymidine  
FT (dT)"  
XX  
PN WO9935288-A1.  
XX  
PD 15-JUL-1999.  
XX  
PF 20-AUG-1998; 98WO-US017311.  
XX  
PR 09-JAN-1998; 98US-00005260.  
XX (MINN ) MINNESOTA MINING & MFG CO.  
PI Wei A, Mach PA;  
XX WPI; 1999-419356/35.  
DR  
XX An enzyme-specific cleavable polynucleotide substrate bearing quenched  
PT fluorescent moieties.  
XX  
PS Example 2; Page 20; 34pp; English.  
XX  
CC The specification describes an enzyme-specific cleavable polynucleotide  
CC substrate bearing quenched fluorescent moieties. The enzyme-specific  
CC cleavable polynucleotide substrate is useful in biological assays for  
CC detection and identification of microorganisms, sterilization assurance,  
CC pharmaceutical discovery, enzyme assays, immunoassays and other  
CC biological assays. The method provides a rapid and convenient approach  
CC for detection and identification of microorganisms. It can be adapted to  
CC sequence-dependent or sequence-independent tests. The invention provides  
CC improved accuracy, faster detection, and overall lower cost in detection  
CC and identification of microorganisms. The presence of nuclease is  
CC measured more accurately and sensitively by red-shifting the emission  
CC wavelength from far UV region (350-400 nm) to the 500-600 nm region of  
CC the electromagnetic spectrum and reducing the effect of background signal  
CC levels of intact reagents. The present sequence is used in the course of  
CC the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;







KW Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;  
KW nuclease resistance; phosphodiester; ss.  
XX Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16  
FT /\*tag= a  
FT /note= "2'-modified T"  
FT modified\_base 17  
FT /\*tag= b  
FT /note= "2'-modified T"  
FT modified\_base 18  
FT /\*tag= c  
FT /note= "2'-modified T"  
FT modified\_base 19  
FT /\*tag= d  
FT /note= "2'-modified T"  
XX  
XX WO200008044-A1.  
PN  
XX  
XX PD 17-FEB-2000.  
XX  
XX PF 06-AUG-1999; 99WO-US017895.  
XX  
XX PR 07-AUG-1998; 98US-00130566.  
XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX  
XX PI Manoharan M, Cook PD;  
XX  
XX WPI; 2000-205668/18.  
XX  
XX Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides  
PT used in diagnostic, therapeutic and research reagents.  
PT  
XX  
XX PS Disclosure; Page 44; 60pp; English.  
XX  
XX CC The present sequence represents an uniform phosphodiester  
CC oligonucleotide. The specification describes oligomeric compounds  
CC containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified  
CC nucleosides include ring structures that position the sugar moiety of the  
CC nucleosides preferentially in 3' endo geometries. The modified oligomeric  
CC compounds have increased binding affinity and increased nuclease  
CC resistance. The oligomeric compounds can be used in diagnostic,  
CC therapeutic and research reagents  
XX  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
RESULT 843  
AAZ61404  
ID AAZ61404 standard; DNA; 19 BP.  
XX  
XX AC AAZ61404;  
XX  
XX DT 19-JUN-2000 (first entry)  
XX  
XX DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.  
XX  
KW Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;  
KW nuclease resistance; phosphorothioate; ss.  
XX  
XX OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT misc\_feature 1. .19  
FT /\*tag= a  
FT /note= "nucleosides linked by phosphodiester linkages"  
FT modified\_base 16. .19  
FT /\*tag= b  
FT /note= "2'-O-[2-N,N-dimethylaminoethyl]oxyethyl-5- methyl  
FT uridine"  
XX  
XX PN WO200008044-A1.  
XX  
XX PD 17-FEB-2000.  
XX  
XX PF 06-AUG-1999; 99WO-US017895.  
XX  
XX PR 07-AUG-1998; 98US-00130566.  
XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX  
XX PI Manoharan M, Cook PD;  
XX  
XX WPI; 2000-205668/18.  
XX  
XX Novel 2'-O-aminoethyloxyethyl modified nucleosides and oligonucleotides  
PT used in diagnostic, therapeutic and research reagents.  
PT  
XX  
XX PS Disclosure; Page 51; 60pp; English.  
XX  
XX CC The present sequence represents an oligomeric compound containing 2'-O-  
CC modified ribosyl nucleosides. The oligomeric compound contains  
CC phosphodiester linkages. The 2'-O-modified nucleosides include ring  
CC structures that position the sugar moiety of the nucleosides  
CC preferentially in 3' endo geometries. The modified oligomeric compounds  
CC have increased binding affinity and increased nuclease resistance. The  
CC oligomeric compounds can be used in diagnostic, therapeutic and research  
CC reagents  
XX  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
RESULT 844  
AAZ61404/c  
ID AAZ61404 standard; DNA; 19 BP.  
XX  
XX AC AAZ61404;  
XX  
XX DT 19-JUN-2000 (first entry)  
XX  
XX DE 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.  
XX  
KW Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;  
KW nuclease resistance; phosphorothioate; ss.  
XX  
XX OS Synthetic.  
XX  
XX FH Key Location/Qualifiers  
FT misc\_feature 1. .19  
FT /\*tag= a  
FT /note= "nucleosides linked by phosphodiester linkages"  
FT modified\_base 16. .19  
FT /\*tag= b  
FT /note= "2'-O-[2-N,N-dimethylaminoethyl]oxyethyl-5- methyl  
FT uridine"  
XX  
XX PN WO200008044-A1.





KW Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;  
KW research reagent; therapeutic; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..15  
FT /\*tag= a  
FT /note= "Phosphorothioate internucleotide linkage"  
FT 15..19  
FT /\*tag= d  
FT /note= "Optionally all phosphorothioate internucleotide  
FT linkages"  
FT 16..19  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Optionally all 3'-O-(2-methoxyethyl) or all 2'-O-  
FT modified\_base 16..19  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Optionally all 3'-O-(2-methoxyethyl) or all 2'-O-  
XX (2-methoxyethyl)"  
PN WO200004189-A1.  
XX  
XX  
PD 27-JAN-2000.  
XX  
XX  
PF 13-JUL-1999; 99WO-US015886.  
XX  
XX 14-JUL-1998; 98US-00115043.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Manoharan M, Cook PD;  
XX  
XX WPI; 2000-182445/16.  
XX  
XX Novel modified oligonucleotides, useful in antisense methodologies,  
PT diagnostics, therapeutics and as research reagents.  
PT  
XX  
PS Example 54; Page 59; 75pp; English.  
XX  
XX This sequence represents a modified oligonucleotide used in the course of  
CC the invention. The invention relates to oligonucleotides comprising  
CC nucleotides covalently linked together by internucleotide linkages where  
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-  
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides  
CC can be used in gene therapy and are also useful in antisense  
CC methodologies, diagnostics, therapeutics and as research reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
RESULT 850  
AAZ95240/c  
ID AAZ95240 standard; DNA; 19 BP.  
XX  
XX AAZ95240;  
AC  
XX 05-JUN-2000 (first entry)  
DT  
XX Modified oligonucleotide #3 ISIS # 22110.  
DE  
XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;  
KW research reagent; therapeutic; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers

FT misc\_feature 1..15  
FT /\*tag= a  
FT /note= "Phosphorothioate internucleotide linkage"  
FT 15..19  
FT /\*tag= d  
FT /note= "Optionally all phosphorothioate internucleotide  
FT linkages"  
FT 16..19  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "Optionally all 3'-O-(2-methoxyethyl) or all 2'-O-  
XX (2-methoxyethyl)"  
PN WO200004189-A1.  
XX  
XX  
PD 27-JAN-2000.  
XX  
XX  
PF 13-JUL-1999; 99WO-US015886.  
XX  
XX 14-JUL-1998; 98US-00115043.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Manoharan M, Cook PD;  
XX  
XX WPI; 2000-182445/16.  
XX  
XX Novel modified oligonucleotides, useful in antisense methodologies,  
PT diagnostics, therapeutics and as research reagents.  
PT  
XX  
PS Example 54; Page 59; 75pp; English.  
XX  
XX This sequence represents a modified oligonucleotide used in the course of  
CC the invention. The invention relates to oligonucleotides comprising  
CC nucleotides covalently linked together by internucleotide linkages where  
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-  
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides  
CC can be used in gene therapy and are also useful in antisense  
CC methodologies, diagnostics, therapeutics and as research reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
RESULT 851  
AAA06839  
ID AAA06839 standard; DNA; 19 BP.  
XX  
XX AAA06839;  
AC  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Modified T-containing oligonucleotide, SEQ ID NO:14.  
XX  
XX Modified nucleoside; aminoxy group;  
KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;  
KW hybridisation; binding affinity; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 16..19  
FT /\*tag= a  
FT /note= "These nucleotides are substituted with 2'-O-(2-  
FT [N-(2-amino)ethyl-N-(methyl)aminoxyethyl] group"  
XX



PN WO200008042-A1.  
XX  
PD 17-FEB-2000.  
XX  
PF 09-AUG-1999; 99WO-US017988.  
XX  
PR 07-AUG-1998; 98US-00130973.  
XX  
PR 07-AUG-1998; 98US-00130973.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;  
XX  
PI WPI; 2000-224020/19.  
XX  
DR Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,  
XX therapeutic and research reagents and for modulating the expression of  
XX protein in organisms.  
XX  
PS Example 99; Page 120; 195pp; English.  
XX  
XX The invention relates to aminoxy-modified nucleosides and  
XX oligonucleotides and to oligonucleotides that elicit RNase H for cleavage  
XX in a complementary nucleic acid strand. It also relates to  
XX oligonucleotides wherein at least some of the nucleotides are  
XX functionalised to be nuclease resistant, at least some of the nucleotides  
XX include a substituent that potentiates hybridisation of the  
XX oligonucleotide to a complementary strand, and at least some of the  
XX nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The  
XX inclusion of one or more aminoxy moieties in such oligonucleotides  
XX provides for improved binding of such oligonucleotides to a complementary  
XX strand. The oligonucleotides of the invention are used as diagnostic,  
XX therapeutic or research reagents, and can be used to modulate gene  
XX expression in organisms. The oligonucleotides containing the modified  
XX nucleosides have increased nuclease resistance and increased binding  
XX affinity to a complementary strand. The present sequence represents an  
XX oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-  
XX amino)ethyl-N-(methyl)]aminoxyethyl) group  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
DB 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 852  
AAA06839/c  
ID AAA06839 standard; DNA; 19 BP.  
XX  
AC AAA06839;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Modified T-containing oligonucleotide, SEQ ID NO:14.  
XX  
KW Modified nucleoside; aminoxy group;  
KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;  
KW hybridisation; binding affinity; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 16.19  
FT /tag= a  
FT /note= "These nucleotides are substituted with 2'-O-(2-[N-(2-amino)ethyl-N-(methyl)]aminoxyethyl) group"  
FT  
XX  
PN WO200008042-A1.  
XX

PD 17-FEB-2000.  
XX  
PF 09-AUG-1999; 99WO-US017988.  
XX  
PR 07-AUG-1998; 98US-00130973.  
XX  
PR (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;  
XX  
PI WPI; 2000-224020/19.  
XX  
DR Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,  
XX therapeutic and research reagents and for modulating the expression of  
XX protein in organisms.  
XX  
PS Example 99; Page 120; 195pp; English.  
XX  
XX The invention relates to aminoxy-modified nucleosides and  
XX oligonucleotides and to oligonucleotides that elicit RNase H for cleavage  
XX in a complementary nucleic acid strand. It also relates to  
XX oligonucleotides wherein at least some of the nucleotides are  
XX functionalised to be nuclease resistant, at least some of the nucleotides  
XX include a substituent that potentiates hybridisation of the  
XX oligonucleotide to a complementary strand, and at least some of the  
XX nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The  
XX inclusion of one or more aminoxy moieties in such oligonucleotides  
XX provides for improved binding of such oligonucleotides to a complementary  
XX strand. The oligonucleotides of the invention are used as diagnostic,  
XX therapeutic or research reagents, and can be used to modulate gene  
XX expression in organisms. The oligonucleotides containing the modified  
XX nucleosides have increased nuclease resistance and increased binding  
XX affinity to a complementary strand. The present sequence represents an  
XX oligonucleotide containing nucleotides substituted with a 2'-O-(2-[N-(2-  
XX amino)ethyl-N-(methyl)]aminoxyethyl) group  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
DB 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 853  
AAA88952  
ID AAA88952 standard; DNA; 19 BP.  
XX  
AC AAA88952;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22115.  
XX  
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; DNA-RNA hybrid; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1.15  
FT /tag= f  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /tag= b  
XX

```

FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT 18
FT modified_base
FT
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT 19
FT misc_RNA
FT
FT /*tag= e
FT /label= RNA
FT 19
FT modified_base
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
FT 19
FT XX
FT PN WO200066509-A1.
FT XX
FT PD 09-NOV-2000.
FT XX
FT PF 03-MAY-2000; 2000WO-US011913.
FT XX
FT PR 03-MAY-1999; 99US-00303586.
FT XX
FT PA (ISIS-) ISIS PHARM INC.
FT XX
FT PI Manoharan M, Mohan V;
FT XX
FT DR WPI; 2000-672833/65.
FT XX
FT PT New oligonucleotides containing sequences with A and B geometry, used to
FT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
FT bacterial infections, bind to single stranded RNA or DNA.
FT XX
FT PS Example 54; Page 69; 132pp; English.
FT XX
FT CC Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
FT phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
FT used in experiments to determine the effects of snake venom
FT phosphodiesterase and liver homogenate on the stability of
FT oligonucleotides. Novel oligonucleotides of the invention have both A-
FT and B-form conformational geometry. The A-form geometry modulates the
FT binding affinity and nuclease resistance of the oligonucleotide. The B-
FT form geometry allows the oligonucleotide to serve as substrate for RNase-
FT H when bound to a target nucleic acid strand. The oligonucleotides can be
FT used to treat psoriasis and other inflammatory skin conditions, skin
FT cancers and viral, bacterial and fungal infections, and in various
FT diagnostic applications
FT XX
FT SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
FT
FT Query Match 0.7%; Score 19; DB 1; Length 19;
FT Best Local Similarity 100.0%; Pred. No. 5.5e+02;
FT Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
FT
FT Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184
FT Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19
FT
FT RESULT 854
FT AAA88952/c
FT ID AAA88952 standard; DNA; 19 BP.
FT XX
FT AC AAA88952;
FT XX
FT DT 05-MAR-2001 (first entry)
FT DE
FT XX Oligonucleotide ISIS 22115.
FT XX
FT KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
FT KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
FT KW diagnosis; DNA-RNA hybrid; ss.
FT OS Synthetic.

```

AC AAA88965;  
XX 05-MAR-2001 (first entry)  
DT 2'-Modified chimeric oligonucleotide.  
DE Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
KW Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
XX WO200066609-A1.  
PN  
XX 09-NOV-2000.  
XX 03-MAY-2000; 2000WO-US011913.  
XX 03-MAY-1999; 99US-00303586.  
XX (ISIS-) ISIS PHARM INC.  
XX Manoharan M, Mohan V;  
XX WPI; 2000-672833/65.  
XX New oligonucleotides containing sequences with A and B geometry, used to  
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and  
PT bacterial infections, bind to single stranded RNA or DNA.  
XX Example 86; Page 102; 132pp; English.  
PS This sequence represents 2'-modified chimeric oligonucleotides containing  
XX 2'-modified T. The nucleotides were used to examine the effects of the  
CC modifications on nuclease resistance. Novel oligonucleotides of the  
CC invention have both A- and B-form conformational geometry. The A-form  
CC geometry modulates the binding affinity and nuclease resistance of the  
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve  
CC as substrate for RNase-H when bound to a target nucleic acid strand. The  
CC oligonucleotides can be used to treat psoriasis and other inflammatory  
CC skin conditions, skin cancers and viral, bacterial and fungal infections,  
CC and in various diagnostic applications  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2184  
|||||

Db 1 TTTT TTTT TTTT TTTT TTTT 19  
RESULT 856  
AAA88965/c  
ID AAA88965 standard; DNA; 19 BP.  
XX  
AC AAA88965;  
XX 05-MAR-2001 (first entry)  
DT 2'-Modified chimeric oligonucleotide.  
DE Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
XX dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
KW Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-  
FT (F), 2'-ara-(OH), -2'-ara-(OMe)"  
XX WO200066609-A1.  
PN  
XX 09-NOV-2000.  
XX 03-MAY-2000; 2000WO-US011913.  
XX 03-MAY-1999; 99US-00303586.  
XX (ISIS-) ISIS PHARM INC.  
XX Manoharan M, Mohan V;  
XX WPI; 2000-672833/65.  
XX New oligonucleotides containing sequences with A and B geometry, used to  
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and  
PT bacterial infections, bind to single stranded RNA or DNA.  
XX Example 86; Page 102; 132pp; English.  
PS This sequence represents 2'-modified chimeric oligonucleotides containing  
XX 2'-modified T. The nucleotides were used to examine the effects of the  
CC modifications on nuclease resistance. Novel oligonucleotides of the  
CC invention have both A- and B-form conformational geometry. The A-form  
CC geometry modulates the binding affinity and nuclease resistance of the  
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve  
CC as substrate for RNase-H when bound to a target nucleic acid strand. The  
CC oligonucleotides can be used to treat psoriasis and other inflammatory  
CC skin conditions, skin cancers and viral, bacterial and fungal infections,  
CC and in various diagnostic applications  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
SQ

Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 857  
AAA88949

ID AAA88949 standard; DNA; 19 BP.  
XX  
AC AAA88949;  
XX

DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22112.  
XX

KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT modified\_base 1. .19  
FT /\*tag= e  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
XX  
PN WO200066609-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US011913.  
XX  
PR 03-MAY-1999; 99US-00303586.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Mohan V;  
XX  
DR WPI; 2000-672833/65.  
XX

New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.

Example 54; Page 69; 132pp; English.

Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the

CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The CC oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, CC and in various diagnostic applications

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTTTT 19

RESULT 858  
AAA88949/c

ID AAA88949 standard; DNA; 19 BP.  
XX  
AC AAA88949;  
XX

DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22112.  
XX

KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
XX

FH Key Location/Qualifiers  
FT modified\_base 1. .19  
FT /\*tag= e  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
XX  
PN WO200066609-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US011913.  
XX  
PR 03-MAY-1999; 99US-00303586.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Mohan V;  
XX  
DR WPI; 2000-672833/65.  
XX

New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.

Example 54; Page 69; 132pp; English.



XX Oligonucleotide ISIS 22112 contains a phosphorothioate backbone and has  
CC 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine  
CC the effects of snake venom phosphodiesterase and liver homogenate on the  
CC stability of oligonucleotides. Novel oligonucleotides of the invention  
CC have both A- and B-form conformational geometry. The A-form geometry  
CC modulates the binding affinity and nuclease resistance of the  
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve  
CC as substrate for RNase-H when bound to a target nucleic acid strand. The  
CC oligonucleotides can be used to treat psoriasis and other inflammatory  
CC skin conditions, skin cancers and viral, bacterial and fungal infections,  
CC and in various diagnostic applications  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
RESULT 859  
AAA88950  
ID AAA88950 standard; DNA; 19 BP.  
XX  
AC AAA88950;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22113.  
XX  
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; DNA-RNA hybrid; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .19  
FT /tag= f  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /tag= a  
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FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 18  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT misc\_RNA 19  
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FT /label= RNA  
FT modified\_base 19  
FT /tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)uridine"  
XX  
PN WO200066609-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US011913.  
XX  
PR 03-MAY-1999; 99US-00303586.  
XX  
PA (ISIS-) ISIS PHARM INC.

XX Manoharan M, Mohan V;  
PI WPI; 2000-672833/65.  
XX  
XX New oligonucleotides containing sequences with A and B geometry, used to  
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and  
PT bacterial infections, bind to single stranded RNA or DNA.  
XX  
PS Example 54; Page 69; 132pp; English.  
XX  
CC Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has  
CC 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine  
CC the effects of snake venom phosphodiesterase and liver homogenate on the  
CC stability of oligonucleotides. Novel oligonucleotides of the invention  
CC have both A- and B-form conformational geometry. The A-form geometry  
CC modulates the binding affinity and nuclease resistance of the  
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve  
CC as substrate for RNase-H when bound to a target nucleic acid strand. The  
CC oligonucleotides can be used to treat psoriasis and other inflammatory  
CC skin conditions, skin cancers and viral, bacterial and fungal infections,  
CC and in various diagnostic applications  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
RESULT 860  
AAA88950/c  
ID AAA88950 standard; DNA; 19 BP.  
XX  
AC AAA88950;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22113.  
XX  
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; DNA-RNA hybrid; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .19  
FT /tag= f  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 18  
FT /tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)thymidine"  
FT misc\_RNA 19  
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FT /label= RNA  
FT modified\_base 19  
FT /tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-O-(2-methoxyethyl)uridine"

XX PN WO200066609-A1.  
XX PD 09-NOV-2000.  
XX PF 03-MAY-2000; 2000WO-US011913.  
XX PR 03-MAY-1999; 99US-00303586.  
XX PA (ISIS-) ISIS PHARM INC.  
XX PI Manoharan M, Mohan V;  
XX PD WPI; 2000-672833/65.  
XX  
PT New oligonucleotides containing sequences with A and B geometry, used to  
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and  
PT bacterial infections, bind to single stranded RNA or DNA.  
XX  
PS Example 54; Page 69; 132pp; English.  
XX  
CC Oligonucleotide ISIS 22113 contains a phosphorothioate backbone and has  
CC 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine  
CC the effects of snake venom phosphodiesterase and liver homogenate on the  
CC stability of oligonucleotides. Novel oligonucleotides of the invention  
CC have both A- and B-form conformational geometry. The A-form geometry  
CC modulates the binding affinity and nuclease resistance of the  
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve  
CC as substrate for RNase-H when bound to a target nucleic acid strand. The  
CC oligonucleotides can be used to treat psoriasis and other inflammatory  
CC skin conditions, skin cancers and viral, bacterial and fungal infections,  
CC and in various diagnostic applications  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 861  
AAA88951  
ID AAA88951 standard; DNA; 19 BP.  
XX  
AC AAA88951;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22114.  
XX  
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .15  
FT /\*tag= e  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 18

FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "3'-O-(2-methoxyethyl)thymidine"  
XX  
PN WO200066609-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 03-MAY-2000; 2000WO-US011913.  
XX  
PR 03-MAY-1999; 99US-00303586.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Mohan V;  
XX  
DR WPI; 2000-672833/65.  
XX  
CC New oligonucleotides containing sequences with A and B geometry, used to  
CC treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and  
CC bacterial infections, bind to single stranded RNA or DNA.  
XX  
PS Example 54; Page 69; 132pp; English.  
XX  
CC Oligonucleotide ISIS 22114 contains a mixed phosphodiester and  
CC phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was  
CC used in experiments to determine the effects of snake venom  
CC phosphodiesterase and liver homogenate on the stability of  
CC oligonucleotides. Novel oligonucleotides of the invention have both A-  
CC and B-form conformational geometry. The A-form geometry modulates the  
CC binding affinity and nuclease resistance of the oligonucleotide. The B-  
CC form geometry allows the oligonucleotide to serve as substrate for RNase-  
CC H when bound to a target nucleic acid strand. The oligonucleotides can be  
CC used to treat psoriasis and other inflammatory skin conditions, skin  
CC cancers and viral, bacterial and fungal infections, and in various  
CC diagnostic applications  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 862  
AAA88951/c  
ID AAA88951 standard; DNA; 19 BP.  
XX  
AC AAA88951;  
XX  
DT 05-MAR-2001 (first entry)  
XX  
DE Oligonucleotide ISIS 22114.  
XX  
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;  
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;  
KW diagnosis; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .15  
FT /\*tag= e  
FT /note= "phosphorothioate linkage"  
FT modified\_base 16

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FT      /*tag= a
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FT      /note= "3'-O-(2-methoxyethyl)thymidine"
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FT      modified_base
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      18
FT      modified_base
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      19
FT      modified_base
FT      /*tag= d
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX PN WO200066609-A1.
XX
XX PD 09-NOV-2000.
XX
XX PF 03-MAY-2000; 2000WO-US011913.
XX
XX PR 03-MAY-1999; 99US-00303586.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Mohan V;
XX
XX PR WPI; 2000-672833/65.
XX
XX PS New oligonucleotides containing sequences with A and B geometry, used to
XX      treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX      bacterial infections, bind to single stranded RNA or DNA.
XX
XX PS Example 54; Page 69; 132pp; English.
XX
XX CC Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
XX      phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
XX      used in experiments to determine the effects of snake venom
XX      phosphodiesterase and liver homogenate on the stability of
XX      oligonucleotides. Novel oligonucleotides of the invention have both A-
XX      and B-form conformational geometry. The A-form geometry modulates the
XX      binding affinity and nuclease resistance of the oligonucleotide. The B-
XX      form geometry allows the oligonucleotide to serve as substrate for RNase-
XX      H when bound to a target nucleic acid strand. The oligonucleotides can be
XX      used to treat psoriasis and other inflammatory skin conditions, skin
XX      cancers and viral, bacterial and fungal infections, and in various
XX      diagnostic applications
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

      Query Match      0.7%; Score 19; DB 1; Length 19;
      Best Local Similarity 100.0%; Pred. No. 5.5e+02;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2804
Db      19 AAAAAAAAAAAAAAAAAA 1

RESULT 863
AAA88947
ID AAA88947 standard; DNA; 19 BP.
XX
XX AC AAA88947;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22110.
XX
XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW      dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW      diagnosis; ss.
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XX OS Synthetic.
XX
XX FH Key
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FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      17
FT      modified_base
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      18
FT      modified_base
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      19
FT      modified_base
FT      /*tag= d
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX PN WO200066609-A1.
XX
XX PD 09-NOV-2000.
XX
XX PF 03-MAY-2000; 2000WO-US011913.
XX
XX PR 03-MAY-1999; 99US-00303586.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Manoharan M, Mohan V;
XX
XX PR WPI; 2000-672833/65.
XX
XX PS New oligonucleotides containing sequences with A and B geometry, used to
XX      treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX      bacterial infections, bind to single stranded RNA or DNA.
XX
XX PS Example 54; Page 69; 132pp; English.
XX
XX CC Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-
XX      O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX      effects of snake venom phosphodiesterase and liver homogenate on the
XX      stability of oligonucleotides. Novel oligonucleotides of the invention
XX      have both A- and B-form conformational geometry. The A-form geometry
XX      modulates the binding affinity and nuclease resistance of the
XX      oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX      as substrate for RNase-H when bound to a target nucleic acid strand. The
XX      oligonucleotides can be used to treat psoriasis and other inflammatory
XX      skin conditions, skin cancers and viral, bacterial and fungal infections,
XX      and in various diagnostic applications
XX
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

      Query Match      0.7%; Score 19; DB 1; Length 19;
      Best Local Similarity 100.0%; Pred. No. 5.5e+02;
      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTTTTTT 2184
Db      1 TTTTTTTTTTTTTTTTTT 19

RESULT 864
AAA88947/c
ID AAA88947 standard; DNA; 19 BP.
XX
XX AC AAA88947;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22110.
```

XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; ss.

XX KW KW

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified\_base 16

XX FT /tag= a

XX FT /mod\_base= OTHER

XX FT /note= "3'-O-(2-methoxyethyl)thymidine"

XX FT modified\_base 17

XX FT /tag= b

XX FT /mod\_base= OTHER

XX FT /note= "3'-O-(2-methoxyethyl)thymidine"

XX FT modified\_base 18

XX FT /tag= c

XX FT /mod\_base= OTHER

XX FT /note= "3'-O-(2-methoxyethyl)thymidine"

XX FT modified\_base 19

XX FT /tag= d

XX FT /mod\_base= OTHER

XX FT /note= "3'-O-(2-methoxyethyl)thymidine"

XX PN WO20006609-A1.

XX PD 09-NOV-2000.

XX PF 03-MAY-2000; 2000WO-US011913.

XX PR 03-MAY-1999; 99US-00303586.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Mohan V;

XX PI WPI; 2000-672833/65.

XX PT New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.

XX PS Example 54; Page 69; 132pp; English.

XX CC Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 5.5e+02;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 865

AAA88948

ID AAA88948 standard; DNA; 19 BP.

XX AC AAA88948;

XX DT 05-MAR-2001 (first entry)

XX DE Oligonucleotide ISIS 22111.

XX KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic; dermatological; cytostatic; virucide; antibacterial; fungicide; therapy; diagnosis; DNA-RNA hybrid; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified\_base 16

XX FT /tag= a

XX FT /mod\_base= OTHER

XX FT /note= "2'-O-(2-methoxyethyl)thymidine"

XX FT modified\_base 17

XX FT /tag= b

XX FT /mod\_base= OTHER

XX FT /note= "2'-O-(2-methoxyethyl)thymidine"

XX FT modified\_base 18

XX FT /tag= c

XX FT /mod\_base= OTHER

XX FT /note= "2'-O-(2-methoxyethyl)thymidine"

XX FT misc\_RNA 19

XX FT /tag= e

XX FT /label= RNA

XX FT modified\_base 19

XX FT /tag= d

XX FT /mod\_base= OTHER

XX FT /note= "2'-O-(2-methoxyethyl)uridine"

XX PN WO20006609-A1.

XX PD 09-NOV-2000.

XX PF 03-MAY-2000; 2000WO-US011913.

XX PR 03-MAY-1999; 99US-00303586.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Manoharan M, Mohan V;

XX PI WPI; 2000-672833/65.

XX PT New oligonucleotides containing sequences with A and B geometry, used to treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and bacterial infections, bind to single stranded RNA or DNA.

XX PS Example 54; Page 69; 132pp; English.

XX CC Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-O-(2-methoxyethyl) chemistry. It was used in experiments to determine the effects of snake venom phosphodiesterase and liver homogenate on the stability of oligonucleotides. Novel oligonucleotides of the invention have both A- and B-form conformational geometry. The A-form geometry modulates the binding affinity and nuclease resistance of the oligonucleotide. The B-form geometry allows the oligonucleotide to serve as substrate for RNase-H when bound to a target nucleic acid strand. The oligonucleotides can be used to treat psoriasis and other inflammatory skin conditions, skin cancers and viral, bacterial and fungal infections, and in various diagnostic applications

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 0.7%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 5.5e+02;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184

Db 1 TTTTTTTTTTTTTTTTTT 19





```
AAA71630/c
ID  AAA71630 standard; DNA; 19 BP.
XX
AC  AAA71630;
XX
DT  14-DEC-2000 (first entry)
XX
DE  Phosphorothioate 20-mer primer DNA #1.
XX
KW  Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX
OS  Synthetic.
XX
FH  Key Location/Qualifiers
FT  modified_base 1..20
FT  /*tag= a
FT  /mod_base= OTHER.
FT  /note= "phosphorothioate linkage"
XX
PN  BP1028124-A2.
XX
PD  16-AUG-2000.
XX
PF  06-SEP-1999; 99EP-00307066.
XX
PR  04-FEB-1999; 99US-0118564P.
PR  09-APR-1999; 99US-00288679.
XX
PA  (ISIS-) ISIS PHARM INC.
XX
PI  Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL;
PI  Guzaev A;
XX
DR  WPI; 2000-500332/45.
XX
PT  Novel method for the production of oligomers with reduced exocyclic
PT  adducts comprises treatment with deprotecting and cleaving reagents.
XX
PS  Example 2; Page 17; 33pp; English.
XX
CC  This invention describes a novel synthetic method (M) comprising: (a)
CC  providing a sample comprising a number of oligomers of formula (I); (b)
CC  contacting the sample with a deprotecting agent to remove R t groups from
CC  the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC  method is used to produce oligomeric compounds for use in antisense and
CC  oligonucleotide therapies. The method enables the synthesis of oligomers
CC  with a reduction in the number acrylonitrile groups attached.
CC  Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC  This sequence represents a phosphorothioate 20-mer primer which is used
CC  in the method of the invention
XX
SQ  Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 869
AAC62454
ID AAC62454 standard; DNA; 19 BP.
XX
AC AAC62454;
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;
XX
```

```
affinity chromatography; sequencing; mutagenesis; DNA preparation;
nucleic acid purification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 10
FT /*tag= a
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Example 3; Page 34; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.5e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 870
AAC62454/c
ID AAC62454 standard; DNA; 19 BP.
XX
AC AAC62454;
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
XX
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 10
FT /*tag= a
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
```

XX  
PR 29-MAR-1999; 99GB-00007245.  
XX (GOLD/) GOLDSBOROUGH A.  
XX WPI; 2000-664908/64.  
DR  
XX Detaching nucleic acid molecule comprising unconventional nucleotide  
PT incorporated at predetermined site from a solid support involves cleaving  
PT the nucleic acid molecule at the site of unconventional nucleotide.  
XX  
PS Example 3; Page 34; 47pp; English.  
XX  
CC The present invention is concerned with the cleavage of nucleic acids  
CC from solid supports. This is carried out by adding a non-conventional  
CC nucleotide into the nucleic acid attached to the support, so that it is  
CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
CC released. This is useful in many molecular biological procedures such as  
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-  
CC based assays, mutagenesis procedures, nucleic acid purification and  
CC affinity chromatography. The present sequence is an oligonucleotide used  
CC in assays to demonstrate the methods of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 871  
AAF31458  
ID AAF31458 standard; DNA; 19 BP.  
XX  
AC AAF31458;  
XX 10-APR-2001 (first entry)  
XX Oligonucleotide ISIS 109989.  
DE  
XX Gene expression; gene therapy; diagnosis; ss.  
KW Synthetic.  
XX WO200102423-A2.  
XX 11-JAN-2001.  
XX 07-JUL-2000; 2000WO-US018609.  
XX 07-JUL-1999; 99US-00349040.  
XX (ISIS-) ISIS PHARM INC.  
XX Manoharan M, Cook PD, Prakash TP, Mohan V;  
XX WPI; 2001-138119/14.  
XX  
XX Guanidium functionalized oligomers prepared from corresponding monomer  
PT units, are hybridizable with a specific RNA or DNA sequence, useful for  
PT diagnostic and therapeutic purposes.  
XX Example 26; Page 54; 108pp; English.  
XX The present invention relates to nucleotide oligomers comprising monomer  
CC units. Oligomers modulate gene expression when hybridized by a single- or  
CC double-stranded nucleic acid. They are useful for gene therapy,  
CC diagnostic and investigative purposes  
XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 872  
AAF31458/C  
ID AAF31458 standard; DNA; 19 BP.  
XX  
AC AAF31458;  
XX 10-APR-2001 (first entry)  
XX Oligonucleotide ISIS 109989.  
DE  
XX Gene expression; gene therapy; diagnosis; ss.  
KW Synthetic.  
XX WO200102423-A2.  
XX 11-JAN-2001.  
XX 07-JUL-2000; 2000WO-US018609.  
XX 07-JUL-1999; 99US-00349040.  
XX (ISIS-) ISIS PHARM INC.  
XX Manoharan M, Cook PD, Prakash TP, Mohan V;  
XX WPI; 2001-138119/14.  
XX  
XX Guanidium functionalized oligomers prepared from corresponding monomer  
PT units, are hybridizable with a specific RNA or DNA sequence, useful for  
PT diagnostic and therapeutic purposes.  
XX Example 26; Page 54; 108pp; English.  
XX The present invention relates to nucleotide oligomers comprising monomer  
CC units. Oligomers modulate gene expression when hybridized by a single- or  
CC double-stranded nucleic acid. They are useful for gene therapy,  
CC diagnostic and investigative purposes  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 873  
AAF31564  
ID AAF31564 standard; DNA; 19 BP.  
XX  
AC AAF31564;  
XX 09-APR-2001 (first entry)  
XX  
XX ISIS sequence 32327.  
XX DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;  
KW atherosclerosis; ss.  
XX







```
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H substrate oligonucleotide #4.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT /*tag= b
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT methoxyethyl)"
FT misc_RNA 19
FT /*tag= c
XX
PN WO200123613-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US026729.
XX
PR 30-SEP-1999; 99US-00409926.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
DR
XX Chimeric oligonucleotides that can serve as substrates for human RNase
PT H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS Example 54; Page 88; 178pp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 879
AAH25738
ID AAH25738 standard; DNA; 19 BP.
XX
AC AAH25738;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H substrate oligonucleotide #5.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
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FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT /*tag= b
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT methoxyethyl)"
FT misc_RNA 19
FT /*tag= c
XX
PN WO200123613-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-US026729.
XX
PR 30-SEP-1999; 99US-00409926.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
DR
XX Chimeric oligonucleotides that can serve as substrates for human RNase
PT H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
PS Example 54; Page 88; 178pp; English.
XX
CC The present invention provides a number of DNA-RNA oligonucleotides which
CC can act as substrates for human RNase HI (a type II RNase). The sequence
CC consists of two portions, one of which is capable of supporting cleavage
CC of a complementary target RNA and the other of which is incapable of
CC supporting such cleavage. These can be used to enhance the effectiveness
CC of antisense therapies. The present sequence is an RNase H substrate used
CC in the exemplification of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.5e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTT 19
RESULT 880
AAH25738/c
ID AAH25738 standard; DNA; 19 BP.
XX
AC AAH25738;
XX
DT 14-AUG-2001 (first entry)
XX
DE Human type II RNase H substrate oligonucleotide #5.
XX
KW Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;
KW gene therapy; primer; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "optionally phosphorothioate backbone"
FT modified_base 16..19
FT /*tag= b
FT
```

```
FT /mod_base= OTHER
FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-
FT methoxyethyl)"
FT 19
FT misc_RNA /*tag= C
XX
XX WO200123613-A1.
XX
XX 05-APR-2001.
XX
XX 29-SEP-2000; 2000WO-US026729.
XX
XX 30-SEP-1999; 99US-00409926.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Crooke ST, Lima WF, Wu H, Manoharan M;
XX WPI; 2001-343164/36.
XX
XX Chimeric oligonucleotides that can serve as substrates for human RNase
XX H1, useful for enhancing the effectiveness of antisense gene therapies.
XX
XX Example 54; Page 88; 178pp; English.
XX
XX The present invention provides a number of DNA-RNA oligonucleotides which
XX can act as substrates for human RNase HI (a type II RNase). The sequence
XX consists of two portions, one of which is capable of supporting cleavage
XX of a complementary target RNA and the other of which is incapable of
XX supporting such cleavage. These can be used to enhance the effectiveness
XX of antisense therapies. The present sequence is an RNase H substrate used
XX in the exemplification of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
SQ
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 881
AAC83664
ID AAC83664 standard; DNA; 19 BP.
XX
XX AAC83664;
AC
XX
XX 02-MAR-2001 (first entry)
DT
XX
XX 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
DE
XX
XX 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KW tumour formation; cancer; protein kinase C expression;
KW cell adhesion molecule expression; multidrug resistance; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
XX
XX US6147200-A.
PN
XX
XX 14-NOV-2000.
PD
XX
XX 19-AUG-1999; 99US-00378568.
XX
XX 19-AUG-1999; 99US-00378568.
PR 19-AUG-1999; 99US-00378568.
```

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XX (ISIS-) ISIS PHARM INC.
PA
XX Manoharan M, Cook PD, Fraser AS, Prakash TP, Kawasaki AM;
PI
XX WPI; 2001-069824/08.
XX
XX New 2'-O-acetamido modified nucleosides (I) used to produce
PT oligonucleotides which have enhanced nuclease resistance and superior
PT hybridization properties than prior art.
XX
XX Example 12; Col 28; 29pp; English.
PS
XX
XX The present sequence is a modified oligonucleotide. 2'-O-acetamido-
XX modified nucleosides were used to produce oligonucleotides which have
XX enhanced nuclease resistance and superior hybridisation properties than
XX prior art. The oligomeric compounds are useful for identification or
XX quantification of ribonucleic acid and deoxyribonucleic acid or for
XX modulating the activity of an ribonucleic acid or deoxyribonucleic acid
XX molecule. They have a modified nucleoside monomer and are specifically
XX hybridisable with a preselected nucleotide sequence of a single-stranded
XX or double-stranded target deoxyribonucleic acid or ribonucleic acid
XX molecule. The oligomers are further useful in a ras-luciferase fusion
XX system using ras-luciferase transactivation. They are useful in abnormal
XX cell proliferation and tumour formation and modulation of expression of
XX protein kinase C and cell adhesion molecules such as ICAM. They are
XX useful in the modulation of proteins related to multidrug resistance and
XX viral genomic nucleic acids such as HOV, herpes viruses, Epstein-Barr
XX virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza
XX virus
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTTTT 19
RESULT 882
AAC83664/C
ID AAC83664 standard; DNA; 19 BP.
XX
XX AAC83664;
AC
XX
XX 02-MAR-2001 (first entry)
DT
XX
XX 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.
DE
XX
XX 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;
KW tumour formation; cancer; protein kinase C expression;
KW cell adhesion molecule expression; multidrug resistance; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"
XX
XX US6147200-A.
PN
XX
XX 14-NOV-2000.
PD
XX
XX 19-AUG-1999; 99US-00378568.
XX
XX 19-AUG-1999; 99US-00378568.
PR 19-AUG-1999; 99US-00378568.
XX
XX (ISIS-) ISIS PHARM INC.
PA
```





XX CC The present invention relates to a method for the qualitative and  
CC quantitative detection of targets in a sample by molecular interaction  
CC between the target and probes in an array. The method can be used to  
CC detect interactions between nucleic acids; antigens and antibodies or  
CC receptor and ligands, particularly in applications such as medical  
CC diagnosis, forensic science, bacterial screening, tissue typing for  
CC transplantation, monitoring gene expression, and genotyping. The present  
CC sequence is a modifying oligonucleotide used in the exemplification of  
CC the invention  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAA 1  
RESULT 885  
ABA91949  
ID ABA91949 standard; DNA; 19 BP.  
XX  
AC ABA91949;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Methyl thioethyl modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
XX  
PN US6277982-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 20-AUG-1999; 99US-00378665.  
XX  
PR 20-AUG-1999; 99US-00378665.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
XX  
XX WPI; 2002-235143/29.  
XX  
PT Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.

XX CC The present sequence is that of a chimeric oligonucleotide having some 2'  
CC -methyl thioethyl modifications. This was compared with oligonucleotides  
CC with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)  
CC modifications for resistance to snake venom phosphodiesterase. The assay  
CC revealed the nuclease resistance of the modified oligomers. The invention  
CC provides methods for the alkylation of alcohols, amines, thiols and their  
CC derivatives by cyclic sulfate intermediates. In particular, methods for  
CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and  
CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl  
CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or  
CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified  
CC nucleosides and their analogues. The methods are especially useful for  
CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside  
CC surrogates that are precursors for the preparation of oligomeric  
CC compounds useful as therapeutics, diagnostics and research reagents  
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTTTT 19  
RESULT 886  
ABA91949/c  
ID ABA91949 standard; DNA; 19 BP.  
XX  
AC ABA91949;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Methyl thioethyl modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
FT modified\_base 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-methyl thioethyl thymidine"  
XX  
PN US6277982-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 20-AUG-1999; 99US-00378665.  
XX  
PR 20-AUG-1999; 99US-00378665.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
XX  
XX WPI; 2002-235143/29.

XX Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.  
XX  
CC The present sequence is that of a chimeric oligonucleotide having some 2'  
CC -methyl thioethyl modifications. This was compared with oligonucleotides  
CC with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)  
CC modifications for resistance to snake venom phosphodiesterase. The assay  
CC revealed the nuclease resistance of the modified oligomers. The invention  
CC provides methods for the alkylation of alcohols, amines, thiols and their  
CC derivatives by cyclic sulfate intermediates. In particular, methods for  
CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and  
CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl  
CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or  
CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified  
CC nucleosides and their analogues. The methods are especially useful for  
CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside  
CC surrogates that are precursors for the preparation of oligomeric  
CC compounds useful as therapeutics, diagnostics and research reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 887  
ABA91951  
ID ABA91951 standard; DNA; 19 BP.  
XX  
AC ABA91951;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Dimethylaminopropyl modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 17 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 18 /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 19 /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
XX  
PN US6277982-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 20-AUG-1999; 99US-00378665.  
XX  
PR 20-AUG-1999; 99US-00378665.

XX (ISIS-) ISIS PHARM INC.  
XX  
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
XX  
DR WPI; 2002-235143/29.  
XX  
PT Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.  
XX  
CC The present sequence is that of a chimeric oligonucleotide having some 2'  
CC -dimethylaminopropyl modifications. This was compared with  
CC oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy  
CC (see ABA91950) modifications for resistance to snake venom  
CC phosphodiesterase. The assay revealed the nuclease resistance of the  
CC modified oligomers. The invention provides methods for the alkylation of  
CC alcohols, amines, thiols and their derivatives by cyclic sulfate  
CC intermediates. In particular, methods for the alkylation of the 2', 3' or  
CC 5'-hydroxy position of nucleosides and their analogues with cyclic  
CC sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are  
CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile  
CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The  
CC methods are especially useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates that are precursors  
CC for the preparation of oligomeric compounds useful as therapeutics,  
CC diagnostics and research reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTTTT 2184  
DB 1 TTTTTTTTTTTTTTTTTTTT 19  
  
RESULT 888  
ABA91951/C  
ID ABA91951 standard; DNA; 19 BP.  
XX  
AC ABA91951;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Dimethylaminopropyl modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
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FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 17 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 18 /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminopropyl thymidine"  
FT modified\_base 19 /\*tag= d  
FT /mod\_base= OTHER  
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XX

PN US6277982-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 20-AUG-1999; 99US-00378665.  
XX  
PR 20-AUG-1999; 99US-00378665.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
XX  
DR WPI; 2002-235143/29.  
XX  
PT Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.  
XX  
CC The present sequence is that of a chimeric oligonucleotide having some 2'  
CC -dimethylaminopropyl modifications. This was compared with  
CC oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy  
CC (see ABA91950) modifications for resistance to snake venom  
CC phosphodiesterase. The assay revealed the nuclease resistance of the  
CC modified oligomers. The invention provides methods for the alkylation of  
CC alcohols, amines, thiols and their derivatives by cyclic sulfate  
CC intermediates. In particular, methods for the alkylation of the 2', 3' or  
CC 5'-hydroxy position of nucleosides and their analogues with cyclic  
CC sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are  
CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile  
CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The  
CC methods are especially useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates that are precursors  
CC for the preparation of oligomeric compounds useful as therapeutics,  
CC diagnostics and research reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 889  
ABA91950  
ID ABA91950 standard; DNA; 19 BP.  
XX  
AC ABA91950;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Methoxyethoxy modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethoxy thymidine"  
FT modified\_base 17 /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethoxy thymidine"  
FT modified\_base 18 /\*tag= c  
FT

FT /mod\_base= OTHER  
FT /note= "2'-methoxyethoxy thymidine"  
FT modified\_base 19 /\*tag= d  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethoxy thymidine"  
XX  
PN US6277982-B1.  
XX  
PD 21-AUG-2001.  
XX  
PF 20-AUG-1999; 99US-00378665.  
XX  
PR 20-AUG-1999; 99US-00378665.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
XX  
DR WPI; 2002-235143/29.  
XX  
PT Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.  
XX  
CC The present sequence is that of a chimeric oligonucleotide having some 2'  
CC -methoxyethoxy modifications. This was compared with oligonucleotides  
CC with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see  
CC ABA91951) modifications for resistance to snake venom phosphodiesterase.  
CC The assay revealed the nuclease resistance of the modified oligomers. The  
CC invention provides methods for the alkylation of alcohols, amines, thiols  
CC and their derivatives by cyclic sulfate intermediates. In particular,  
CC methods for the alkylation of the 2', 3' or 5'-hydroxy position of  
CC nucleosides and their analogues with cyclic sulfates to form the 2', 3'  
CC or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of  
CC the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-  
CC modified nucleosides and their analogues. The methods are especially  
CC useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and  
CC nucleoside surrogates that are precursors for the preparation of  
CC oligomeric compounds useful as therapeutics, diagnostics and research  
CC reagents  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 890  
ABA91950/c  
ID ABA91950 standard; DNA; 19 BP.  
XX  
AC ABA91950;  
XX  
DT 23-MAY-2002 (first entry)  
XX  
DE Methoxyethoxy modified oligonucleotide.  
XX  
KW 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16 /\*tag= a  
FT /mod\_base= OTHER  
FT

FT modified\_base /note= "2'-methoxyethoxy thymidine"  
FT 17  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT modified\_base /note= "2'-methoxyethoxy thymidine"  
FT 18  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT modified\_base /note= "2'-methoxyethoxy thymidine"  
FT 19  
FT /\*tag= d  
FT /mod\_base= OTHER  
FT modified\_base /note= "2'-methoxyethoxy thymidine"  
FT 19  
XX

PN US6277982-B1.  
XX  
XX 21-AUG-2001.  
XX  
XX 20-AUG-1999; 99US-00378665.  
XX  
XX 20-AUG-1999; 99US-00378665.  
PR  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;  
PI  
XX WPI; 2002-235143/29.  
DR

XX Alkylation of alcohols, amines, or thiols, useful for preparing  
PT nucleosides that are precursors for preparation of oligomeric compounds  
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.  
XX  
PS Example 15; Col 35; 45pp; English.

XX The present sequence is that of a chimeric oligonucleotide having some 2'-  
CC -methoxyethoxy modifications. This was compared with oligonucleotides  
CC with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see  
CC ABA91951) modifications for resistance to snake venom phosphodiesterase.  
CC The assay revealed the nuclease resistance of the modified oligomers. The  
CC invention provides methods for the alkylation of alcohols, amines, thiols  
CC and their derivatives by cyclic sulfate intermediates. In particular,  
CC methods for the alkylation of the 2', 3' or 5'-hydroxy position of  
CC nucleosides and their analogues with cyclic sulfates to form the 2', 3'  
CC or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of  
CC the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-  
CC modified nucleosides and their analogues. The methods are especially  
CC useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and  
CC nucleoside surrogates that are precursors for the preparation of  
CC oligomeric compounds useful as therapeutics, diagnostics and research  
CC reagents

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 891  
ABL51520  
ID ABL51520 standard; DNA; 19 BP.  
XX  
AC ABL51520;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.  
XX  
KW Tailing reaction; tailed primer; primer; probe; identification;

KW detection; linear amplification scheme; chain extending enzyme;  
KW telomerase; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "biotinylated"  
FT 19  
FT misc\_RNA  
FT /\*tag= b  
XX

PN US2002031776-A1.  
XX  
XX 14-MAR-2002.  
XX  
XX 26-JUL-2001; 2001US-00917138.  
XX  
XX 28-MAY-1999; 99US-0136545P.  
PR  
PR 25-MAY-2000; 2000US-00580358.  
XX  
XX (TULL/) TULLIS R H.  
PA (STRE/) STREIFEL J A.  
XX  
XX Tullis RH, Streifel JA;  
PI  
XX WPI; 2002-361176/39.  
DR

XX Identifying and detecting nucleic acids, particularly DNA hybridization  
PT probes, involves employing chain extending enzymes (e.g. telomerase) to  
PT elongate probes to render them readily detectable.

PS Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid  
CC probe, which comprises using chain extending enzymes to elongate probes.  
CC The method comprises: (a) treating the sample with a chain terminating  
CC reagent to prevent polynucleotide chain growth from the nucleic acid in  
CC the sample; (b) contacting the sample with the probe containing a  
CC terminus capable of elongation by a chain extending enzyme, where the  
CC probe hybridises to the nucleic acid in the sample; (c) contacting the  
CC sample with a chain extending enzyme and its substrates, which elongates  
CC the probe; and (d) detecting the elongated hybridised probe. Also  
CC described is a method comprising: (a) treating nucleic acid molecules or  
CC modified nucleic acids in a sample with a reagent or reagents that render  
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;  
CC (b) hybridising the treated molecules with a nucleic acid probe that  
CC includes an extendable terminus, under conditions where hybrids form; and  
CC (c) treating any hybrids formed with a non-template dependent chain  
CC elongating enzyme and its substrates, where any hybridised probe is  
CC extended. The method is useful for identifying and detecting nucleic  
CC acids, particularly DNA hybridisation probes. The present sequence  
CC represents a tailing reaction exemplary primer, which is used in an  
CC example from the present invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 5.5e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 892  
ABL51520/c  
ID ABL51520 standard; DNA; 19 BP.  
XX  
AC ABL51520;  
XX





KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX Unidentified.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 15. .18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethoxy (MOE) residues"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
DR WPI; 2002-546338/58.  
XX  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 31; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 895  
AAD42002  
ID AAD42002 standard; DNA; 19 BP.  
XX  
AC AAD42002;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #5 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX Unidentified.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16. .19  
FT /\*tag= a  
FT /mod\_base= OTHER

FT /note= "5-methyl, 2'-methoxyethyl residues"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
DR WPI; 2002-546338/58.  
XX  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 33; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 896  
AAD42002/c  
ID AAD42002 standard; DNA; 19 BP.  
XX  
AC AAD42002;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #5 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX Unidentified.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16. .19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-methoxyethyl residues"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.

XX (ISIS-) ISIS PHARM INC.  
PA Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX WPI; 2002-546338/58.  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
XX for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX Example 46; Col 33; 24pp; English.  
XX The present invention relates to a novel method of selective alkylation  
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 897  
AAD42004  
ID AAD42004 standard; DNA; 19 BP.  
XX  
AC AAD42004;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #7 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 18 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-dimethylaminooxyethyl residue"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX WPI; 2002-546338/58.  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving

PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX Example 46; Col 33; 24pp; English.  
XX The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184  
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 898  
AAD42004/c  
ID AAD42004 standard; DNA; 19 BP.  
XX  
AC AAD42004;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #7 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 18 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-dimethylaminooxyethyl residue"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX WPI; 2002-546338/58.  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 33; 24pp; English.  
XX The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention

CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 899  
AAD42010  
ID AAD42010 standard; DNA; 19 BP.  
XX  
AC AAD42010;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #13 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16. .19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE) "  
FT modified\_base 18. .19  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 35; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide

CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTT 19  
  
RESULT 900  
AAD42010/C  
ID AAD42010 standard; DNA; 19 BP.  
XX  
AC AAD42010;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #13 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 16. .19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE) "  
FT modified\_base 18. .19  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate backbone"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 35; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;





```
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 904
AAD42001/c
ID AAD42001 standard; DNA; 19 BP.
XX
AC AAD42001;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #4 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
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FT /note= "5-methyl, 2'-dimethylaminooxyethyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804
Db 19 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 905
AAD42011
ID AAD42011 standard; DNA; 19 BP.
XX
AC AAD42011;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #14 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
```

XX (ISIS-) ISIS PHARM INC.  
PA  
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
PI  
XX WPI; 2002-546338/58.  
DR  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
XX for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
PT  
XX Example 46; Col 37; 24pp; English.  
PS  
XX The present invention relates to a novel method of selective alkylation  
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 906  
AAD42011/C  
ID AAD42011 standard; DNA; 19 BP.  
XX  
AC AAD42011;  
XX  
XX 04-NOV-2002 (first entry)  
DT  
XX Oligonucleotide #14 used to illustrate the method of the invention.  
DE  
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
KW  
XX Unidentified.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 16.19  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving

PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 37; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 907  
AAD42005  
ID AAD42005 standard; DNA; 19 BP.  
XX  
AC AAD42005;  
XX  
XX 04-NOV-2002 (first entry)  
DT  
XX Oligonucleotide #8 used to illustrate the method of the invention.  
DE  
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
KW  
XX Unidentified.  
OS  
XX Key Location/Qualifiers  
FH modified\_base 18  
FT /tag= a  
FT /mod\_base= OTHER  
FT /note= "5-methyl, 2'-methoxyethyl residues"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
PT  
XX Example 46; Col 33; 24pp; English.  
PS  
XX The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
PT  
XX Example 46; Col 33; 24pp; English.  
PS  
XX The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with

CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

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Query Match... 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	2166		2184
D <sub>b</sub>	1		19

RESULT 908  
AAD42005/c  
ID AAD42005 standard; DNA; 19 BP.  
XX  
XX AC AAD42005;  
XX  
XX DT 04-NOV-2002 (first entry)  
XX  
XX DE Oligonucleotide #8 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.

	Key	Location/Qualifiers
PH	modified_base	18
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "5-methyl, 2'-methoxyethyl residues"

PN	US6403779-B1.	
XX		
PD	11-JUN-2002.	
XX		
PF	08-JAN-1999;	99US-00227782.
XX		
PR	08-JAN-1999;	99US-00227782.
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Kawasaki AM,	Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX		
DR	WPI; 2002-546338/58.	

Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.

Example 46; Col 33; 24pp; English.

The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match	0.7%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 5.5e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
|||  
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 909  
AAD42003  
ID AAD42003 standard; DNA; 19 BP.

AC AAD42003;

04-NOV-2002 (first entry)

DE Oligonucleotide #6 used to illustrate the method of the invention.

Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity; nuclear resistance; alkylation; therapeutic; diagnostic; ss.

OS Unidentified.

	Key	Location/Qualifiers
FT	modified_base	16..19
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "5-methyl, 2'-O-propyl residues"

PN US6403779-B1.

PD 11-JUN-2002.

PF 08-JAN-1999; 99US-00227782.

PR 08-JAN-1999; 99US-00227782.

PA (ISIS-) ISIS PHARM INC.

PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI: 2002-546338/58.

Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used for preparation of 2'-O-alkylated compounds comprises dissolving nucleoside in aprotic solvent, cooling, treating with base, warming, cooling and reacting with ester.

PS Example 46; Col 33; 24pp; English;

The present invention relates to a novel method of selective alkylation of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside. The method involves dissolving the nucleoside in at least one aprotic solvent, cooling, treating with base, warming, cooling and reacting with a reactive ester. The method is useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside surrogates used for preparation of oligomeric compounds having improved hybridisation affinity and nuclear resistance, which are useful as therapeutics, diagnostics and research reagents. The present sequence is a modified oligonucleotide used to illustrate the method of the invention

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match	0.7%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 5.5e+02;		
Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19



```

RESULT 910
AAD42003/c
ID AAD42003 standard; DNA; 19 BP.
XX
AC AAD42003;
XX
AC AAD42003;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #6 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-O-propyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
DR Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 911
AAD41998
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #1 used to illustrate the method of the invention.
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XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
DR Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
DB 1 TTTTTTTTTTTTTTTTTT 19

RESULT 912
AAD41998/c
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #1 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
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FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminooxyethoxy (2'-AOE) residues"
XX
PN US6403779-B1.
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 913
AAD41999
ID AAD41999 standard; DNA; 19 BP.
XX
AC AAD41999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxyethoxy (2'-DMAOE)
FT residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
DR
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XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 31; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 914
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
AC AAD41999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxyethoxy (2'-DMAOE)
FT residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
DR
```

XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 31; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 915  
AAD42009  
ID AAD42009 standard; DNA; 19 BP.  
XX  
AC AAD42009;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #12 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 15..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 35; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation

CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 916  
AAD42009/c  
ID AAD42009 standard; DNA; 19 BP.  
XX  
AC AAD42009;  
XX  
DT 04-NOV-2002 (first entry)  
XX  
DE Oligonucleotide #12 used to illustrate the method of the invention.  
XX  
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;  
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 15..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-dimethylaminooxyethyl thymidine (T-2'DMAOE)"  
XX  
PN US6403779-B1.  
XX  
PD 11-JUN-2002.  
XX  
PF 08-JAN-1999; 99US-00227782.  
XX  
PR 08-JAN-1999; 99US-00227782.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;  
XX  
DR WPI; 2002-546338/58.  
XX  
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used  
PT for preparation of 2'-O-alkylated compounds comprises dissolving  
PT nucleoside in aprotic solvent, cooling, treating with base, warming,  
PT cooling and reacting with ester.  
XX  
PS Example 46; Col 35; 24pp; English.  
XX  
CC The present invention relates to a novel method of selective alkylation  
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.  
CC The method involves dissolving the nucleoside in at least one aprotic  
CC solvent, cooling, treating with base, warming, cooling and reacting with  
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl  
CC nucleotides, nucleosides and nucleoside surrogates used for preparation  
CC of oligomeric compounds having improved hybridisation affinity and  
CC nuclear resistance, which are useful as therapeutics, diagnostics and  
CC research reagents. The present sequence is a modified oligonucleotide  
CC used to illustrate the method of the invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 917  
ABZ58336  
ID ABZ58336 standard; DNA; 19 BP.  
XX AC ABZ58336;  
XX DT 28-APR-2003 (first entry)  
XX Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.  
DE Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;  
KW DNA-RNA hybrid; ss.  
XX Synthetic.  
OS Key Location/Qualifiers  
FH modified\_base 16 /\*tag= a /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 17 /\*tag= b /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 18 /\*tag= c /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 19 /\*tag= d /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
XX WO2003004603-A2.  
PN 16-JAN-2003.  
XX 01-JUL-2002; 2002WO-US020940.  
XX 03-JUL-2001; 2001US-0302683P.  
PR 28-JAN-2002; 2002US-00058740.  
XX (ISIS-) ISIS PHARM INC.  
XX Prakash TP, Manoharan M;  
PI WPI; 2003-239204/23.  
DR Increasing binding of oligomeric compound to proteins useful in  
XX preparation of antisense therapeutics, involves use of modified  
PT oligomeric compound having oligonucleotide group.  
PS Example 27; Page 72; 122pp; English.  
XX The present sequence is an example of an oligonucleotide of the invention  
CC containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-  
CC methyluridine) modifications. In examples of the invention, 2'-O-MTE was  
CC incorporated into oligonucleotides and evaluated for antisense properties  
CC in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)  
CC modification. The 2'-O-MTE modified oligonucleotides exhibited similar  
CC binding affinity to target RNA as their 2'-O-MOE equivalent while binding

CC to human serum albumin was improved. The modification can be used to  
CC modulate the pharmacokinetics of oligonucleotides, e.g. in antisense  
CC therapy  
XX Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;  
SQ Query Match 0.7%; Score 19; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 5.5e+02;  
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTUUUU 19  
RESULT 918  
ABZ58336/c  
ID ABZ58336 standard; DNA; 19 BP.  
XX AC ABZ58336;  
XX DT 28-APR-2003 (first entry)  
XX Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.  
DE Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;  
KW DNA-RNA hybrid; ss.  
XX Synthetic.  
OS Key Location/Qualifiers  
FH modified\_base 16 /\*tag= a /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 17 /\*tag= b /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 18 /\*tag= c /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
FT modified\_base 19 /\*tag= d /mod\_base= OTHER  
FT /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"  
XX WO2003004603-A2.  
PN 16-JAN-2003.  
XX 01-JUL-2002; 2002WO-US020940.  
XX 03-JUL-2001; 2001US-0302683P.  
PR 28-JAN-2002; 2002US-00058740.  
XX (ISIS-) ISIS PHARM INC.  
XX Prakash TP, Manoharan M;  
PI WPI; 2003-239204/23.  
DR Increasing binding of oligomeric compound to proteins useful in  
XX preparation of antisense therapeutics, involves use of modified  
PT oligomeric compound having oligonucleotide group.  
PS Example 27; Page 72; 122pp; English.  
XX The present sequence is an example of an oligonucleotide of the invention  
CC containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-  
CC methyluridine) modifications. In examples of the invention, 2'-O-MTE was  
CC incorporated into oligonucleotides and evaluated for antisense properties





DT 25-MAR-2003 (revised)  
DT 21-AUG-1994 (first entry)  
XX  
DE Sequence of synthetic RNA oligo which is a target nucleotide for a novel  
DE receptor.  
XX  
KW Novel receptor; nucleic acid; transport; oligo; ss.  
XX  
OS Synthetic.  
XX  
XX WO9404194-A1.  
PN  
XX  
PD 03-MAR-1994.  
XX  
XX 13-AUG-1993; 93WO-US007603.  
PF  
XX  
PR 14-AUG-1992; 92US-00930087.  
XX  
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
PA  
XX  
XX Usman N, Rebek J, De Mendoza J;  
PI  
XX WPI; 1994-082846/10.  
DR  
XX Transport of nucleic acid derivs. across membranes - using new receptors  
PT which use salt bridging, aromatic stacking, hydrogen bonding and  
PT chelation.  
XX  
XX Example; Table 1, page 38; 103pp; English.  
PS  
XX The inventors claim a method of transporting a nucleic acid deriv. accros  
CC a membrane which comprises using a receptor that uses salt bridgin,  
CC aromatic stacking, H bonding and chelation to recognise the nucleic acid  
CC deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the  
CC examples. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 922  
AAQ94205/c  
ID AAQ94205 standard; DNA; 20 BP.  
XX  
AC AAQ94205;  
XX  
DT 25-MAR-2003 (revised)  
DT 24-AUG-1995 (first entry)  
XX  
DE Alpha-anomeric oligonucleotide ligand 1803 for oestradiol haptten.  
XX  
KW Oligonucleotide ligand; steroid hormone; haptten; immobilisation;  
KW immunodetection; estradiol; alpha-anomer; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 1. .21  
FT /\*tag= b  
FT /note= "the glycosidic bonds between nucleotides are all  
FT in the alpha-anomer form"  
FT modified\_base 20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "carries a group derived ffrom aminopropanediol"  
XX

PN WO9429723-A1.  
XX  
PD 22-DEC-1994.  
XX  
PF 10-JUN-1994; 94WO-FR000689.  
XX  
PR 11-JUN-1993; 93FR-00007093.  
XX  
XX (CROS/) CROS P.  
PA (KURF/) KURFURST R.  
PA (BATT/) BATTAIL N.  
PA (PIGA/) PIGA N.  
XX  
XX Cros P, Kurfurst R, Battail N, Piga N;  
PI WPI; 1995-036665/05.  
DR  
XX Assay device for haptten or its specific antibodies - comprises support  
PT having competitive reagent immobilised via nucleic acid ligand to improve  
PT orientation and accessibility.  
XX  
PS Example 1; Page 10; 39pp; French.  
XX  
CC Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.  
CC The ligands are covalently linked to a haptten (esp. a steroid hormone) to  
CC form a conjugate which is then immobilised on a solid support for  
CC interaction with antibodies against the haptten. Nucleic acid ligands are  
CC less likely to be recognised by the antibodies than are peptide ligands  
CC and nucleic acids are also less likely to undergo intramolecular  
CC organisation which interferes with accessibility of the haptten to the  
CC antibodies. For immunodiagnosis of oestradiol, the active haptten  
CC oestradiol-6-carboxymethoxime-N- hydroxysuccinimide ester was used.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 923  
AAQ90405/c  
ID AAQ90405 standard; DNA; 20 BP.  
XX  
AC AAQ90405;  
XX  
DT 08-JAN-1996 (first entry)  
XX  
DE T2 (synthetic DNA probe with 5' amino terminal #4).  
XX  
KW T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;  
KW ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 1  
FT /\*tag= a  
FT /note= "3' aminolink2 Thymine; allows binding to any  
FT amine"  
XX  
XX WO9512808-A1.  
PN  
XX 11-MAY-1995.  
PD  
XX 26-OCT-1994; 94WO-US012270.  
PF  
XX 01-NOV-1993; 93US-00146504.  
PR

XX PA (NANO-) NANOGEN INC.  
XX PI Heller MJ, Tu E;  
XX DR WPI; 1995-185870/24.  
XX PT New self-addressable electronic devices - used for multi-step and  
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics  
PT and bio:polymer synthesis.  
XX PS Example 1; Page 41; 86pp; English.  
XX CC The sequences represented by, AAQ90402-15 are synthetic DNA probes  
CC containing 5' amino termini. The sequences shown in AAQ90390-401 are  
CC synthetic DNA probes with 3' ribonucleoside termini. These sequences were  
CC specific for the polymorphisms of HLA gene dQa. The sequences were used  
CC in the device of the invention. This is a self-addressable electronic  
CC device (SAED) that can be used to carry out multi-step and multiplex  
CC reactions, such as nucleic acid hybridisations. The advantages of this  
CC method are that these reactions can be carried out with complete and  
CC precise electronic control, and that the rate, specificity and  
CC sensitivity of these reactions are greatly improved at micro-locations  
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 20 AAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 924  
AAV07752/C  
ID AAV07752 standard; DNA; 20 BP.  
XX AC AAV07752;  
XX DT 07-DEC-1998 (first entry)  
XX DE Phosphorothioate oligonucleotide.  
XX KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;  
KW antisense; EDITH; Beaucage reagent; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT misc\_feature 1..20  
FT /\*tag= a  
FT /note= "phosphorothioate internucleotide linkages"  
XX PN WO9741130-A2.  
XX PD 06-NOV-1997.  
XX PF 29-APR-1997; 97WO-US007118.  
XX PR 30-APR-1996; 96US-00641920.  
XX PA (MINU ) UNIV MINNESOTA.  
PA (LOUU ) UNIV LOUISIANA STATE & AGRIC.  
XX PI Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;  
XX DR WPI; 1997-549671/50.  
XX PT Sulphurisation of phosphorus-containing compounds, e.g.  
PT oligo:nucleotide(s) - by contacting the compound with a di:sulphide-  
PT containing five-membered heterocycle.

XX PS Example 7; Page 30; 51pp; English.  
XX CC The present invention provides a method for sulphurising phosphorus-  
CC containing compounds. It comprises contacting the phosphorus-containing  
CC compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-  
CC substituted-1,2,4-dithiazolin-5-one compound. The method is especially  
CC useful for incorporation of phosphorothioate linkages into biologically  
CC important molecules such as DNA, RNA and phosphopeptides. Molecules  
CC containing such linkages are useful e.g. as antisense compounds for  
CC inhibiting gene expression, as reagents for studying DNA-protein or RNA-  
CC protein interactions, or as catalytic RNA. The present sequence  
CC represents an oligonucleotide with phosphorothioate linkages prepared by  
CC the method of the invention  
XX SQ Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 925  
AAT63649/C  
ID AAT63649 standard; DNA; 20 BP.  
XX AC AAT63649;  
XX DT 06-JUN-1997 (first entry)  
XX DE Anti-HTLV antisense reference oligonucleotide HT.  
XX KW antisense; complementary; tax gene; inhibit; HTLV-1;  
KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.  
XX OS Synthetic.  
XX PN JP09052898-A.  
XX PD 25-FEB-1997.  
XX PF 09-AUG-1995; 95JP-00224606.  
XX PR 09-AUG-1995; 95JP-00224606.  
XX PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.  
XX DR WPI; 1997-197252/18.  
XX PT Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of  
PT tax gene from human T-cell lymphotropic virus type 1 and inhibits viral  
PT antigen expression.  
XX PS Example 1; Page 8; 10pp; Japanese.  
XX CC Oligonucleotides having a partial sequence consisting of at least 15  
CC bases of AAT63641 (an antisense oligo complementary to a region of the  
CC tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-  
CC 1) viral antigen expression) are claimed. In an example, six antisense  
CC oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos  
CC derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1  
CC (p21), R1 (rex), RR1 (rex response element), E1 (env) and G1 (gag), four  
CC reference oligonucleotides TIS (tax-sense), HC (dc20), HT (dt20)  
CC (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen  
CC expression inhibiting test. Oligonucleotide T1 gave the best results  
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 926  
AAV34591  
ID AAV34591 standard; DNA; 20 BP.  
XX AC AAV34591;  
XX DT 25-AUG-1998 (first entry)  
XX DE M. vaccae antigenic sequence hybridising oligo AD12.  
XX KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
XX KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
XX KW mycobacteria infection; vaccine; cancer; ss.  
XX OS Synthetic.  
XX OS Mycobacterium vaccae.  
XX PN WO9808542-A2.  
XX PD 05-MAR-1998.  
XX PF 28-AUG-1997; 97WO-NZ000105.  
XX PR 29-AUG-1996; 96US-00705347.  
XX PR 12-JUN-1997; 97US-00873970.  
XX PA (GENE-) GENESIS RES & DEV CORP.  
XX PI Tan P, Hiyama J, Visser E, Skinner MA, Scott LM, Prestidge RL;  
XX WPI; 1998-216926/19.  
XX PT Mycobacterium vaccae polypeptides - used to develop products for use in  
XX PT detection, therapy and prevention of mycobacteria infections or as immune  
XX PT response enhancers.  
XX PS Example 8; Page 99; 153pp; English.  
XX SS This oligonucleotide is used in the DNA cloning strategies of the  
CC Mycobacterium vaccae antigens. The invention provides M. vaccae  
CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae  
CC antigen, or a variant, where the antigen induces an immune response in  
CC patients previously exposed to a mycobacterium. Such M. vaccae  
CC polypeptides can be used in methods for enhancing non-specific immune  
CC response. The methods and products can be used for the detection,  
CC treatment and prevention of infectious diseases caused by mycobacteria  
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
CC the ability to induce cell proliferation and cytokine production (e.g.  
CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B  
CC cells, or macrophages. They can be used for enhancing immune responses  
CC for use in vaccines or immunotherapy of infectious diseases and cancers  
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 927  
AAT86606/c

Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 928  
AAX27533/c  
ID AAX27533 standard; RNA; 20 BP.  
XX AC AAX27533;

AAT86606 standard; DNA; 20 BP.  
AAT86606;  
04-JUN-1998 (first entry)  
Oligonucleotide separated by capillary affinity gel electrophoresis.  
Capillary affinity gel electrophoresis; separation; polymer-gel;  
polyacrylamide; ss.  
Synthetic.  
WO9745721-A1.  
04-DEC-1997.  
23-MAY-1997; 97WO-EP002647.  
24-MAY-1996; 96CH-00001320.  
(NOVS ) NOVARTIS AG.  
Muscate A, Paulus A, Natt F;  
WPI; 1998-041763/04.  
Separation of electrically charged target molecules - by capillary  
affinity gel electrophoresis using polymer-gel to which receptors for  
target molecules are bound.  
Example D3; Page 25; 41pp; English.  
A mixture of oligonucleotides (AAT86604-7) were separated by a new  
process using capillary affinity gel electrophoresis. The invention  
relates to selective separation of electrically charged target molecules  
in an analytical mixture. It comprises capillary affinity gel  
electrophoresis using a capillary tube which is at least partly filled  
with a polymer gel. Receptors for target molecules are covalently bound  
to the polymer. An electric field of at least 50 volts/cm is applied. The  
capillary tube is charged with the analytical mixture. In a first  
separation stage, the target molecules in the mixture are bound to the  
receptors and the remaining components are eluted, optionally whilst  
splitting open. In a second stage, the elution conditions are changed,  
optionally in stages, so that the affinity of the target molecules for  
the receptor is eliminated and the target molecules are eluted and  
detected, optionally whilst splitting open. The process is useful for  
selective separation and/or determination of charged organic compounds,  
such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.  
for isolation of specific proteins and DNA molecules, purification of  
antibodies, analysis of antisense compounds or screening for enzyme  
inhibitors. The process achieves higher resolution and selectivity than  
prior art processes, especially in the case of complex biological  
analytical mixtures. It has high sensitivity, even with small amounts of  
samples. The derivatised polymers may be synthesised specifically using  
standard methods  
Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 928  
AAX27533/c  
ID AAX27533 standard; RNA; 20 BP.  
XX AC AAX27533;



XX 27-MAY-1999 (first entry)  
DT Synthetic RNA sequence produced by the method of the invention.  
XX  
DE Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;  
XX cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.  
KW  
XX Synthetic.  
OS  
XX WO9909044-A1.  
PN  
XX 25-FEB-1999.  
PD  
XX 17-AUG-1998; 98WO-EP005215.  
PF  
XX 18-AUG-1997; 97CH-00001931.  
PR  
XX (PITS/) PITSCH S.  
PA (WEIS/) WEISS P A.  
PA (JENN/) JENNY L.  
XX  
PI Pitsch S, Weiss PA, Jenny L;  
XX  
XX WPI; 1999-180963/15.  
DR  
XX 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have  
PT high purity, use in machine synthesis of ribonucleic acids, enable longer  
PT oligonucleotide chain construction, and larger amounts.  
XX  
PS Example 6; Page 25; 38pp; English.  
XX  
CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides  
CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are  
CC intermediates for synthesis of RNA-oligonucleotides with predetermined  
CC nucleotide sequence, particularly by machine synthesis. The groups  
CC specified above, apart from those on silyl, are those particularly for  
CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide  
CC products in diagnosis, therapy, and as research tools, are well known,  
CC and are not dealt with in detail. (II) is an intermediate for (I). The  
CC silyloxymethyl halide reagent is easy to prepare, and yields are high.  
CC introduction of the silyloxymethyl group into the ribonucleoside is  
CC simple and rapid, and the acetal bond formed does not migrate,  
CC eliminating particularly the prior art problem of 2' to 3' isomerisation.  
CC The methylenedioxy group spacer between the silyl group and nucleoside  
CC ring results in less steric hindrance than bulky direct silyloxy  
CC linkages, enabling first, a range of choices for the silyl substituents,  
CC to provide, e.g., acid or base stability; and second, higher yields in  
CC coupling. Purer products are therefore obtained than in prior art,  
CC enabling larger quantities and longer chains of oligoribonucleotides to  
CC be synthesised successfully, and in shorter times  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 929  
AAZ11326  
ID AAZ11326 standard; DNA; 20 BP.  
XX  
AC AAZ11326;  
XX 25-OCT-1999 (first entry)  
DT  
XX Mycobacterial 16S rRNA specific oligo AD12.  
DE  
XX

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;  
KW dendritic cell maturation; infectious disease; immune disorder; cancer;  
KW respiratory system; mycobacterial infection; allergy; tuberculosis;  
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;  
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;  
KW squamous cell carcinoma; melanoma; PCR primer; ss.  
XX  
OS Synthetic.  
OS Mycobacterium vaccae.  
XX  
PN WO9932634-A2.  
XX  
PD 01-JUL-1999.  
XX  
PF 23-DEC-1998; 98WO-NZ000189.  
XX  
PR 23-DEC-1997; 97US-00396624.  
PR 23-DEC-1997; 97US-00997080.  
PR 23-DEC-1997; 97US-00997362.  
PR 11-JUN-1998; 98US-00095855.  
PR 17-SEP-1998; 98US-00156181.  
PR 04-DEC-1998; 98US-00205426.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
XX Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;  
PI WPI; 1999-430163/36.  
XX  
DR Enhancing immune response to an antigen.  
XX  
XX Example 15; Page 177; 243pp; English.  
PS  
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant  
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T  
CC cells and natural killer cells, to stimulate the production of cytokines,  
CC to enhance the expression of co-stimulatory molecules on dendritic cells  
CC and monocytes, and to enhance dendritic cell maturation and function. The  
CC proteins can be expressed by standard recombinant methodology.  
CC Pharmaceutical compositions comprising the proteins or nucleic acid  
CC sequences encoding the proteins can be used for the treatment,  
CC prevention, and detection of disorders including infectious diseases,  
CC immune disorders and cancer. In particular, the compounds and methods are  
CC used for treatment of diseases of the respiratory system, such as  
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,  
CC sarcoidosis and lung cancers, and disorders of the skin such as  
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,  
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell  
CC carcinoma and melanoma  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
RESULT 930  
AAA40449  
ID AAA40449 standard; DNA; 20 BP.  
XX  
AC AAA40449;  
XX  
DT 13-NOV-2000 (first entry)  
XX  
DE Electrochemical detection method sample DNA target.  
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;  
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;

KW plasma; serum; urine; lymph diagnosis; ss.  
XX  
OS Synthetic.  
XX  
PN EP1018646-A2.  
XX  
PD 12-JUL-2000.  
XX  
XX  
PF 07-JAN-2000; 2000EP-00100126.  
XX  
XX  
PR 06-JAN-1999; 99JP-00001111.  
PR 24-MAY-1999; 99JP-00143599.  
XX  
PA (FUJF ) FUJI PHOTO FILM CO LTD.  
XX  
PI Ogawa M, Takenaka S, Takagi M;  
XX  
XX WPI; 2000-444372/39.  
DR  
XX  
XX Quantitative analysis of a biochemical compound such as glucose, in body  
PT a body fluid such as blood, comprising detecting enhanced electron  
PT transfer between an oxidase and a DNA-immobilized electrode, useful for  
PT diagnosis of disease.  
XX  
PS Example 1; Page 8; 14pp; English.  
XX  
CC This invention describes a novel method for quantitatively analysing a  
CC biochemical compound (I) which comprises contacting (I) with double  
CC stranded DNA fixed to the surface of an electrode at their terminals in  
CC which electrochemically active threading intercalators are intercalated,  
CC in an aqueous medium under application of electric potential to the  
CC electrode in the presence of an oxidase which oxidizes the biochemical  
CC compound and becomes reduced, and detecting electric current flowing  
CC between the electrode and a second electrode in the aqueous medium. The  
CC method is useful for detection of biochemical compounds such as glucose,  
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
CC for diagnosis of various diseases. The method allows detection of  
CC biochemical compounds quickly and easily with a high sensitivity using a  
CC simple apparatus. This sequence represents DNA fragment used as a target  
CC sample in the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 931  
AAA40448/c  
ID AAA40448 standard; DNA; 20 BP.  
XX  
AC AAA40448;  
XX  
DT 13-NOV-2000 (first entry)  
XX  
DE Electrochemical detection method fixed probe DNA.  
XX  
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;  
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;  
KW plasma; serum; urine; lymph diagnosis; probe; ss.  
XX  
OS Synthetic.  
XX  
PN EP1018646-A2.  
XX  
PD 12-JUL-2000.  
XX

PF 07-JAN-2000; 2000EP-00100126.  
XX  
PR 06-JAN-1999; 99JP-00001111.  
PR 24-MAY-1999; 99JP-00143599.  
XX  
PA (FUJF ) FUJI PHOTO FILM CO LTD.  
XX  
PI Ogawa M, Takenaka S, Takagi M;  
XX  
XX WPI; 2000-444372/39.  
DR  
XX  
XX Quantitative analysis of a biochemical compound such as glucose, in body  
PT a body fluid such as blood, comprising detecting enhanced electron  
PT transfer between an oxidase and a DNA-immobilized electrode, useful for  
PT diagnosis of disease.  
XX  
PS Example 1; Page 7; 14pp; English.  
XX  
CC This invention describes a novel method for quantitatively analysing a  
CC biochemical compound (I) which comprises contacting (I) with double  
CC stranded DNA fixed to the surface of an electrode at their terminals in  
CC which electrochemically active threading intercalators are intercalated,  
CC in an aqueous medium under application of electric potential to the  
CC electrode in the presence of an oxidase which oxidizes the biochemical  
CC compound and becomes reduced, and detecting electric current flowing  
CC between the electrode and a second electrode in the aqueous medium. The  
CC method is useful for detection of biochemical compounds such as glucose,  
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic  
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph  
CC for diagnosis of various diseases. The method allows detection of  
CC biochemical compounds quickly and easily with a high sensitivity using a  
CC simple apparatus. This sequence represents DNA fragment used as fixed  
CC probe DNA in the method of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 932  
AAZ91117/c  
ID AAZ91117 standard; DNA; 20 BP.  
XX  
AC AAZ91117;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Oligonucleotide #5 for conjugation to abietane derivative.  
XX  
KW Abietane derivative; labelling; diagnostic test; biotin substitute; ss.  
XX  
OS Synthetic.  
XX  
PN FR2781802-A1.  
XX  
PD 04-FEB-2000.  
XX  
PF 31-JUL-1998; 98FR-00010084.  
XX  
PR 31-JUL-1998; 98FR-00010084.  
XX  
PA (INMR ) BIO MERIEUX.  
XX  
PI Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;  
XX  
DR WPI; 2000-239603/21.  
XX

PT Saturated and unsaturated derivatives of abietic acid and their  
PT conjugated derivatives with natural and synthetic polymers, having use in  
PT diagnostics, chemical reactions and analysis.  
XX  
PS Example 5; Page 20; 39pp; French.  
XX  
CC The invention relates to novel saturated and unsaturated abietane  
CC derivatives. The new compounds may be used directly or indirectly in the  
CC development of new diagnostic tests, to follow infections, especially  
CC viral infections, to follow and/or measure chemical products, especially  
CC potential pollutants. In diagnostic tests they may be used as markers, or  
CC to form a universal solid phase after immobilization on a solid support,  
CC to produce monoclonal antibodies or polyclonal antibodies having  
CC diagnostic uses. The oligonucleotides AAZ91113-Z91117 represent examples  
CC of sequences that can be labeled with the new abietane derivatives. The  
CC new derivatives may be used to substitute for biotin in diagnostic tests,  
CC but because they are not found naturally in humans the risk of potential  
CC interactions with biological molecules is eliminated  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 933  
AAA50193/c  
ID AAA50193 standard; DNA; 20 BP.  
XX  
AC AAA50193;  
XX  
DT 07-NOV-2000 (first entry)  
XX  
DE 2'-Methoxyethoxy-modified oligonucleotide.  
XX  
KW Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..19  
FT /\*tag= a  
FT /note= "2'-methoxyethoxy modified thymidine"  
XX  
PN WO200047593-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 11-FEB-2000; 2000WO-US003543.  
XX  
PR 12-FEB-1999; 99US-00250075.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Maier MA;  
XX  
DR WPI; 2000-558188/51.  
XX  
PT Preparation of mixed backbone oligomeric compounds useful as e.g. primers  
PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside  
PT linkages to phosphodiester internucleoside linkages.  
XX  
PS Example 12; Page 34; 49pp; English.  
XX  
CC The present sequence is that of a phosphodiester oligonucleotide  
CC containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5'  
CC ribosyl sugar moiety. It is an example of an oligomeric compound produced  
CC according to the methods of the invention. The invention provides

CC compounds and methods for the preparation of mixed backbone oligomeric,  
CC or chimeric, compounds having phosphodiester internucleoside linkages in  
CC addition to phosphorothioate and/or phosphoramidate internucleoside  
CC linkages. The methods also include incorporation of boranophosphate  
CC internucleoside linkages. The methods utilise H-phosphonate intermediates  
CC that are coupled together forming contiguous regions of 1 or more H-  
CC phosphonate internucleoside linkages. Each contiguous region is  
CC subsequently oxidized to phosphodiester, phosphorothioate,  
CC phosphoroamidate or boranophosphate internucleoside linkages prior to  
CC further elongation. Mixed backbone oligomeric compounds are prepared in  
CC this manner by oxidizing adjacent regions with different reagents.  
CC Oligomeric compounds of the invention are prepared using novel oxidation  
CC steps that oxidize a region of 1 or more H-phosphonate internucleoside  
CC linkages without degrading existing linkages that have been previously  
CC oxidized. The oligonucleotides obtained are useful as primers in PCR,  
CC probes, linkers, gene fragments and for other diagnostic tests on e.g.  
CC biological tissue, fluid, cells etc., as research reagents, and as  
CC antiviral agents  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 934  
AAC87238/c  
ID AAC87238 standard; DNA; 20 BP.  
XX  
AC AAC87238;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.  
XX  
KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;  
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;  
KW antagonist; mimic; inhibitor; drug screening;  
KW cellular target identification; oligonucleotide optimisation;  
KW immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO200067023-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011697.  
XX  
PR 29-APR-1999; 99US-0131830P.  
PR 03-MAR-2000; 2000US-0186845P.  
XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Noll BO, Schetter C, Krieg AM;  
XX  
DR WPI; 2001-016002/02.  
XX  
PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA  
PT functional modifiers, immunostimulatory DNA binding competitors and to  
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.  
XX  
PS Example 1; Page 45; 95pp; English.  
XX  
CC The invention relates to the use of an immunostimulatory single-stranded  
CC DNA-binding protein in screening assays to identify compounds which bind



CC to it and thereby act as functional modifiers of immunostimulatory  
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.  
CC Immunostimulatory DNA-binding proteins can also be used in screening  
CC methods to identify immunostimulatory DNA binding competitors, and to  
CC optimize an immunostimulatory ODN for immune stimulation. Isolated  
CC complexes of an immunostimulatory DNA-binding protein bound to an  
CC immunostimulatory ODN can additionally be used to screen a panel of  
CC candidate target molecules to identify the cellular target molecules of  
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins  
CC used in the methods of the invention are the RNA-binding proteins  
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening  
CC methods are useful for identifying a compound that inhibits interaction  
CC between immunostimulatory DNA and an immunostimulatory DNA-binding  
CC protein and for identifying agonists useful in immunotherapy. The complex  
CC is useful in screening for immunostimulatory DNA cellular target  
CC molecules. The candidate immunostimulatory ODN competitors allow the  
CC investigation of structure/activity relationships of immunostimulatory  
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
CC represents an oligonucleotide used in an exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 935  
AAC87230/c  
ID AAC87230 standard; DNA; 20 BP.  
XX  
AC AAC87230;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.  
XX  
KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;  
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;  
KW antagonist; mimic; inhibitor; drug screening;  
KW cellular target identification; oligonucleotide optimisation;  
KW immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO200067023-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011697.  
XX  
PR 29-APR-1999; 99US-0131830P.  
PR 03-MAR-2000; 2000US-0186845P.  
XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Noll BO, Schetter C, Krieg AM;  
XX WPI; 2001-016002/02.  
XX  
PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA  
PT functional modifiers, immunostimulatory DNA binding competitors and to  
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.  
XX  
PS Example 1; Page 45; 95pp; English.

XX The invention relates to the use of an immunostimulatory single-stranded  
CC DNA-binding protein in screening assays to identify compounds which bind  
CC to it and thereby act as functional modifiers of immunostimulatory  
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity  
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory  
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.  
CC Immunostimulatory DNA-binding proteins can also be used in screening  
CC methods to identify immunostimulatory DNA binding competitors, and to  
CC optimize an immunostimulatory ODN for immune stimulation. Isolated  
CC complexes of an immunostimulatory DNA-binding protein bound to an  
CC immunostimulatory ODN can additionally be used to screen a panel of  
CC candidate target molecules to identify the cellular target molecules of  
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins  
CC used in the methods of the invention are the RNA-binding proteins  
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening  
CC methods are useful for identifying a compound that inhibits interaction  
CC between immunostimulatory DNA and an immunostimulatory DNA-binding  
CC protein and for identifying agonists useful in immunotherapy. The complex  
CC is useful in screening for immunostimulatory DNA cellular target  
CC molecules. The candidate immunostimulatory ODN competitors allow the  
CC investigation of structure/activity relationships of immunostimulatory  
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence  
CC represents an oligonucleotide used in an exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 936  
AAC87241/c  
ID AAC87241 standard; DNA; 20 BP.  
XX  
AC AAC87241;  
XX  
DT 09-MAR-2001 (first entry)  
XX  
DE Poly T oligonucleotide, SEQ ID NO:20.  
XX  
KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;  
KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;  
KW hnRNP A1; lupus La protein; functional modifier identification; agonist;  
KW antagonist; mimic; inhibitor; drug screening;  
KW cellular target identification; oligonucleotide optimisation;  
KW immunotherapy; ss.  
XX  
OS Synthetic.  
XX  
PN WO200067023-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011697.  
XX  
PR 29-APR-1999; 99US-0131830P.  
PR 03-MAR-2000; 2000US-0186845P.  
XX  
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Noll BO, Schetter C, Krieg AM;  
XX WPI; 2001-016002/02.  
XX  
PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA  
PT functional modifiers, immunostimulatory DNA binding competitors and to



PT optimize immunostimulatory oligodeoxynucleotides for stimulation.

XX

PS Example 1; Page 45; 95pp; English.

XX

CC The invention relates to the use of an immunostimulatory single-stranded

CC DNA-binding protein in screening assays to identify compounds which bind

CC to it and thereby act as functional modifiers of immunostimulatory

CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity

CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory

CC DNA mimics, and immunostimulatory DNA agonists and antagonists.

CC Immunostimulatory DNA-binding proteins can also be used in screening

CC methods to identify immunostimulatory DNA binding competitors, and to

CC optimize an immunostimulatory ODN for immune stimulation. Isolated

CC complexes of an immunostimulatory DNA-binding protein bound to an

CC immunostimulatory ODN can additionally be used to screen a panel of

CC candidate target molecules to identify the cellular target molecules of

CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins

CC used in the methods of the invention are the RNA-binding proteins

CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening

CC methods are useful for identifying a compound that inhibits interaction

CC between immunostimulatory DNA and an immunostimulatory DNA-binding

CC protein and for identifying agonists useful in immunotherapy. The complex

CC is useful in screening for immunostimulatory DNA cellular target

CC molecules. The candidate immunostimulatory ODN competitors allow the

CC investigation of structure/activity relationships of immunostimulatory

CC DNA-binding proteins and immunostimulatory ODNs. The present sequence

CC represents an oligonucleotide used in an exemplification of the invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 937

AAS10402/C

ID AAS10402 standard; DNA; 20 BP.

XX

AC AAS10402;

XX

DT 24-OCT-2001 (first entry)

XX

DE DNA template for 3' end labeling of an RNA molecule, #14.

XX

KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.

XX

OS Synthetic.

XX

PN US6238865-B1.

XX

PD 29-MAY-2001.

XX

PF 16-OCT-1998; 98US-00173936.

XX

PR 17-OCT-1997; 97US-0063757P.

XX

PA (CHEN/) CHEN G.

PA (HUAN/) HUANG Z.

PA (SZOS/) SZOSTAK J W.

XX

PI Huang Z, Szostak JW;

XX

DR WPI; 2001-366470/38.

XX

PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for

PT labeling and modifying 3'-termini of other nucleic acids, comprises using

PT a synthetic nucleotide template with a defined overhang nucleotide.

XX

PS Example 5; Col 13; 22pp; English.

XX

CC The sequence represents a synthetic DNA template molecule used to

CC demonstrate the method of the invention. The invention relates to a

CC method of modifying (e.g. 3' end labeling with 32P dATP) the 3' terminus

CC of an RNA molecule by providing a DNA oligonucleotide, complementary to

CC the 3' end of the RNA molecule, with an overhang at the 5' end which

CC allows incorporation of the labeling nucleotide into the RNA molecule.

CC The method, based on the synthesis of Okazaki fragments, is useful for

CC labeling and modifying the 3'-termini of other nucleic acids such as DNA

CC fragments. The method is a simple and efficient way of labeling or

CC modifying RNA 3'-termini using DNA polymerase and a synthetic template

CC with defined overhang nucleotides

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 938

AAD16997/C

ID AAD16997 standard; DNA; 20 BP.

XX

AC AAD16997;

XX

DT 29-NOV-2001 (first entry)

XX

DE Capture probe CP5'.

XX

KW Scaffold protein; antibody mimic; fibronectin type III domain;

KW randomised loop; randomised beta-sheet; diagnostic purpose;

KW protein designing; probe; tenth module of human Fn3; 10Fn3;

KW fibronectin module of type III; Fn3; ss.

XX

OS Unidentified.

XX

PN WO200164942-A1.

XX

PD 07-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US006414.

XX

PR 29-FEB-2000; 2000US-00515260.

XX

PA (PHYL-) PHYLLOS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2001-557782/62.

XX

PT Fibronectin scaffold protein array for obtaining a protein/compound which

PT binds to a compound/protein, comprises a fibronectin type III domain

PT having a randomized loop, a randomized beta-sheet or their combination.

XX

PS Disclosure; Page 41; 67pp; English.

XX

CC The present invention relates to an array of proteins (antibody mimics)

CC comprising a fibronectin type III domain having a randomised loop, a

CC randomised beta-sheet, or their combination, and has the capacity to bind

CC to a compound that is not bound by a corresponding naturally- occurring

CC fibronectin, immobilised onto a solid support. The antibody mimics is

CC useful for detecting a compound preferably a protein, in a biological

CC sample. It is also useful to detect one or more different analytes

CC simultaneously in a sample. Hence is useful for diagnostic purposes. It

CC is also useful for the purpose of designing proteins capable of binding

CC to virtually any compound of interest. The present sequence is a capture

CC probe used to self-assemble and anchor the tenth module of human

CC fibronectin module of type III (Fn3) (10Fn3) which is used in an  
CC exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other; 0;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAA 2  
  
RESULT 939  
AAF60896  
ID AAF60896 standard; DNA; 20 BP.  
XX  
AC AAF60896;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Conjugate forming oligonucleotide ON5 SEQ ID 5.  
XX  
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;  
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;  
KW tumor therapy; drug; phosphodiester linkage; ss.  
XX  
OS Unidentified.  
XX  
PN DE19935302-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-1999; 99DE-01035302.  
XX  
PR 28-JUL-1999; 99DE-01035302.  
XX  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
XX  
PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;  
XX  
DR WPI; 2001-203679/21.  
XX  
PT New substituted aryl conjugates of parent molecules, especially  
PT oligonucleotides, having improved transmembrane and intracellular  
PT transport properties, useful as medicaments or diagnostic agents.  
XX  
PS Disclosure; Page 9; 28pp; German.  
XX  
CC This invention describes a novel conjugate (I) which consists of (A) a  
CC molecule to be transported and (B) at least one aryl residue of formula -  
CC Ar-(X-C(Y)-R<sub>1</sub>)<sub>n</sub> (II). Ar = group containing at least one aromatic ring;  
CC X = O or N (sic); Y = O, S or NH-R<sub>2</sub> (sic); R<sub>1</sub> = optionally substituted  
CC 1-23C alkyl (optionally containing double and/or triple bonds); R<sub>2</sub> =  
CC optionally substituted 1-18C alkyl (optionally containing double and/or  
CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or  
CC via a chemical group, provided that the chemical group is other than CH<sub>2</sub>  
CC -S if the bond is via a phosphodiester linkage of (A). The invention also  
CC describes (i) the preparation of a conjugate (I') of (A') a molecule to  
CC be transported and (B') at least one aryl residue (not restricted to  
CC (II)), by preparing (A') containing a reactive function at the position  
CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');  
CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical  
CC group) for transporting (A) across biological membranes. The products of  
CC the invention have cytostatic, virucide, vasotropic, dermatological,  
CC antipsoriatic and antiasthmatic activity and can be used for gene  
CC therapy. Conjugation of (A) with (B) is useful for transporting (A)  
CC across biological membranes or into eukaryotic or prokaryotic cells  
CC (specifically bacterial, yeast or mammalian cells, including human cells,  
CC particularly tumor cells). Medicaments, diagnostic agents and test kits  
CC containing (I) are also claimed. Typically (I) are antisense  
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for

CC treating viral infections or diseases associated with integrins or cell-  
CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or  
CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ  
CC hybridization. Conjugation with (B) markedly improves the cellular uptake  
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,  
CC in which case the conjugates (I) are fluorescently labeled, allowing  
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)  
CC is superior to that obtained using other conjugated groups related to  
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within  
CC the scope of (B)) have superior uptake to corresponding fluorescein  
CC conjugates  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 940  
AAS63428  
ID AAS63428 standard; DNA; 20 BP.  
XX  
AC AAS63428;  
XX  
DT 29-JAN-2002 (first entry)  
XX  
DE Oligonucleotide-nanoparticle probe #52.  
XX  
KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;  
KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;  
KW ss.  
XX  
OS Synthetic.  
XX  
PN WO200173123-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 28-MAR-2001; 2001WO-US010071.  
XX  
PR 28-MAR-2000; 2000US-0192699P.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
PR 26-JUN-2000; 2000US-0213906P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Park S, Li Z;  
XX  
DR WPI; 2001-656926/75.  
XX  
PT Detecting and separating nucleic acid, useful e.g. for diagnosis,  
PT comprises reaction with nanoparticles that carry oligonucleotides  
PT complementary to parts of the target.  
XX  
PS Example 18; Page 158; 404pp; English.  
XX  
CC The invention relates to a method for detection of nucleic acid (I)  
CC having at least 2 portions, comprising treatment with nanoparticles that  
CC carry oligonucleotides complementary to at least 2 parts of (I), where  
CC detectable change caused by hybridisation of the oligonucleotide to (I)  
CC is observed. The method is used to detect (or to separate) specific (I),  
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic

CC analysis etc., and generally to detect analytes other than (I). The  
CC oligonucleotide-derivatised nanoparticles are also useful for preparing  
CC nanostructures useful, for example, as biochips, biofilters, mechanical  
CC devices, separation membranes, chemical sensors, in computers, and for  
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be  
CC produced, allowing their direct use (as probes) in polymerase chain  
CC reaction, i.e. they survive multiple heating/cooling cycles so do not  
CC need to be added after amplification. (I) are detected by simple colour  
CC change, without the need for special equipment, making possible rapid  
CC field testing for e.g. pathogens. AAS63374-AAS63448 represent  
CC oligonucleotide-nanoparticle probes, and related sequences, used in the  
CC method of the invention

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 941

AAF28481  
ID AAF28481 standard; DNA; 20 BP.

XX  
AC AAF28481;

XX  
DT 03-APR-2001 (first entry)

XX  
DE Random oligonucleotide, SEQ ID NO: 53.

XX  
KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;  
KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;  
KW cell line authentication; gene therapy; ss.

XX  
OS Synthetic.

XX  
PN WO200100876-A1.

XX  
PD 04-JAN-2001.

XX  
PF 26-JUN-2000; 2000WO-US017507.

XX  
PR 25-JUN-1999; 99US-00344667.

XX  
PR 26-APR-2000; 2000US-0200161P.

XX  
PA (MIRK/) MIRKIN C A.

PA (LETS/) LETSINGER R L.

PA (MUCI/) MUCIC R C.

PA (STOR/) STORHOFF J J.

PA (ELGH/) ELGHANIAN R.

PA (TATO/) TATON T A.

XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;

XX  
DR WPI; 2001-061976/07.

XX  
PT Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics  
PT and DNA sequencing, comprises observing detectable change brought about  
PT by hybridization of nucleic acid with substrate or particle bound  
PT oligonucleotides.

XX  
PS Disclosure; Page 199; 205pp; English.

XX  
CC The present sequence is an oligonucleotide used in a method for detecting  
CC a nucleic acid having at least 2 portions. The method comprises  
CC hybridising the nucleic acid with oligonucleotides, such as the present  
CC sequence, attached to a substrate and/or particle and detecting a change  
CC in colour, conductivity or optical density. The method is useful for the

CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,  
CC for paternity testing, for cell line authentication and for monitoring  
CC gene therapy. Detecting nucleic acids based upon observing a colour  
CC change is cheap, fast, simple, and does not require specialised or  
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain  
CC stable for at least 6 months. A single base mismatch and as little as 20  
CC femtomoles (fM) of target can be detected using the conjugates

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 942

AAS10371  
ID AAS10371 standard; DNA; 20 BP.

XX  
AC AAS10371;

XX  
DT 24-OCT-2001 (first entry)

XX  
DE Oligonucleotide-cyclic disulphide linker, d.

XX  
KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
KW DNA isolation; genetic disease; bacterial disease; viral disease;  
KW forensic science; paternity testing; gene therapy; ss.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers

FT misc\_feature 1

FT /\*tag= a

FT /note= "A is covalently linked to a cyclic-disulphide moiety"

XX  
PN WO200151665-A2.

XX  
PD 19-JUL-2001.

XX  
PF 12-JAN-2001; 2001WO-US001190.

XX  
PR 13-JAN-2000; 2000US-0176409P.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

PR 12-JAN-2001; 2001US-00760500.

XX  
PA (NANO-) NANOSPHERE INC.

XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Li Z;

XX  
DR WPI; 2001-451868/48.

XX  
PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or  
PT viral diseases, by contacting the nucleic acid with oligonucleotides  
PT attached to nanoparticles and having sequences complementary a portion of  
PT the nucleic acid.

XX  
PS Example 24; Fig 44; 323pp; English.

XX  
CC The sequence represents a cyclic disulphide linked oligonucleotide which  
CC may be coupled with colloidal gold particles (nanoparticles) and used to  
CC demonstrate the method of the invention. The invention relates to  
CC isolating or detecting a nucleic acid of interest, in a mixture of  
CC nucleic acids, by binding it to 2 or more complementary nucleotides which  
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.  
CC colloidal gold) are used to both isolate and detect (e.g. by linking the



CC particle to a fluorescent probe) the resultant complex. The methods are  
CC useful for detecting nucleic acids, natural or synthetic, and modified or  
CC unmodified. The methods may also be applied in the diagnosis of genetic,  
CC bacterial and viral diseases, in forensics, in DNA sequencing, for  
CC paternity testing, for cell line authentication, and for monitoring gene  
CC therapy. The methods are further useful in research and analytical  
CC laboratories in DNA sequencing, in the field to detect the presence of  
CC specific pathogens, for quick identification of an infection to assist in  
CC drug prescription, and in homes and health centres for inexpensive first-  
CC line screening. The methods, which are based on observing colour change  
CC with the naked eye, are cheap, fast, simple, robust (reagents are  
CC stable), do not require specialised or expensive equipment, and little or  
CC no instrumentation is required

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 943  
AAF99427/C  
ID AAF99427 standard; DNA; 20 BP.  
XX  
AC AAF99427;  
XX  
DT 12-JUN-2001 (first entry)  
XX  
DE Immunostimulatory nucleic acid #543.  
XX  
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

OS Synthetic.  
XX  
PN WO200122972-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 25-SEP-2000; 2000WO-US026383.  
XX  
PR 25-SEP-1999; 99US-0156113P.  
PR 27-SEP-1999; 99US-0156135P.  
PR 23-AUG-2000; 2000US-0227436P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX  
PI Krieg AM, Schetter C, Vollmer J;

XX  
DR WPI; 2001-273485/28.  
XX  
PT Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.

PS Claim 101; Page 49; 338pp; English.  
XX  
CC The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or

CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 944  
AAF99099/c  
ID AAF99099 standard; DNA; 20 BP.  
XX  
AC AAF99099;  
XX  
DT 12-JUN-2001 (first entry)  
XX  
DE Immunostimulatory nucleic acid #215.  
XX  
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

OS Synthetic.  
XX  
PN WO200122972-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 25-SEP-2000; 2000WO-US026383.  
XX  
PR 25-SEP-1999; 99US-0156113P.  
PR 27-SEP-1999; 99US-0156135P.  
PR 23-AUG-2000; 2000US-0227436P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.

XX  
PI Krieg AM, Schetter C, Vollmer J;  
XX  
DR WPI; 2001-273485/28.  
XX  
PT Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.

PS Claim 101; Page 42; 338pp; English.

XX  
CC The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone

XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;



```
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 945
AAF99431
ID AAF99431 standard; DNA; 20 BP.
XX AC AAF99431;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #547.
XX KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Vollmer J;
XX WPI; 2001-273485/28.
XX Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids.
XX Claim 101; Page 49; 338pp; English.
XX The present invention relates to a method for stimulating an immune
XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells. Note: the
XX present sequence may have a phosphorothioate backbone
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAA 19
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RESULT 946
AAH46465/C
ID AAH46465 standard; DNA; 20 BP.
XX AC AAH46465;
XX DT 14-SEP-2001 (first entry)
XX DE Oligonucleotide #13.
XX KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All bases are phosphorothioate"
FT modified_base 1
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Modified with 2'-O-methyl"
XX US6242591-B1.
XX PN 05-JUN-2001.
XX PD 11-JAN-2000; 2000US-00481486.
XX PF 15-OCT-1997; 97US-00950779.
XX PR (ISIS-) ISIS PHARM INC.
XX PA Cole DL, Ravikumar VT, Cheruvallath ZS;
XX PI WPI; 2001-407218/43.
XX DR Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
XX useful in biological research, comprises phosphorylating the 5'-hydroxyl
XX of a nucleic acid having a nucleoside with a 2' modification.
XX Example 23; Col 11; 7pp; English.
XX The present invention relates to a method for preparing phosphorothioate
XX oligonucleotides having at least one nucleoside with a 2' modification.
XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
XX group having at least one nucleoside with a 2' modification in an
XX acetonitrile. The present sequence was used to illustrate the method of
XX the present invention. The method is useful for synthesising sulphurised
XX 2' substituted phosphorothioate oligonucleotides, which may be used in
XX molecular biological research, in applications such as anti-viral
XX therapy, and for determining the stereochemical pathways of certain
XX enzymes which recognise nucleic acids
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAA 2

RESULT 947
AAH78547
ID AAH78547 standard; cDNA; 20 BP.
XX AC AAH78547;
XX
```

DT 10-DEC-2001 (first entry)  
XX Nucleotide sequence of a cDNA sequence.  
DE  
XX  
KW Nucleic acid identification; DNA library screening; ss.  
XX  
OS Synthetic.  
XX  
PN US6274321-B1.  
XX  
PD 14-AUG-2001.  
XX  
PF 03-DEC-1999; 99US-00454704.  
XX  
PR 03-DEC-1999; 99US-00454704.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Blumberg B;  
XX  
DR WPI; 2001-588900/66.  
XX  
PT Screening nucleic acids (NA) in pool of interest comprises pooling,  
PT expressing NA to form expression product pool and identifying NA in NA  
PT pool corresponding to expression product pool having interaction with  
PT target moiety.  
XX  
PS Disclosure; Col 22; 19pp; English.  
XX  
CC The specification describes a method for identifying a nucleic acid in a  
CC pool of interest. The method comprises pooling individually identifiable  
CC nucleic acids into at least two pools of one nucleic acid each;  
CC expressing nucleic acid pools to obtain protein expression product pools;  
CC assaying protein expression product pools for products having interaction  
CC with target molecule; selecting nucleic acid pools corresponding to  
CC identified protein expression product pools; and identifying individual  
CC nucleic acids in identified nucleic acid pools. The method is useful for  
CC identifying a nucleic acid (e.g. cDNA) in a pool of interest and for  
CC functionally screening several nucleic acids. The method is also useful  
CC for screening genomic DNA libraries or other source of individual cDNAs,  
CC mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries.  
CC The present sequence was used in the course of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 948  
AAF28351  
ID AAF28351 standard; DNA; 20 BP.  
XX  
AC AAF28351;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE DNA oligomer #1.  
XX  
KW Deoxynucleic S-Methythiourea; DNmt; antisense therapy;  
KW cardiovascular disease; inflammatory disease; neurocellular disease;  
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;  
KW influenza; herpes; infection; ss.  
XX  
OS Unidentified.  
XX  
PN US6169176-B1.  
XX

PD 02-JAN-2001.  
XX  
PF 28-SEP-1999; 99US-00407675.  
XX  
PR 02-JUL-1998; 98US-0091481P.  
PR 11-DEC-1998; 98US-0111800P.  
PR 02-JUL-1999; 99US-00347443.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Dev AP, Bruice TC;  
XX  
DR WPI; 2001-122276/13.  
XX  
PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in  
PT antisense therapy, by synthesizing oligonucleotides comprising backbone  
PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.  
XX  
PS Example 7; Fig 16; 48pp; English.  
XX  
CC The present sequence was used to demonstrate the ability of deoxynucleic  
CC S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An  
CC increase in the C content of the oligos resulted in a large decrease in  
CC binding. This experiment was performed as an example of a method for  
CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy  
CC thiourea linkages. The method is useful for preparing oligonucleotides  
CC for use in antisense or antigenic therapy, to inhibit production of  
CC proteins associated with genetic diseases, cardiovascular, inflammatory  
CC and neurocellular diseases, and for antiviral therapy, e.g. to treat  
CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes  
CC infections. The compounds are also useful as diagnostic reagents to  
CC detect the presence or absence of the target DNA or RNA sequences to  
CC which they specifically bind and by antagonising the normal biological  
CC activity of a target protein, they can be used in the manipulation of  
CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue  
CC cultures. The method provides an efficient and rapid solid-phase method  
CC for the synthesis of thiourea and S-methylthiourea  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 949  
ABS77742/C  
ID ABS77742 standard; DNA; 20 BP.  
XX  
AC ABS77742;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #226.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
PD 11-JUL-2002.



PS Claim 2; Page 29; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma, and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

XX acid of the invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 952

ABL39402/c

ID ABL39402 standard; DNA; 20 BP.

XX

AC ABL39402;

XX

DT 16-APR-2002 (first entry)

XX

DE Immunostimulatory nucleic acid SEQ ID NO: 838.

XX

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.

KW

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "phosphorothioate backbone"

XX

PN WO200197843-A2.

XX

PD 27-DEC-2001.

XX

PF 22-JUN-2001; 2001WO-US020154.

XX

PR 22-JUN-2000; 2000US-0213346P.

XX

PA (IOWA ) UNIV IOWA RES FOUND.

XX

PI Weiner G, Hartmann G;

XX

DR WPI; 2002-154611/20.

XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

XX

PS Disclosure; Page 309; 312pp; English.

XX

CC The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

PS Claim 2; Page 29; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma, and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

XX acid of the invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 952

ABL38648

ID ABL38648 standard; DNA; 20 BP.

XX

AC ABL38648;

XX

DT 16-APR-2002 (first entry)

XX

DE Immunostimulatory nucleic acid SEQ ID NO: 2.

XX

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

KW angiogenesis; metastasis; cytostatic; ss.

KW

XX

OS Synthetic.

XX

XX WO200197843-A2.

PN

PD 27-DEC-2001.

XX

PF 22-JUN-2001; 2001WO-US020154.

XX

PR 22-JUN-2000; 2000US-0213346P.

XX

PA (IOWA ) UNIV IOWA RES FOUND.

XX

PI Weiner G, Hartmann G;

XX

DR WPI; 2002-154611/20.

XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

XX

PS Disclosure; Page 95; 312pp; English.

XX

CC The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression

PS Claim 2; Page 29; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma, and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic

XX acid of the invention

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 953

ABL38648

ID ABL38648 standard; DNA; 20 BP.

XX

AC ABL38648;

XX

DT 16-APR-2002 (first entry)

XX

DE Immunostimulatory nucleic acid SEQ ID NO: 2.

XX

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;

KW angiogenesis; metastasis; cytostatic; ss.

KW

XX

OS Synthetic.

XX

XX WO200197843-A2.

PN

PD 27-DEC-2001.

XX

PF 22-JUN-2001; 2001WO-US020154.

XX

PR 22-JUN-2000; 2000US-0213346P.

XX

PA (IOWA ) UNIV IOWA RES FOUND.

XX

PI Weiner G, Hartmann G;

XX

DR WPI; 2002-154611/20.

XX

PT Treating or preventing cancer, such as basal cell carcinoma, comprises

PT administering immunostimulatory nucleic acids that induce expression of

PT cell surface antigens and antibodies to a subject having or at risk of

PT developing cancer.

XX

PS Disclosure; Page 95; 312pp; English.

XX

CC The present invention relates to methods for treating or preventing

CC cancer, involving administering to a subject having or at risk of

CC developing cancer immunostimulatory nucleic acids that induce expression



```
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 954
ABL39403/C
ID ABL39403 standard; DNA; 20 BP.
XX AC ABL39403;
XX DT 16-APR-2002 (first entry)
XX DE Immunostimulatory nucleic acid SEQ ID NO: 839.
XX KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
XX KW angiogenesis; metastasis; cytostatic; ss.
XX OS Synthetic.
XX PN WO200197843-A2.
XX PD 27-DEC-2001.
XX PF 22-JUN-2001; 2001WO-US020154.
XX PR 22-JUN-2000; 2000US-0213346P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Weiner G, Hartmann G;
XX WPI; 2002-154611/20.
XX DR Treating or preventing cancer, such as basal cell carcinoma, comprises
XX PT administering immunostimulatory nucleic acids that induce expression of
XX PT cell surface antigens and antibodies to a subject having or at risk of
XX PT developing cancer.
XX PS Disclosure; Page 309; 312pp; English.
XX CC The present invention relates to methods for treating or preventing
XX CC cancer, involving administering to a subject having or at risk of
XX CC developing cancer immunostimulatory nucleic acids that induce expression
XX CC of cell surface antigens and antibodies. The methods are useful for
XX CC treating or preventing cancer such as basal cell carcinoma, bladder
XX CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX CC breast cancer, cervical cancer, colon and rectum cancer, connective
XX CC tissue cancer, oesophageal cancer; eye cancer, kidney cancer, larynx
XX CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
XX CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX CC present sequence is an immunostimulatory oligonucleotide described in the
XX CC exemplification of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2
```

```
RESULT 955
ABL54775/C
ID ABL54775 standard; DNA; 20 BP.
XX AC ABL54775;
XX DT 10-JUN-2002 (first entry)
XX DE CD14 receptor PCR primer SEQ ID NO 9.
XX KW Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;
XX KW single-nucleotide polymorphism; PCR; primer; ss.
XX OS Synthetic.
XX PN JP2002034599-A.
XX PD 05-FEB-2002.
XX PF 26-JUL-2000; 2000JP-00225354.
XX PR 26-JUL-2000; 2000JP-00225354.
XX PA (TOYM ) TOYOCO KK.
XX WPI; 2002-275727/32.
XX DR Detecting 1 base polymorphism on a sequence of a chromosome or it's
XX PT fragment.
XX PT Example 2; Page 10; 10pp; Japanese.
XX PS The invention relates to a method for detecting 1 base polymorphism on
XX CC the sequence of a chromosome or its fragment in which a sample nucleic
XX CC acid is reacted with a reaction liquor containing a nucleic acid primer
XX CC having a base adjacent to the polymorphic base at its 3'-end, one
XX CC dideoxynucleotide corresponding to a polymorphic base having a
XX CC distinguishable feature or its mixture, DNA polymerase and a composition
XX CC required for its activity expression to detect the presence of taking
XX CC dideoxynucleotide in the nucleic acid primer and to detect the type of
XX CC the base to be specified. The method is used for detecting 1 base
XX CC polymorphism on the sequence of a chromosome or its fragment. The present
XX CC sequence is that of a PCR primer, useful in examples of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 956
ABK65035
ID ABK65035 standard; DNA; 20 BP.
XX AC ABK65035;
XX DT 02-JUL-2002 (first entry)
XX DE Nanoparticle-oligonucleotide #55.
XX KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
XX KW ss.
XX OS Synthetic.
XX PN WO200218643-A2.
```



PN EP1176151-A1.  
XX  
PD 30-JAN-2002.  
XX  
PF 27-JUL-2001; 2001BP-00118360.  
XX  
PR 28-JUL-2000; 2000US-00627249.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;  
XX  
DR WPI; 2002-156732/21.  
XX  
PT Synthesis of polynucleotide useful during fabrication of an array.  
PT involves coupling nucleoside phosphoramidite and a solid-supported  
PT nucleoside and treating the product with an oxidation/deprotection  
PT composition.  
XX  
PS Example 1; Page 15; 36pp; English.  
XX  
CC The present invention relates to a method for the synthesis of a  
CC polynucleotide which involves coupling a second nucleoside to a first  
CC nucleoside through a phosphite linkage, where the second nucleoside has a  
CC non-carbonate protecting group protecting a hydroxyl, and exposing the  
CC product to a composition which concurrently oxidizes the phosphite formed  
CC to a phosphate and deprotects the protected hydroxyl of the second  
CC nucleoside. The method is useful for synthesizing the polynucleotides,  
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for  
CC fabricating an addressable array of polynucleotides on a substrate. The  
CC present sequence is an oligonucleotide produced to demonstrate the method  
CC of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAA 2  
  
RESULT 959  
ABL36232  
ID ABL36232 standard; DNA; 20 BP.  
XX  
AC ABL36232;  
XX  
DT 08-APR-2002 (first entry)  
XX  
DE M tuberculosis rRNA probe SEQ ID NO: 83.  
XX  
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;  
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;  
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;  
KW Th2 immune response; immunomodulatory; probe; ss.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN US6328978-B1.  
XX  
PD 11-DEC-2001.  
XX  
PF 02-JUN-1999; 99US-00324542.  
XX  
PR 23-DEC-1997; 97US-00997080.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Watson JD, Tan PLJ, Prestidge R;  
XX

DR WPI; 2002-138361/18.  
XX  
PT Inhibiting skin inflammation associated with skin disorder e.g.  
PT psoriasis, by administering composition comprising delipidated and  
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae  
PT culture filtrate.  
XX  
PS Example 5; Col 99-100; 116pp; English.  
XX  
CC The present invention relates to a method of inhibiting skin inflammation  
CC associated with a skin disorder selected from psoriasis, atopic  
CC dermatitis and allergic contact dermatitis, which involves administering  
CC a composition containing delipidated and deglycolipidated Mycobacterium  
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be  
CC treated may also include alopecia areata, and skin cancers such as basal  
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition  
CC acts by inhibiting the Th2 immune response. The present sequence is a  
CC probe described in the exemplification of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 960  
ABS64673  
ID ABS64673 standard; DNA; 20 BP.  
XX  
AC ABS64673;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Nucleic acid detection method associated polynucleotide #55.  
XX  
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;  
KW nanoparticle; viral RNA detection; bacterial DNA detection;  
KW fungal DNA detection; nanoprobe conjugate; ss.  
XX  
OS Synthetic.  
XX  
PN WO200246472-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 07-DEC-2001; 2001WO-US046418.  
XX  
PR 08-DEC-2000; 2000US-0254392P.  
PR 08-DEC-2000; 2000US-0254418P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 11-DEC-2000; 2000US-0255236P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
PR 09-APR-2001; 2001US-0282640P.  
PR 10-AUG-2001; 2001US-00927777.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
DR WPI; 2002-608256/65.  
XX  
PT Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change.  
XX  
PS Example 18; Page 437; 442pp; English.

XX The invention describes a method of detecting (M1) a nucleic acid having  
CC two portions, involving providing nanoparticles having oligonucleotides  
CC attached to it, which has a sequence complementary to sequence of two  
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to  
CC allow hybridisation of oligonucleotides with two or more portions of  
CC nucleic acid, and observing a detectable change brought about by  
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide  
CC conjugates (II) and the aggregate probe are useful for detecting two or  
CC more nucleic acids (from a biological source) having at least two  
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated  
CC with a disease, synthetic, or structurally-modified natural or synthetic  
CC RNA or DNA, or a product of a polymerase chain reaction amplification.  
CC (II) is useful for preparing a nanoprobe conjugate for detecting an  
CC analyte, and for detecting a nucleic acid bound to an electrode surface.  
CC (I) and (II) are useful for fabrication, and for separating a selected  
CC nucleic acid having two portions from other nucleic acids. (I), (II) and  
CC the aggregate probe are useful for detecting an analyte (especially  
CC polyvalent analyte) in a sample. This sequence represents a  
CC polynucleotide used to demonstrate the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19  
RESULT 961  
ABS64688  
ID ABS64688 standard; DNA; 20 BP.  
XX  
AC ABS64688;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Nucleic acid detection method associated polynucleotide #70.  
XX  
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;  
KW nanoparticle; viral RNA detection; bacterial DNA detection;  
KW fungal DNA detection; nanoprobe conjugate; ss.  
XX  
OS Synthetic.  
XX  
PN WO200246472-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 07-DEC-2001; 2001WO-US046418.  
XX  
PR 08-DEC-2000; 2000US-0254392P.  
PR 08-DEC-2000; 2000US-0254418P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 11-DEC-2000; 2000US-0255236P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
PR 09-APR-2001; 2001US-0282640P.  
PR 10-AUG-2001; 2001US-00927777.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX WPI; 2002-608256/65.  
DR  
XX  
XX Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change.

XX Example 24; Fig 44; 442pp; English.  
XX  
CC The invention describes a method of detecting (M1) a nucleic acid having  
CC two portions, involving providing nanoparticles having oligonucleotides  
CC attached to it, which has a sequence complementary to sequence of two  
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to  
CC allow hybridisation of oligonucleotides with two or more portions of  
CC nucleic acid, and observing a detectable change brought about by  
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide  
CC conjugates (II) and the aggregate probe are useful for detecting two or  
CC more nucleic acids (from a biological source) having at least two  
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated  
CC with a disease, synthetic, or structurally-modified natural or synthetic  
CC RNA or DNA, or a product of a polymerase chain reaction amplification.  
CC (II) is useful for preparing a nanoprobe conjugate for detecting an  
CC analyte, and for detecting a nucleic acid bound to an electrode surface.  
CC (I) and (II) are useful for fabrication, and for separating a selected  
CC nucleic acid having two portions from other nucleic acids. (I), (II) and  
CC the aggregate probe are useful for detecting an analyte (especially  
CC polyvalent analyte) in a sample. This sequence represents a  
CC polynucleotide used to demonstrate the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19  
RESULT 962  
ABN87103/C  
ID ABN87103 standard; DNA; 20 BP.  
XX  
AC ABN87103;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE Capture probe CP5' SEQ ID NO:23.  
XX  
KW Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO200232925-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 16-OCT-2001; 2001WO-US032233.  
XX  
PR 16-OCT-2000; 2000US-00688566.  
XX  
PA (PHYL-) PHYLOS INC.  
XX  
PI Lipovsek D, Wagner RW, Kuimelis RG;  
XX WPI; 2002-444238/47.  
DR  
XX  
XX New non-antibody proteins having an immunoglobulin fold, useful in  
PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
PT designing proteins with specific properties, e.g. for binding any antigen  
PT of interest.  
XX  
XX Disclosure; Page 58; 94pp; English.  
XX  
CC The present invention describes a non-antibody protein, comprising a  
CC domain having an immunoglobulin-like fold, derived from a reference  
CC protein having a mutated amino acid sequence, where the non-antibody



CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
CC not bound as tightly by the reference protein. The non-antibody protein  
CC is useful as scaffolds for selecting or designing a protein framework  
CC with specific and favourable properties, e.g. for binding any antigen of  
CC interest, or for destroying or inactivating antibody molecules. The non-  
CC antibody protein is also useful in all areas where antibodies are used,  
CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
CC binding proteins useful in the above-mentioned fields. The present  
CC proteins have thermodynamic properties superior to those of natural  
CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
CC antibody mimics exhibit improved biophysical properties, such as  
CC stability under reducing conditions and solubility at high  
CC concentrations. In addition, these molecules are readily expressed and  
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention

XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 963

ABZ88267  
ID ABZ88267 standard; DNA; 20 BP.

XX  
AC ABZ88267;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiqunone.

XX Disclosure; SEQ ID NO 3509; 872pp; English.

PS  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiqunone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiqunone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 964

ABZ88565  
ID ABZ88565 standard; DNA; 20 BP.

XX  
AC ABZ88565;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiqunone.

XX Disclosure; SEQ ID NO 3807; 872pp; English.

PS  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 965

ABZ88619  
ID ABZ88619 standard; DNA; 20 BP.

XX  
AC ABZ88619;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 3861; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 966

ABZ89705

ID ABZ89705 standard; DNA; 20 BP.

XX  
AC ABZ89705;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4947; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 967

ABZ88816  
ID ABZ88816 standard; DNA; 20 BP.

XX  
AC ABZ88816;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX  
PD 31-OCT-2002.

XX  
PF 23-APR-2002; 2002WO-US013135.

XX  
PR 24-APR-2001; 2001US-0286137P.

XX  
PA (EPIG-) EPIGENESIS PHARM INC.

XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX  
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX  
PS Disclosure; SEQ ID NO 4058; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 968

ABZ88881

ID ABZ88881 standard; DNA; 20 BP.

XX  
AC ABZ88881;

XX  
DT 17-OCT-2003 (first entry)

XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX  
PD 31-OCT-2002.

XX  
PF 23-APR-2002; 2002WO-US013135.

XX  
PR 24-APR-2001; 2001US-0286137P.

XX  
PA (EPIG-) EPIGENESIS PHARM INC.

XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX  
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX  
PS Disclosure; SEQ ID NO 4123; 872pp; English.

XX



CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 969

ABZ89706  
ID ABZ89706 standard; DNA; 20 BP.

XX ABZ89706;

AC ABZ89706;

XX 17-OCT-2003 (first entry)

DT Human oligonucleotide sequence.

DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4948; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 970

ABZ88620  
ID ABZ88620 standard; DNA; 20 BP.

XX ABZ88620;

XX 17-OCT-2003 (first entry)

DT Human oligonucleotide sequence.

DE Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 3862; 872pp; English.



CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 971  
ABZ88380  
ID ABZ88880 standard; DNA; 20 BP.

XX  
AC ABZ88880;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4122; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 972  
ABZ89179  
ID ABZ89179 standard; DNA; 20 BP.

XX  
AC ABZ89179;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4421; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 2 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 973

ABZ88814  
ID ABZ88814 standard; DNA; 20 BP.

XX AC ABZ88814;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.

XX PS Disclosure; SEQ ID NO 4056; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 974

ABZ89241  
ID ABZ89241 standard; DNA; 20 BP.

XX AC ABZ89241;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX respiration, has oligo(s) antisense to specific gene(s) or its  
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX ubiquinone.

XX PS Disclosure; SEQ ID NO 4483; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 975  
ABZ90650  
ID ABZ90650 standard; DNA; 20 BP.

XX  
AC ABZ90650;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 5892; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||||  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 976  
ABZ99050  
ID ABZ99050 standard; DNA; 20 BP.

XX  
AC ABZ99050;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 14292; 872pp; English.

XX







CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 979  
ABZ85435/c  
ID ABZ85435 standard; DNA; 20 BP.

XX  
AC ABZ85435;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Claim 15; SEQ ID NO 677; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 980  
ABZ88817  
ID ABZ88817 standard; DNA; 20 BP.

XX  
AC ABZ88817;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4059; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 981  
ABZ88939  
ID ABZ88939 standard; DNA; 20 BP.  
XX  
AC ABZ88939;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4181; 872pp; English.  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 982  
ABZ89302  
ID ABZ89302 standard; DNA; 20 BP.  
XX  
AC ABZ89302;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4544; 872pp; English.  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 983  
ABZ87681  
ID ABZ87681 standard; DNA; 20 BP.

XX  
AC ABZ87681;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
PT

XX Disclosure; SEQ ID NO 2923; 872pp; English.  
PS  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTT 19

RESULT 984  
ABZ88566  
ID ABZ88566 standard; DNA; 20 BP.

XX  
AC ABZ88566;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
PT

XX Disclosure; SEQ ID NO 3808; 872pp; English.  
PS  
XX



CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 985  
ABZ89086  
ID ABZ89086 standard; DNA; 20 BP.  
XX  
AC ABZ89086;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4328; 872pp; English.  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 986  
ABZ85533  
ID ABZ85533 standard; DNA; 20 BP.  
XX  
AC ABZ85533;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
antisense gene therapy; respiratory; lung; adenosine sensitivity;  
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
Miller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
respiration, has oligo(s) antisense to specific gene(s) or its  
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
ubiquinone.

Claim 15; SEQ ID NO 775; 872pp; English.





CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 989

ABZ89016  
ID ABZ89016 standard; DNA; 20 BP.

XX ABZ89016;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Millier S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4258; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 990

ABZ89120

ID ABZ89120 standard; DNA; 20 BP.

XX ABZ89120;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

OS WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4362; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 991  
ABZ89704  
ID ABZ89704 standard; DNA; 20 BP.  
XX  
AC ABZ89704;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
PN  
XX 31-OCT-2002.  
PD  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
PI  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 4946; 872pp; English.  
XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 992  
ACD27320  
ID ACD27320 standard; DNA; 20 BP.  
XX  
AC ACD27320;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #54.

XX Nanotechnology; ss; nucleic acid detection; nanoparticle;  
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;  
KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;  
KW sexually transmitted disease; inherited disorder; forensic;  
KW paternity testing; cell line authentication.

XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "

XX US2002155461-A1.  
PN  
XX 24-OCT-2002.  
PD  
XX 12-OCT-2001; 2001US-00976378.  
PF  
XX 29-JUL-1996; 96US-0031809P.  
PR  
XX 21-JUL-1997; 97WO-US012783.  
PR  
XX 29-JAN-1999; 99US-00240755.  
PR  
XX 25-JUN-1999; 99US-00344667.  
PR  
XX 26-APR-2000; 2000US-0200161P.  
PR  
XX 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;



XX WPI; 2003-228115/22.

DR Detecting nucleic acids having 2 portions e.g. for detecting disease,

XX comprises use of nanoparticles which have oligonucleotides attached to

PT them that are complementary to portions of the nucleic acid sequence.

PT

XX

PS Example 18; Page 44; 130pp; English.

XX

CC This invention relates to a novel method for detecting a nucleic acid

CC having 2 portions. The method comprises providing nanoparticles having

CC oligonucleotides attached, where the oligonucleotide on each nanoparticle

CC has a sequence complementary to a sequence of 2 portions of nucleic acid.

CC The nucleic acid and nanoparticle are contacted to allow hybridisation of

CC the oligonucleotide on the nanoparticle with two or more portions of

CC nucleic acid and observing a detectable change brought about by the

CC hybridisation. The method of the invention is useful for separating a

CC selected nucleic acid having 2 portions, from other nucleic acids, and

CC for detecting nucleic acids having 2 portions. The method of the

CC invention is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.

CC Preferably, the method is useful for detecting nucleic acids for

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency

CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr

CC virus), bacterial diseases, sexually transmitted diseases, inherited

CC disorders, in forensics, in DNA sequencing, for paternity testing, for

CC cell line authentication, for monitoring gene therapy, etc. This method

CC involves detecting nucleic acids based on observing a colour change with

CC the naked eye so is cheap, fast, simple and robust, and does not require

CC specialised expensive equipment. The present sequence represents a thiol

CC modified oligonucleotide sequence used to demonstrate the method of the

CC invention

XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 993

ACC58867/c

ID ACC58867 standard; DNA; 20 BP.

XX

AC ACC58867;

XX

DT 08-SEP-2003 (first entry)

XX

DE Doubly labelled DNA probe.

XX

KW Probe; nucleic acid detection; ss.

XX

OS Synthetic.

XX

PN WO2003043402-A2.

XX

PD 30-MAY-2003.

XX

PF 21-OCT-2002; 2002WO-US033699.

XX

PR 19-OCT-2001; 2001US-0336432P.

XX

XX (PROL-) PROLIGO LLC.

XX

PI Bruce I, Davies M, Wolter A;

XX

DR WPI; 2003-505122/47.

XX

PT Detection or quantification of nucleic acid analyte, by hybridizing a

PT nucleic acid probe having non-identical covalently attached dyes, with

PT nucleic acid analyte, and measuring change in fluorescence of the probes.

XX

PS Example 9; Page 32; 110pp; English.

XX

CC The present sequence is an example of nucleic acid probes of the

CC invention. The probe may be doubly labelled with non-identical covalently

CC attached dyes, e.g. the fluorescent intercalator ethidium, which serves

CC as the detector dye and the fluorescent dye fluorescein, which serves as

CC the donor dye of a fluorescent resonance energy transfer (FRET) system. A

CC bifunctional linker was used to attach the dyes to the oligonucleotide.

CC The probe generates a fluorescent signal upon hybridisation to a

CC complementary nucleic acid based on the interaction of the intercalator

CC with the formed double-stranded DNA. Nucleic acid probes of the invention

CC can be used in homogeneous assays, real-time PCR monitoring,

CC transcription assays, expression analysis on nucleic acid microarrays and

CC other microarray applications such as genotyping

XX

SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 20 AAAAAAAAAAAAAAAAAA 2

RESULT 994

ABZ22916/c

ID ABZ22916 standard; DNA; 20 BP.

XX

AC ABZ22916;

XX

DT 08-APR-2003 (first entry)

XX

DE Phosphorothioate 20-mer oligonucleotide #1.

XX

KW Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages"

XX

PN WO2002102815-A2.

XX

PD 27-DEC-2002.

XX

PF 13-JUN-2002; 2002WO-US018581.

XX

PR 14-JUN-2001; 2001US-00881535.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Ravikumar VT;

XX

DR WPI; 2003-157021/15.

XX

PT Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp

PT enantiomer, by coupling a synthon with 2'-substituted nucleoside in

PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp

PT enantiomer.

XX

PS Example 1; Page 31; 65pp; English.

XX

CC The present invention describes a method (M1) for preparing an

CC internucleotide phosphorothioate linkage enriched in the Sp or Rp

CC enantiomer between a synthon having a hydroxyl moiety at the 5' position





CC sequence that encodes (IId) is used to alter the translation profile in  
CC plants. Since (I) are derived from potato, their promoters and  
CC terminators provide high level transgene expression in potato, with  
CC improved tissue specificity and inducibility, and can also be used to  
CC control endogenous genes. The present sequence is that of a PCR primer  
CC used in the first strand synthesis of cDNAs derived from Potato  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 997  
ABX79181  
ID ABX79181 standard; DNA; 20 BP.  
XX  
AC ABX79181;  
XX  
DT 15-APR-2003 (first entry)  
XX  
DE Thio-modified 20dA oligonucleotide.  
XX  
KW Nanoparticle; ss; nucleic acid detection; viral disease; probe;  
KW human immunodeficiency virus infection; hepatitis virus infection;  
KW herpes virus infection; cytomegalovirus infection; forensic science;  
KW Epstein-Barr virus infection; bacterial disease; gene therapy;  
KW sexually transmitted disease; inherited disorder; DNA sequencing;  
KW paternity testing; cell line authentication.  
XX  
OS Synthetic.  
XX  
PN US2002155462-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 12-OCT-2001; 2001US-00976577.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-198491/19.  
XX  
PT Detecting nucleic acids having at least 2 portions comprises use of  
PT nanoparticles which have oligonucleotides attached to them that are  
PT complementary to portions of the nucleic acid sequence.  
XX  
PS Example 18; Page 44; 130pp; English.  
XX  
CC The invention relates to detecting a nucleic acid (NA) having at least 2  
CC portions, comprises providing a type of nanoparticles (NP) having  
CC attached to oligonucleotides (O) (O) on each NP has a sequence  
CC complementary to sequence of at least 2 portions of NA), contacting NA  
CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,  
CC and observing a detectable change brought about by hybridisation of (O)  
CC on NP with NA. The nanoparticle is useful for separating a selected  
CC nucleic acid having at least 2 portions, from other nucleic acids, and  
CC for detecting nucleic acids having at least 2 portions. The method of  
CC using NP is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.  
CC Preferably, the method is useful for detecting nucleic acids for  
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency  
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr  
CC virus), bacterial diseases, sexually transmitted diseases, inherited  
CC disorders, in forensics, in DNA sequencing, for paternity testing, for  
CC cell line authentication and for monitoring gene therapy. The method is  
CC useful in research and analytical laboratories in DNA sequencing and in  
CC the field to detect the presence of specific pathogens. Detecting nucleic  
CC acids based on observing a colour change with the naked eye is cheap,  
CC fast, simple and robust, and do not require specialised expensive  
CC equipment. The present sequence is a nanoparticle (e.g. gold particles)  
CC labelled probe used to demonstrate the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 998  
ABX92177  
ID ABX92177 standard; DNA; 20 BP.  
XX  
AC ABX92177;  
XX  
DT 12-MAY-2003 (first entry)  
XX  
DE Nanoparticle-associated oligonucleotide SEQ ID 55.  
XX  
KW Nonoparticle; nucleic acid detection; hybridisation; diagnosis;  
KW sequencing; viral infection; human immunodeficiency virus; HIV;  
KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;  
KW bacterial infection; sexually transmitted disease; inherited disorder;  
KW forensic; paternity testing; cell line authentication; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
PN US2002155458-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 28-SEP-2001; 2001US-00967409.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-182627/18.  
XX  
PT Detecting nucleic acids having at least two portions involves use of  
PT nanoparticles which have oligonucleotides attached to them that are  
PT complementary to portions of the nucleic acid sequence.  
XX  
PS Disclosure; Page 59; 130pp; English.  
XX  
CC This invention describes a novel method of detecting nucleic acid having  
CC at least two portions. The method involves providing nanoparticles  
CC attached to oligonucleotides, where the oligonucleotide on each  
CC nanoparticle have a sequence complementary to a sequence of at least two

CC portions of nucleic acid, contacting nucleic acid and nanoparticle to  
CC allow hybridisation of the oligonucleotide on the nanoparticle with two  
CC or more portions of nucleic acid and observing a detectable change  
CC brought about by hybridisation of the oligonucleotide nanoparticle with  
CC nucleic acid. The method is useful for separating a selected nucleic acid  
CC having at least two portions, from other nucleic acids and for detecting  
CC nucleic acids having at least two portions. The method is useful for  
CC detecting any type of nucleic acids which may be used for diagnosis of  
CC disease and in sequencing of nucleic acids. Preferably, the method is  
CC useful for detecting nucleic acids for diagnosis and/or monitoring of  
CC viral infections (human immunodeficiency virus (HIV), hepatitis virus,  
CC herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial  
CC diseases, sexually transmitted diseases, inherited disorders, in  
CC forensics, in DNA sequencing, for paternity testing, for cell line  
CC authentication, and for monitoring gene therapy. The method is useful in  
CC research and analytical laboratories in DNA sequencing, in the field to  
CC detect the presence of specific pathogens. Detecting nucleic acids based  
CC on observing a colour change with the naked eye is cheap, fast, simple  
CC and robust and does not require specialised expensive equipment. ABX92123  
CC -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the  
CC method of the invention  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 999

ACD27255  
ID ACD27255 standard; DNA; 20 BP.

XX ACD27255;

XX 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method associated #54.

KW Nanotechnology; ss; nucleic acid detection; nanoparticle;  
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;  
KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;  
KW sexually transmitted disease; inherited disorder; forensic;  
KW paternity testing; cell line authentication.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "

XX US2002155459-A1.

XX 24-OCT-2002.

XX 11-OCT-2001; 2001US-00975062.

XX 29-JUL-1996; 96US-0031809P.

XX 21-JUL-1997; 97WO-US012783.

XX 29-JAN-1999; 99US-00240755.

XX 25-JUN-1999; 99US-00344667.

XX 26-APR-2000; 2000US-0200161P.

XX 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;  
XX  
DR WPI; 2003-228114/22.

XX Detecting nucleic acids having 2 portions e.g. for detecting disease,  
PT comprises use of nanoparticles which have oligonucleotides attached to  
PT them that are complementary to portions of the nucleic acid sequence.

PS Example 18; Page 43; 129pp; English.

XX This invention relates to a novel method for detecting a nucleic acid  
CC having 2 portions. The method comprises providing nanoparticles having  
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle  
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.  
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of  
CC the oligonucleotide on the nanoparticle with two or more portions of  
CC nucleic acid and observing a detectable change brought about by the  
CC hybridisation. The method of the invention is useful for separating a  
CC selected nucleic acid having 2 portions, from other nucleic acids, and  
CC for detecting nucleic acids having 2 portions. The method of the  
CC invention is useful for detecting any type of nucleic acids which may be  
CC used for diagnosis of disease and in sequencing of nucleic acids.  
CC Preferably, the method is useful for detecting nucleic acids for  
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency  
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr  
CC virus), bacterial diseases, sexually transmitted diseases, inherited  
CC disorders, in forensics, in DNA sequencing, for paternity testing, for  
CC cell line authentication, for monitoring gene therapy, etc. This method  
CC involves detecting nucleic acids based on observing a colour change with  
CC the naked eye so is cheap, fast, simple and robust, and does not require  
CC specialised expensive equipment. The present sequence represents a thiol  
CC modified oligonucleotide sequence used to demonstrate the method of the  
CC invention  
XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1000

ACD27125

ID ACD27125 standard; DNA; 20 BP.

XX ACD27125;

XX 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;  
KW DNA sequencing; paternity testing; cell line authentication.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "

XX US2002164605-A1.

XX 07-NOV-2002.

XX 28-SEP-2001; 2001US-00966312.

XX 29-JUL-1996; 96US-0031809P.



PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-247253/24.  
XX  
PT Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change,  
PT useful in forensics.  
XX  
PS Example 18; Page 44; 130pp; English.  
XX  
CC This invention relates to a novel method for detecting nucleic acid  
CC sequences having two portions. The method involves providing  
CC nanoparticles having oligonucleotides attached to them, which has a  
CC sequence complementary to sequence of two portions of nucleic acid,  
CC contacting nucleic acid and nanoparticles, to allow hybridisation of  
CC oligonucleotides with two or more portions of nucleic acid, and observing  
CC a detectable change brought about by hybridisation. The method of the  
CC invention and the aggregate probes are useful for detecting two or more  
CC nucleic acids (from a biological source) having at least two portions,  
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with  
CC a disease, synthetic, or structurally- modified natural or synthetic RNA  
CC or DNA, or a product of a polymerase chain reaction amplification.  
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the  
CC invention are useful for nanofabrication, and for separating a selected  
CC nucleic acid having two portions from other nucleic acids. The method of  
CC the invention is useful in forensics, DNA sequencing, for paternity  
CC testing, cell line authentication, and monitoring gene therapy.  
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates  
CC of the invention improve the sensitivity of the nucleic acid detection  
CC assay. The present invention represents a thiol modified oligonucleotide  
CC sequence used to demonstrate the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1001  
ACD27385  
ID ACD27385 standard; DNA; 20 BP.  
XX  
AC ACD27385;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #54.  
XX  
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;  
KW pathogen detection.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "

XX US2002182611-A1.  
XX  
PD 05-DEC-2002.  
XX  
PF 28-SEP-2001; 2001US-00966491.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-596264/56.  
XX  
PT Detection of nucleic acid for, e.g. research and analytical laboratories  
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid  
PT with nanoparticles having oligonucleotides.  
XX  
PS Example 18; Page 43; 109pp; English.  
XX  
CC This invention relates to a novel method for detecting a nucleic acid by  
CC contacting a nucleic acid with at least two types of nanoparticles having  
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides  
CC on the nanoparticles, and observing a detectable change. The  
CC oligonucleotides on each nanoparticle have a sequence complementary to  
CC its respective portion of the sequence of the nucleic acid to be  
CC detected. The method of the invention may be used for the detection of a  
CC nucleic acid used in, e.g. research and analytical laboratories in DNA  
CC sequencing, in the field to detect the presence of specific pathogens, in  
CC the doctor's office for quick identification of an infection to assist in  
CC prescribing a drug for treatment, and in homes and health centres for  
CC inexpensive first-line screening. The method of the invention detects  
CC nucleic acids based on observing a colour change with the naked eye. This  
CC method is cheap, fast, simple, robust and does not require specialised or  
CC expensive equipment. The present sequence represents a thiol modified  
CC oligonucleotide sequence used to demonstrate the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1002  
ACD27190  
ID ACD27190 standard; DNA; 20 BP.  
XX  
AC ACD27190;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #54.  
XX  
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.  
KW Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER



/\*tag= a  
/mod\_base= OTHER  
/note= "OTHER= Thiol modified" "

FT

FT

FT

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PN

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PD

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PF

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PR

PR

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/note= "OTHER= Thiol modified" "

US2002182613-A1.

05-DEC-2002.

12-OCT-2001; 2001US-00976971.

29-JUL-1996; 96US-0031809P.

21-JUL-1997; 97WO-US012783.

29-JAN-1999; 99US-00240755.

25-JUN-1999; 99US-00344667.

26-APR-2000; 2000US-0200161P.

26-JUN-2000; 2000US-00603830.

(NANO-) NANOSPHERE INC.

Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

Taton TA;

WPI; 2003-596265/56.

Detection of nucleic acid for, e.g. research and analytical laboratories in deoxyribonucleic acid sequencing, involves contacting nucleic acid with nanoparticles having oligonucleotides.

Example 18; Page 43; 107pp; English.

This invention relates to a novel method for detecting a nucleic acid by contacting nucleic acid with at least two types of nanoparticles having oligonucleotides, allowing hybridisation of the oligonucleotides on the nanoparticles, and observing a detectable change. The oligonucleotides on each nanoparticle have a sequence complementary to its respective portion of the sequence of the nucleic acid. The method of the invention may be used for the detection of a nucleic acid used in, e.g. research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, in the doctor's office for quick identification of an infection to assist in prescribing a drug for treatment, and in homes and health centres for inexpensive first-line screening. The inventive method of detecting nucleic acids based on observing a colour change with the naked eye are cheap, fast, simple, robust (the reagents are stable), do not require specialised or expensive equipment, and little or no instrumentation is required. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

|||||

1 AAAAAAAAAAAAAAAAAA 19

RESULT 1003

ACD27060

ID ACD27060 standard; DNA; 20 BP.

XX ACD27060;

XX 15-OCT-2003 (first entry)

XX Nanotechnology nucleic acid detection method oligonucleotide #54.

XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified\_base 1

FT

FT

FT

XX

PN

XX

XX

PD

XX

XX

PF

US2003044805-A1.

06-MAR-2003.

15-OCT-2001; 2001US-00981344.

29-JUL-1996; 96US-0031809P.

21-JUL-1997; 97WO-US012783.

29-JAN-1999; 99US-00240755.

25-JUN-1999; 99US-00344667.

26-APR-2000; 2000US-0200161P.

26-JUN-2000; 2000US-00603830.

(NANO-) NANOSPHERE INC.

Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

Taton TA;

WPI; 2003-521746/49.

Detection of nucleic acid having -2 portions used to prepare biomaterials and in nanofabrication methods, comprises providing nanoparticles, contacting nucleic acid and nanoparticles, and observing change.

Example 18; Page 44; 130pp; English.

This invention relates to a novel method for detecting nucleic acids. The method comprises providing nanoparticles with oligonucleotides attached to them, which have a sequence complementary to a sequence of two portions of nucleic acid, contacting the nucleic acid and nanoparticles to allow hybridisation of the oligonucleotides with two or more portions of the nucleic acid, and observing a detectable change brought about by the hybridisation. The nucleic acid to be detected must have at least two portions and the distances between these are chosen so that when the nanoparticle-oligonucleotide conjugate binds the target sequence a detectable change occurs. The method of the invention is useful for detecting two or more nucleic acids (from a biological source) having at least two portions, such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic, or structurally-modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. Nanoparticle-oligonucleotide conjugates of the invention are useful for preparing a nanoprobe conjugate for detecting an analyte, and for detecting a nucleic acid bound to an electrode surface. Nanoparticles and nanoparticle conjugates of the invention are useful for nanofabrication and for separating a selected nucleic acid having two portions from other nucleic acids. Diagnostic assays employing nanoparticle-oligonucleotide conjugates improve the sensitivity of nucleic acid detection methods and can be used to detect nucleic acids that are present in only small amounts in a sample. The invention also provides highly desirable nanoparticle-oligonucleotide conjugates. These conjugates are stable with tailored hybridisation abilities. The present sequence represents a thiol modified oligonucleotide sequence used to demonstrate the method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

|||||

1 AAAAAAAAAAAAAAAAAA 19

RESULT 1004

ACH00064

ID ACH00064 standard; DNA; 20 BP.

XX

ACH00064;  
15-OCT-2003 (first entry)  
Nanotechnology nucleic acid detection method oligonucleotide #54.  
Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
Synthetic.  
Key Location/Qualifiers  
modified\_base 1 /\*tag= a  
/mod\_base= OTHER  
/note= "OTHER= Thiol modified" "  
US2003049631-A1.  
13-MAR-2003.  
10-OCT-2001; 2001US-00974500.  
29-JUL-1996; 96US-0031809P.  
21-JUL-1997; 97WO-US012783.  
29-JAN-1999; 99US-00240755.  
25-JUN-1999; 99US-00344667.  
26-APR-2000; 2000US-0200161P.  
26-JUN-2000; 2000US-00603830.  
(NANO-) NANOSPHERE INC.  
Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
Taton TA;  
WPI; 2003-634854/60.  
Detection of nucleic acid having at least two portions, by contacting  
nucleic acid and nanoparticles under conditions, which allows  
hybridization of oligonucleotides on nanoparticles with at least two  
portions of nucleic acid.  
Example 18; Page 44; 108pp; English.  
This invention relates to a novel method for detecting nucleic acids. The  
method comprises providing nanoparticles with oligonucleotides attached  
to them, which have a sequence complementary to a sequence of two  
portions of nucleic acid, contacting the nucleic acid and nanoparticles  
to allow hybridisation of the oligonucleotides with two or more portions  
of the nucleic acid, and observing a detectable change brought about by  
the hybridisation. The nucleic acid to be detected must have at least two  
portions and the distances between these are chosen so that when the  
nanoparticle-oligonucleotide conjugate binds the target sequence a  
detectable change occurs. The method of the invention is useful for  
detecting two or more nucleic acids (from a biological source) having at  
least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
associated with a disease, synthetic, or structurally- modified natural  
or synthetic RNA or DNA, or a product of a polymerase chain reaction  
amplification. Nanoparticle-oligonucleotide conjugates of the invention  
are useful for preparing a nanoprobe conjugate for detecting an analyte,  
and for detecting a nucleic acid bound to an electrode surface.  
Nanoparticles and nanoparticle conjugates of the invention are useful for  
nanofabrication and for separating a selected nucleic acid having two  
portions from other nucleic acids. Diagnostic assays employing  
nanoparticle-oligonucleotide conjugates improve the sensitivity of  
nucleic acid detection methods and can be used to detect nucleic acids  
that are present in only small amounts in a sample. The invention also  
provides highly desirable nanoparticle-oligonucleotide conjugates. These  
conjugates are stable with tailored hybridisation abilities. The present  
sequence represents a thiol modified oligonucleotide sequence used to  
demonstrate the method of the invention  
Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19  
|||||  
RESULT 1005  
ACD99851  
ID ACD99851 standard; DNA; 20 BP.  
XX  
AC ACD99851;  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #537.  
XX  
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
XX OS  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX  
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 23; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 19  
|||||  
RESULT 1006  
ACD99847/C  
ID ACD99847 standard; DNA; 20 BP.  
XX  
AC ACD99847;  
XX

DT 25-SEP-2003 (first entry)  
XX Immunostimulatory nucleic acid #533.  
DE  
XX  
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
OS Synthetic.  
XX  
PN US2003050268-A1.  
XX  
PD 13-MAR-2003.  
XX  
PF 29-MAR-2002; 2002US-00112653.  
XX  
PR 29-MAR-2001; 2001US-0279642P.  
XX  
PA (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX  
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
PS Disclosure; Page 23; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db |||||  
20 AAAAAAAAAAAAAAAAAA 2  
RESULT 1007  
ACD99532/c  
ID ACD99532 standard; DNA; 20 BP.  
XX  
AC ACD99532;  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #218.  
XX  
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX  
OS Synthetic.  
XX  
PN US2003050268-A1.  
XX  
PD 13-MAR-2003.  
XX

PF 29-MAR-2002; 2002US-00112653.  
XX  
PR 29-MAR-2001; 2001US-0279642P.  
XX  
PA (KRIE/) KRIEG A M.  
PA (BERG/) BERG D J.  
XX  
PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX  
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
PS Disclosure; Page 14; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db |||||  
20 AAAAAAAAAAAAAAAAAA 2  
RESULT 1008  
ADA14838  
ID ADA14838 standard; DNA; 20 BP.  
XX  
AC ADA14838;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Hairpin target sequence, #2, used in an example of the invention.  
XX  
KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;  
KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;  
KW rhodamine B-labelled dye; detection; gold support; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1..20  
FT /\*tag= a  
FT /bound moiety= "Hairpin oligonucleotide #2"  
FT /note= "Forms a double-stranded region with the hairpin  
FT oligonucleotide shown in examples 3, 4 and 5"  
XX  
PN US2003013109-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 21-JUN-2002; 2002US-00176055.  
XX  
PR 21-JUN-2001; 2001US-0299460P.  
XX  
PA (BALL/) BALLINGER C T.  
PA (LOCA/) LOCASCIO M.  
PA (LAND/) LANDRY D P.  
XX  
PI Ballinger CT, Locascio M, Landry DP;



XX WPI; 2003-596312/56.

XX Hairpin sensor useful for detecting a target nucleotide sequence in a

PT sample, comprises a hairpin loop assembly including a complementary probe

PT and a quenchable fluorescing agent.

XX

PS Example 3; Page 11; 16pp; English.

XX

CC The invention discloses a hairpin sensor comprising a hairpin loop

CC assembly including a complementary probe positioned between a first

CC inverse repeat arm and a second inverse repeat arm, and a quenchable

CC fluorescing agent joined, directly or indirectly, to the end of the

CC second inverse repeat arm of the hairpin loop assembly opposite the

CC complementary probe. Also claimed is a microarray comprising the hairpin

CC sensor, where the end of the first inverse repeat arm opposite the

CC complementary probe is bound, directly or indirectly, to a support, a kit

CC for detecting a target nucleotide sequence in a sample comprising the

CC hairpin sensor, and a support, and a hairpin sensor system, in which the

CC particle is conductive or semi-conductive, including at least one of the

CC above hairpin sensor assemblies. The hairpin sensor further comprises a

CC functional group joined to the end of the first inverse repeat arm

CC opposite the complementary probe, or first spacer opposite the first

CC inverse repeat arm, the functional group selected from amino, carboxyl,

CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned

CC between the second inverse repeat arm and the quenchable fluorescing

CC agent, where the ligand is selected from mercapto, hydroxyl, amino,

CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The

CC second spacer is positioned between the second inverse repeat arm and the

CC quenchable fluorescing agent which comprises a semiconductor nanocrystal

CC or rhodamine B-labelled dye. Within the microarray the support is capable

CC of accepting a charge. At least one hairpin sensor comprises two or more

CC hairpin sensors. The two or more hairpin sensors include complementary

CC probes that are the same or different and respective quenchable

CC fluorescing agents that are the same or different. The two or more

CC hairpin sensors are arranged in a spatially-defined pattern. The sensor

CC and system are useful for detecting a target nucleotide sequence in a

CC sample. Further, the method involves identifying the target nucleotide

CC sequence by the location of the complementary probe to which the target

CC nucleotide sequence binds. The two or more hairpin sensors include

CC complementary probes or quenchable fluorescing agents, that are

CC different. The sequence presented is the hairpin oligonucleotide target

CC sequence, #2, used in an example of the invention.

XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1009

ADA06159

ID ADA06159 standard; DNA; 20 BP.

XX

AC ADA06159;

XX

DT 06-NOV-2003 (first entry)

XX

DE Nanoparticle labelled oligonucleotides, spacer DNA #2.

XX

KW ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;

KW nanostructure; viral disease; human immunodeficiency virus infection;

KW hepatitis virus infection; herpes virus infection;

KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;

KW sexually transmitted disease; inherited disorders; paternity testing;

XX cell line authentication; gene therapy.

OS Synthetic.

XX US2003068622-A1.

XX

PD 10-APR-2003.

XX

PF 12-OCT-2001; 2001US-00976863.

XX

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX

DR WPI; 2003-576420/54.

XX

PT Detecting nucleic acids having at least 2 portions comprises use of

PT nanoparticles which have oligonucleotides attached to them that are

PT complementary to portions of the target nucleic acid sequence.

XX

PS Example 18; Page 44; 130pp; English.

XX

CC The invention relates to detecting a nucleic acid (NA) having at least 2

CC portions comprising providing a type of nanoparticles (NP, e.g. colloidal

CC gold) having oligonucleotides (O) attached (where (O) on each NP has a

CC sequence complementary to sequence of at least two portions of NA),

CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more

CC portions of NA, and observing a detectable change brought about by

CC hybridization of (O) on NP with NA. Also included are aggregate probes,

CC core probes, substrate having NP attached to it, a metallic or

CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures

CC comprising nanoparticles and methods of nanofabrication utilising

CC nanoparticles and satellite probes. The methods, probes nucleic acids,

CC nanoparticles and oligonucleotides are useful for separating a selected

CC nucleic acid having at least two portions, from other nucleic acids, and

CC for detecting nucleic acids having at least two portions, for detecting

CC NA having at least two portions. The method is useful for detecting any

CC type of nucleic acids which may be used for diagnosis of disease and in

CC sequencing of nucleic acids. Preferably, the method is useful for

CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases

CC (human immunodeficiency virus, hepatitis virus, herpes virus,

CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually

CC transmitted diseases, inherited disorders, in forensics, in DNA

CC sequencing, for paternity testing, for cell line authentication, for

CC monitoring gene therapy, etc. The method is useful in research and

CC analytical laboratories in DNA sequencing, in the field to detect the

CC presence of specific pathogens, etc. Detecting nucleic acids based on

CC observing a colour change with the naked eye is cheap, fast, simple and

CC robust, and do not require specialised expensive equipment. The present

CC sequence is a spacer oligonucleotide used to illustrate the method of the

CC invention.

XX

SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1010

ACD26995

ID ACD26995 standard; DNA; 20 BP.

XX

AC ACD26995;



XX 15-OCT-2003 (first entry)  
DT Nanotechnology nucleic acid detection method oligonucleotide #54.  
XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
DE Synthetic.  
KW Key Location/Qualifiers  
XX modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= Thiol modified" "  
XX US2003049630-A1.  
PN 13-MAR-2003.  
XX 20-SEP-2001; 2001US-00957318.  
PF 29-JUL-1996; 96US-0031809P.  
XX 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX (NANO-) NANOSPHERE INC.  
PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
XX Taton TA;  
PI WPI; 2003-615795/58.  
XX Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change.  
XX Example 18; Page 43; 129pp; English.  
PS This invention relates to a novel method for detecting nucleic acids. The  
XX method comprises providing nanoparticles with oligonucleotides attached  
CC to them, which have a sequence complementary to a sequence of two  
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles  
CC to allow hybridisation of the oligonucleotides with two or more portions  
CC of the nucleic acid, and observing a detectable change brought about by  
CC the hybridisation. The nucleic acid to be detected must have at least two  
CC portions and the distances between these are chosen so that when the  
CC nanoparticle-oligonucleotide conjugate binds the target sequence a  
CC detectable change occurs. The method of the invention is useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic, or structurally- modified natural  
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
CC and for detecting a nucleic acid bound to an electrode surface.  
CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
CC nanofabrication and for separating a selected nucleic acid having two  
CC portions from other nucleic acids. Diagnostic assays employing  
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
CC nucleic acid detection methods and can be used to detect nucleic acids  
CC that are present in only small amounts in a sample. The present sequence  
CC represents a thiol modified oligonucleotide sequence used to demonstrate  
CC the method of the invention  
XX  
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
RESULT 1011  
ADB36933  
ID ADB36933 standard; DNA; 20 BP.  
XX  
AC ADB36933;  
XX 04-DEC-2003 (first entry)  
DT Immunostimulatory nucleic acid #547.  
DE ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.  
KW Synthetic.  
XX US2003087848-A1.  
PN 08-MAY-2003.  
PD 02-FEB-2001; 2001US-00776479.  
XX 03-FEB-2000; 2000US-0179991P.  
PR (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Disclosure; Page 13; 221pp; English.  
PS The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
RESULT 1012  
ADB36601/c  
ID ADB36601 standard; DNA; 20 BP.  
XX  
AC ADB36601;  
XX 04-DEC-2003 (first entry)  
DT Immunostimulatory nucleic acid #215.  
DE ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
XX hypo-responsive subject; immunostimulatory.  
KW Synthetic.  
XX

XX US2003087848-A1.  
PN 08-MAY-2003.  
XX  
PD 02-FEB-2001; 2001US-00776479.  
XX PF 03-FEB-2000; 2000US-0179991P.  
XX PR (BRAT/) BRATZLER R L.  
XX PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
XX  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX  
PT Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 8; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db ||||||||||||||||  
20 AAAAAAAAAAAAAAAAAA 2

RESULT 1013  
ADB36929/c  
ID ADB36929 standard; DNA; 20 BP.  
XX  
AC ADB36929;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #543.  
XX  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
OS Synthetic.  
XX  
PN US2003087848-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 02-FEB-2001; 2001US-00776479.  
XX  
PR 03-FEB-2000; 2000US-0179991P.  
XX  
PA (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX  
PT Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 13; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db ||||||||||||||||  
20 AAAAAAAAAAAAAAAAAA 2

RESULT 1014  
AAQ75598/c  
ID AAQ75598 standard; DNA; 20 BP.  
XX  
AC AAQ75598;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2784 TGAATAAAAAAAAAAAAAA 2802  
Db ||||||||||||||||  
19 TGAATAAAAAAAAAAAAAA 1

```

PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
SQ
    Query Match          0.7%; Score 19; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 6.3e+02;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 2784 TGAAAAAAAAAAAAAAAAAAAA 2802
    DB 19 TGAAAAAAAAAAAAAAAAAAAA 1
    |||||
RESULT 1017
AAQ75581
ID AAQ75581 standard; DNA; 20 BP.
AC
XX AAQ75581;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
KW
XX Synthetic.
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ

```





primitive progenitor cells, esp. for treating disorders involving blood cells.

Example 3; Fig 12C; 127pp; English.

AAT04915-T04922 are oligonucleotide primers and probes used for the amplification and sequencing of mammalian stem cell factor (SCF). Non-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

```

Query Match          0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2785 GAAAAAAAAAAAAAAAAA 2803  
|||  
Db 19 GAAAAAAAAAAAAAAAAA 1

RESULT 1022	
AAA13753	
ID	AAA13753 standard; DNA; 20 BP.
XX	
XX	AAA13753;
XX	
DT	27-JUL-2000 (first entry)
XX	
DE	Stem cell factor universal oli
XX	
KW	Stem cell factor; SCF; haemato
KW	primitive progenitor cell; haem
KW	allogeneic; autologous bone ma
KW	transfection; haematopoietic s
KW	cancer; ss.
XX	
OS	Synthetic.
XX	
PN	EP992579-A1.
XX	
PD	12-APR-2000.
XX	
PF	04-OCT-1990; 99EP-00122861.
XX	
PR	16-OCT-1989; 89US-00422383.
PR	11-JUN-1990; 90US-00537198.
PR	24-AUG-1990; 90US-00573616.
PR	28-SEP-1990; 90WO-US005548.
PR	01-OCT-1990; 90US-00589701.
PR	04-OCT-1990; 90EP-00310899.
XX	
PA	{AMGE-} AMGEN INC.
XX	
PI	Zsebo KM, Suggs SV, Bosselma
XX	
DR	WPI; 2000-259135/23.

Production of hematopoietic cells suitable for administration to a subject using progenitor cells and expanding the cells using stem cell factor.





CC induces cell proliferation, and introducing (I) to (III) in vitro.  
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.  
CC The method is useful for enhancing the efficiency of the transfer of a  
CC polynucleotide into a target mammalian cell in vitro. The method is  
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to  
CC AAB98390 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAATAAAAAAAAAA 2803  
Db 19 GAAAAAATAAAAAAAAAA 1  
  
RESULT 1027  
AAS04112  
ID AAS04112 standard; DNA; 20 BP.  
XX  
AC AAS04112;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
XX  
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6207417-B1.  
XX  
PD 27-MAR-2001.  
XX  
PF 07-JUN-1995; 95US-00482918.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 21-DEC-1993; 93US-00172329.  
XX  
PA (ZSEB/) ZSEBO K M.  
PA (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX WPI; 2001-298941/31.  
DR  
XX Novel nucleic acids encoding stem cell factor useful for treating  
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's  
PT disease, Kala azar, anemia and septicemia.  
XX  
PS Example 3; Fig 12C; 209pp; English.  
XX  
CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal  
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
CC including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells

CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
XX disorders such as piebaldism and vitiligo  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2169 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 19  
  
RESULT 1028  
AAS04113/C  
ID AAS04113 standard; DNA; 20 BP.  
XX  
AC AAS04113;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.  
XX  
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6207417-B1.  
XX  
PD 27-MAR-2001.  
XX  
PF 07-JUN-1995; 95US-00482918.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 21-DEC-1993; 93US-00172329.  
XX  
PA (ZSEB/) ZSEBO K M.  
PA (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX WPI; 2001-298941/31.  
DR  
XX Novel nucleic acids encoding stem cell factor useful for treating  
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's  
PT disease, Kala azar, anemia and septicemia.  
XX  
PS Example 3; Fig 12C; 209pp; English.  
XX  
CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal  
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
CC including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple



Query Match	0.7%	Score 19;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No.	6.3e+02;	

RESULT 1031  
AAS05714/C  
ID AAS05714 standard: DNA; 20 BP.



PA (CYGE-) CYGENE INC.  
PA (OSTE/) OSTE C C.  
XX  
PI Oste CC, Ramberg ER;  
XX  
DR WPI; 2001-343488/36.  
XX  
XX Analyzing target nucleic acid sequences, useful for population genetics,  
PT drug development and diagnosing cancer, comprises hybridizing triple  
PT forming oligonucleotide and probe to target sequence.  
XX  
XX Example 2; Page 66; 14lpp; English.  
PS  
XX The sequence is a second reverse phase triplex forming oligonucleotide,  
CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the  
CC method of the invention. The invention relates to analysing target  
CC nucleic acid sequences comprising restricting isolated DNA, hybridising  
CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',  
CC exonuclease to form a protected nucleic acid sequence (PNAS) tail  
CC structure, hybridising the captured structure with a single nucleotide  
CC polymorphisms (SNP) identification probe and determining the SNP score.  
CC The methods can be used for analysing target nucleic acid sequences,  
CC especially genomic DNA sequences, to determine if they contain SNPs or  
CC short tandem repeats (STRs). The methods can be used to detect SNPs for  
CC use in population genetics, drug development, forensics, cancer, genetic  
CC disease research, genomic analysis, diagnostics and therapeutics in  
CC humans, plants and animals  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 1033  
AAH23891/C  
ID AAH23891 standard; DNA; 20 BP.  
XX  
AC AAH23891;  
XX  
DT 07-AUG-2001 (first entry)  
XX  
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.  
XX  
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6204363-B1.  
XX  
PD 20-MAR-2001.  
XX  
PF 25-NOV-1992; 92US-00982255.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 10-APR-1991; 91US-00684535.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX  
XX WPI; 2001-256683/26.

XX New stem cell factor polypeptides and their analogs which stimulate  
PT growth of early hematopoietic progenitors, useful for treating aplastic  
PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's  
PT disease.  
XX  
PS Example 3; Fig 12C; 166pp; English.  
XX  
CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal  
CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the  
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
CC including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides  
CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicaemia, malaria, vitamin  
CC B12 and folic acid deficiency, pyridoxine deficiency, and  
CC hypopigmentation disorders such as piebaldism and vitiligo  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2803  
Db 19 GAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 1034  
AAH23890  
ID AAH23890 standard; DNA; 20 BP.  
XX  
AC AAH23890;  
XX  
DT 07-AUG-2001 (first entry)  
XX  
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
XX  
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6204363-B1.  
XX  
PD 20-MAR-2001.  
XX  
PF 25-NOV-1992; 92US-00982255.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 10-APR-1991; 91US-00684535.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX  
XX WPI; 2001-256683/26.  
XX  
PT New stem cell factor polypeptides and their analogs which stimulate  
PT growth of early hematopoietic progenitors, useful for treating aplastic





CC cells including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides  
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
CC disorders such as piebaldism and vitiligo

XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1037  
AAS10449/C

ID AAS10449 standard; DNA; 20 BP.

XX AC AAS10449;

XX DT 24-OCT-2001 (first entry)

XX DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.

XX KW Human; stem cell factor; SCF; haematopoietic progenitor cell;  
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

XX OS Homo sapiens.

XX PN US6248319-B1.

XX PD 19-JUN-2001.

XX PF 24-MAY-1995; 95US-00449653.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 10-APR-1991; 91US-00684535.

XX PR 25-NOV-1992; 92US-00982255.

XX PR 21-DEC-1993; 93US-00172329.

XX PA (ZSEB/) ZSEBO K M.

XX PA (BOSS/) BOSSELMAN R A.

XX PA (SUGG/) SUGGS S V.

XX PA (MART/) MARTIN F H.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX XX WPI; 2001-407312/43.

XX PT Increasing the number of early hematopoietic progenitor cells in the  
XX peripheral blood useful for the treatment of blood disorders including  
XX Hodgkin's disease comprises the administration of human stem cell factor.  
XX Example 3; Fig 12C; 210pp; English.

XX CC The present sequence for universal PCR primer 220-11 is 1 of 19 PCR  
XX primers (AAS10435-AAS10453) used to amplify various portions of the human  
XX SCF cDNA sequence. The sequence is described in an invention relating to  
XX novel stem cell factors, the polynucleotides encoding them and methods  
XX for producing the stem cell factors. The methods involve increasing the

CC number of early haematopoietic progenitor cells in human peripheral blood  
CC by administering a haematopoietically effective human stem cell factor  
CC polypeptide. The methods are useful for the treatment of blood disorders,  
CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic  
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,  
CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation  
CC disorders i.e. piebaldism and viral induced disorders, including AIDS

XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1038  
AAS10448

ID AAS10448 standard; DNA; 20 BP.

XX AC AAS10448;

XX DT 24-OCT-2001 (first entry)

XX DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.

XX KW Human; stem cell factor; SCF; haematopoietic progenitor cell;  
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

XX OS Homo sapiens.

XX PN US6248319-B1.

XX PD 19-JUN-2001.

XX PF 24-MAY-1995; 95US-00449653.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 10-APR-1991; 91US-00684535.

XX PR 25-NOV-1992; 92US-00982255.

XX PR 21-DEC-1993; 93US-00172329.

XX PA (ZSEB/) ZSEBO K M.

XX PA (BOSS/) BOSSELMAN R A.

XX PA (SUGG/) SUGGS S V.

XX PA (MART/) MARTIN F H.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX XX WPI; 2001-407312/43.

XX PT Increasing the number of early hematopoietic progenitor cells in the  
XX peripheral blood useful for the treatment of blood disorders including  
XX Hodgkin's disease comprises the administration of human stem cell factor.  
XX Example 3; Fig 12C; 210pp; English.

XX CC The present sequence for universal PCR primer 220-7 is 1 of 19 PCR  
XX primers (AAS10435-AAS10453) used to amplify various portions of the human  
XX SCF cDNA sequence. The sequence is described in an invention relating to  
XX novel stem cell factors, the polynucleotides encoding them and methods  
XX for producing the stem cell factors. The methods involve increasing the  
XX number of early haematopoietic progenitor cells in human peripheral blood  
XX by administering a haematopoietically effective human stem cell factor  
XX polypeptide. The methods are useful for the treatment of blood disorders,



PT engraftment of bone marrow during transplantation in a mammal.  
XX  
PS Example 3; Fig 12C; 217pp; English.  
XX  
CC The present invention relates to novel non-naturally-occurring stem cell  
CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
CC duplicative of that of naturally-occurring SCF to allow possession of  
CC haematopoietic biological activity of naturally occurring SCF. Sequences  
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,  
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
CC engraftment of bone marrow during transplantation in mammals and chemical  
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
CC are also useful for treating acquired immune deficiency in a human, nerve  
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
CC damage in a mammal. SCF sequences are useful for preparing biologically  
CC active polymer polypeptide adducts, for enhancing transfection of early  
CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,  
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
CC splenic pancytopenia, disseminated fungus disease, malaria, military  
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12  
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
CC and vitiligo. The present sequence is a PCR primer which is used for  
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
CC exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1041  
ABS73849  
ID ABS73849 standard; DNA; 20 BP.  
XX  
AC ABS73849;  
XX  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE SCF universal oligonucleotide 220-7.  
XX  
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;  
KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
KW disseminated fungus disease; haematopoietic; tuberculostatic;  
KW antianaemic; antifungal; antimalarial; dermatological; ss.  
XX  
OS Synthetic.  
XX  
PN EP1241258-A2.  
XX  
PD 18-SEP-2002.  
XX  
PF 04-OCT-1990; 2002EP-00008587.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
PR 04-OCT-1990; 90EP-00310899.  
PR 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.  
PA  
XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
PI  
XX WPI; 2002-684093/74.  
DR  
XX  
XX Production of a human stem cell factor (SCF) polypeptide for treating  
PT disorders involving blood cells, such as leukemia, comprises culturing  
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
PT encoding the human SCF.  
XX  
XX Example 3; Fig 12C; 120pp; English.  
XX  
XX The present invention relates to novel stem cell factors (SCFs),  
CC polynucleotide sequences encoding the SCFs, and methods of producing  
CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
CC mammals, particularly humans. The method of the invention is useful for  
CC the production of human SCF. The stem cell factors are useful to treat  
CC disorders involving blood cells e.g. metastatic carcinoma, acute  
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
CC disease, malaria, and vitiligo. The present sequence representing a  
CC universal oligonucleotide for SCF DNA is used in the examples of the  
CC present invention  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2169 TTTTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 1042  
ABS73850/c  
ID ABS73850 standard; DNA; 20 BP.  
XX  
AC ABS73850;  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE SCF universal oligonucleotide 220-11.  
XX  
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;  
KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
KW disseminated fungus disease; haematopoietic; tuberculostatic;  
KW antianaemic; antifungal; antimalarial; dermatological; ss.  
XX  
OS Synthetic.  
XX  
PN EP1241258-A2.  
XX  
PD 18-SEP-2002.  
XX  
PF 04-OCT-1990; 2002EP-00008587.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
PR 04-OCT-1990; 90EP-00310899.  
PR 04-OCT-1990; 95EP-00105391.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;



XX WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating

PT disorders involving blood cells, such as leukemia, comprises culturing

PT mammalian cells comprising non-human SCF promoter DNA linked to DNA

PT encoding the human SCF.

XX

PS Example 3; Fig 12C; 120pp; English.

XX

CC The present invention relates to novel stem cell factors (SCFs),

CC polynucleotide sequences encoding the SCFs, and methods of producing

CC them. SCFs are involved in the blood-forming (haematopoietic) system in

CC mammals, particularly humans. The method of the invention is useful for

CC the production of human SCF. The stem cell factors are useful to treat

CC disorders involving blood cells e.g. metastatic carcinoma, acute

CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory

CC erythroblastic anaemia,iliary tuberculosis, disseminated fungus

CC disease, malaria, and vitiligo. The present sequence representing a

CC universal oligonucleotide for SCF DNA is used in the examples of the

CC present invention.

XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2803

Db 19 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1043

ABZ88618

ID ABZ88618 standard; DNA; 20 BP.

XX

AC ABZ88618;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 3860; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred.No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804

Db 2 AAAAAAAAAAAAAAAAAAAAA 20

RESULT 1044

ABZ88618/c

ID ABZ88618 standard; DNA; 20 BP.

XX

AC ABZ88618;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 3860; 872pp; English.



XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 1045  
ABZ89678/c  
ID ABZ89678 standard; DNA; 20 BP.

XX AC ABZ89678;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4920; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 6.3e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 1046  
ABZ89677/c  
ID ABZ89677 standard; DNA; 20 BP.

XX AC ABZ89677;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4919; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

```

Query Match          0.7%;   Score 19;   DB 1;   Length 20;
Best Local Similarity 95.0%;   Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY	2166	TTTTTTTTTTTTTTTTTTT	2185
		{ }	
Dd	20	TNNTTTTTTTTTTTTTTTT	1

RESULT 1047  
ABZ89085  
ID ABZ89085 standard; DNA; 20 BP.  
XX  
AC ABZ89085;  
XX  
17-OCT-2003 (first entry)  
XX  
Human oligonucleotide sequence.  
DE  
XX  
Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
KW

OS Homo sapiens.  
XX  
XX  
PN WO200285308-A2.  
XX  
XX  
PD 31-OCT-2002.  
XX  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX  
DR WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

PS Disclosure; SEQ ID NO 4327; 872pp; English.

XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published pct sequences

Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

```
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2785 GAAAAAAAAAAAAAAAAA 2803  
 |||||  
 Db 2 GAAAAAAAAAAAAAAAAA 20

RESULT 1048  
ABZ88694/c  
ID ABZ88694 standard; DNA; 20 BP.

XX	ABZ88694;
AC	
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
antisense gene therapy; respiratory; lung; adenosine sensitivity;  
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
lung inflammation; respiratory disease; ds.

OS	Homo sapiens.
XX	
PN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra
PI	Miller S, Tang L, Shahabudd
XX	
DR	WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

PS Disclosure; SEQ ID NO 3936; 872bp; English.





XX WPI; 2003-851459/79.

XX New non-natural stem cell factor, useful for treating e.g. leucopenia or

PT immune deficiency, also related nucleic acid and antibodies.

XX

PS Disclosure; SEQ ID NO 34; 217pp; English.

XX

CC The invention relates to stem cell factor (SCF) polypeptides with

CC haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and military tuberculosis. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAAAAAA 2803

Db 19 GAAAAAATAAAAAAAAAA 1

RESULT 1051

ADE52461

ID ADE52461 standard; DNA; 20 BP.

XX

AC ADE52461;

XX

DT 29-JAN-2004 (first entry)

XX

DE Stem cell factor (SCF) related DNA #32.

XX

KW Stem cell factor; SCF; haematopoietic activity; infertility;

KW intestinal damage; myeloproliferative disorder; leucopenia;

KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

KW military tuberculosis; haematopoietic progenitor cell; ss.

XX

OS Synthetic.

XX

PN US2002031491-A1.

XX

PD 14-MAR-2002.

XX

PF 31-DEC-1998; 98US-00224683.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX

PA (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX

DR WPI; 2003-851459/79.

XX

PT New non-natural stem cell factor, useful for treating e.g. leucopenia or

PT immune deficiency, also related nucleic acid and antibodies.

XX

PS Disclosure; SEQ ID NO 33; 217pp; English.

XX

CC The invention relates to stem cell factor (SCF) polypeptides with

CC haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and military tuberculosis. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTT 2187

Db 1 TTTTTTTTTTTTTTTT 19

RESULT 1052

AAX26973/c

ID AAX26973 standard; cDNA; 21 BP.

XX

AC AAX26973;

XX

DT 25-JUN-1999 (first entry)

XX

DE Primer used to reverse transcribe mammaglobin RNA.

XX

KW Human; mammary-specific protein; mammaglobin; antigen; vaccine;

KW mammaglobin-expressing cancer; breast cancer;

KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.

XX

OS Synthetic.

XX

PN WO9914230-A1.

XX

PD 25-MAR-1999.

XX

PF 18-SEP-1998; 98WO-US017991.

XX

PR 18-SEP-1997; 97US-00933149.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Watson MA, Fleming TP;

XX

DR WPI; 1999-244021/20.

XX

PT Mammaglobin, secreted protein overexpressed in breast cancer.

XX

PS Example 2; Page 55; 60pp; English.

XX



CC The present primer was used to reverse transcribe RNA encoding a human  
CC mammary-specific protein, designated mammaglobin. The specification  
CC describes a protein comprising a mammaglobin antigen that is recognized  
CC by B and/or Tc cells specific for the natural, secreted and glycosylated  
CC form of mammaglobin polypeptide. This protein, or recombinant vectors  
CC that express it, are used in vaccines for treating mammaglobin-  
CC expressing cancers, specifically of the breast. Such cancers can also be  
CC treated using autologous tumor lymphocytes activated ex vivo with an  
CC mammaglobin antigen, then returned to the patient. Expression of  
CC mammaglobin is elevated in 27% of stage I primary breast cancers, so it  
CC represents a marker useful for diagnosis of this disease  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1053  
AAZ44350/C  
ID AAZ44350 standard; DNA; 21 BP.

XX AAZ44350;  
XX  
DT 04-APR-2000 (first entry)  
XX  
DE Protein kinase inhibiting primer #12.

XX Antimicrobial; cytostatic; immunosuppressive; protein kinase;  
KW prophylactic; therapy; treatment; cancer; autoimmune disease;  
KW pathogenic microorganism; primer; ss.

XX Unidentified.

XX US5998596-A.

XX 07-DEC-1999.

XX 04-APR-1995; 95US-00416214.

XX 04-APR-1995; 95US-00416214.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Bergan R, Neckers L;

XX WPI; 2000-104623/09.

XX Oligonucleotides inhibiting protein kinase, useful for treating diseases  
PT such as cancer and autoimmune disease.

XX Example 8; Col 27-28; 26pp; English.

XX This invention describes novel purified aptameric oligonucleotides which  
CC have antimicrobial, cytostatic and immunosuppressive activity. The  
CC oligonucleotides are useful for binding to and preventing or inhibiting  
CC the biological function of a protein kinase or a target molecule and for  
CC detecting the presence or absence of a target molecule in biological  
CC samples. The oligonucleotides are also useful for prophylactic and  
CC therapeutic treatment of diseases such as cancer, autoimmune diseases and  
CC diseases caused by pathogenic microorganisms. This sequence represents a  
CC primer used in the method of the invention  
XX

SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1054

AAF99707/C

ID AAF99707 standard; DNA; 21 BP.

XX AAF99707;

XX 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #823.

XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX Synthetic.

XX WO200122972-A2.

XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US026383.

XX 25-SEP-1999; 99US-0156113P.

XX 27-SEP-1999; 99US-0156135P.

XX 23-AUG-2000; 2000US-0227436P.

XX (IOWA ) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

XX Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.

XX Claim 101; Page 56; 338pp; English.

XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone

XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 7.1e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1055

AAH42480/c

ID AAH42480 standard; DNA; 21 BP.  
XX AC AAH42480;  
XX DT 01-OCT-2001 (first entry)  
XX DE Oligonucleotide used to produce branched chain compounds.  
XX KW Branched chain compound; nucleic acid synthesis; primer extension;  
KW reverse transcription; nucleic acid hybridization;  
KW nucleic acid amplification; ss.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /\*note= "NH2-C6 attached"  
FT modified\_base 4  
FT /\*tag= b  
FT /\*note= "NH2-C6 attached"  
FT misc\_feature 6..7  
FT /\*tag= c  
FT /\*note= "branch present"  
XX EP11111068-A1.  
PN 27-JUN-2001.  
PD 21-DEC-1999; 99EP-00125484.  
XX 21-DEC-1999; 99EP-00125484.  
PA (LION-) LION BIOSCIENCE AG.  
PA (VBCG-) VBC GENOMICS GMBH.  
PI Schmidt W, Hiller R, Huber M, Mueller M;  
XX WPI; 2001-466959/51.  
DR Branched compounds useful in e.g. nucleic acid synthesis reaction  
XX comprises nucleic acid moieties optionally extended by a polymerase.  
XX Example 1; Page 10; 31pp; English.  
PS The specification describes branched compounds containing nucleic acid  
XX moieties optionally extended by a polymerase. The branched chain  
CC compounds of the invention are used in nucleic acid synthesis reaction,  
CC primer extension reaction, reverse transcription reaction of RNA into  
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a  
CC nucleic acid), and nucleic acid amplification experiment (for analysing  
CC the expression pattern of genes). The compounds are also used in solid-  
CC phase enzymatic reactions. The present sequence was used in the course of  
CC the invention to produce branched chain compounds  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3  
RESULT 1056  
ABS78428/c  
ID ABS78428 standard; DNA; 21 BP.  
XX AC ABS78428;  
XX DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #912.  
DE  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX WO200253141-A2.  
PN 11-JUL-2002.  
PD 14-DEC-2001; 2001WO-US048458.  
XX PF 14-DEC-2000; 2000US-0255534P.  
PR (COLE-) COLEY PHARM GROUP INC.  
XX PA Bratzler RL;  
XX PI WPI; 2002-566690/60.  
DR Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.  
PS Claim 2; Page 35; 276pp; English.  
XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3  
RESULT 1057  
ABL39404/c  
ID ABL39404 standard; DNA; 21 BP.  
XX AC ABL39404;  
XX DT 16-APR-2002 (first entry)  
XX Immunoestimulatory nucleic acid SEQ ID NO: 840.  
DE Antibody-induced cell lysis; cancer; immunoestimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.  
XX OS Synthetic.

XX FH Key Location/Qualifiers  
FT modified\_base 1..21  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate backbone"

XX PN WO200197843-A2.

XX PD 27-DEC-2001.

XX PF 22-JUN-2001; 2001WO-US020154.

XX PR 22-JUN-2000; 2000US-0213346P.

XX PA (IOWA ) UNIV IOWA RES FOUND.

XX PI Weiner G, Hartmann G;

XX DR WPI; 2002-154611/20.

XX PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.

XX PS Disclosure; Page 309; 312pp; English.

XX CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1058  
AAD51323/c  
ID AAD51323 standard; DNA; 21 BP.

XX AC AAD51323;

XX DT 16-APR-2003 (first entry)

XX DE Regular oligo dT primer used to illustrate the method of the invention.  
XX KW Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;  
KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;  
KW musculoskeletal damage; ss.

XX OS Unidentified.

XX PN WO200290579-A1.

XX PD 14-NOV-2002.

XX PF 03-MAY-2002; 2002WO-AU000553.  
XX PR 04-MAY-2001; 2001AU-00004809.  
XX PR 29-JUN-2001; 2001US-00896941.  
XX PA (GENO-) GENOMICS RES PARTNERS PTY LTD.  
XX PI Brandon RB;  
XX DR WPI; 2003-120558/11.

XX PT Assessing condition e.g. athletic ability, stage of disease, presence of  
PT drugs, response to exercise, response to vaccines, therapies, nutritional  
PT states, of performance animal involves analyzing nucleic acid expression.

XX PS Disclosure; Page 46; 87pp; English.

XX CC The invention relates to a method for assessing a condition of a  
CC performance animal. The method involves determining in sample abundance  
CC of expressed target nucleic acid; transmitting digital sample signal to  
CC remote diagnostic server; processing digital sample signal at remotely  
CC located database to correlate digital signal with digital information and  
CC returning report of particular condition of animal. The method is useful  
CC for assessing a condition of a performance animal preferably human, dog  
CC or camel. The condition can be an athletic ability and a condition that  
CC enhances, hinders, impedes or does not change an expected ability of the  
CC performance animal; and also normal, pre-clinical, overt progress and/or  
CC stage of disease, undiagnosed of unclassified conditions, presence of  
CC drugs, response to exercise, response to vaccines, therapies, nutritional  
CC states and response to environmental conditions. Diseases assessed by the  
CC invention include laminitis, lameness, viral or bacterial disease,  
CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,  
CC musculoskeletal damage or disorders and joint diseases. The present  
CC sequence is a primer used to illustrate the method of the invention

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1059  
ACH03246/c  
ID ACH03246 standard; DNA; 21 BP.

XX AC ACH03246;

XX DT 25-SEP-2003 (first entry)

XX DE Immunostimulatory nucleic acid #881.

XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX OS Synthetic.

XX PN US2003050268-A1.

XX PD 13-MAR-2003.

XX PF 29-MAR-2002; 2002US-00112653.

XX PR 29-MAR-2001; 2001US-0279642P.

XX PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.  
XX  
PI Krieg AM, Berg DJ;  
XX  
XX  
DR WPI; 2003-521815/49.  
XX  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX  
XX  
PS Disclosure; Page 33; 229pp; English.  
XX  
CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAA 3  
  
RESULT 1060  
ADB37209/c  
ID ADB37209 standard; DNA; 21 BP.  
XX  
AC ADB37209;  
XX  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #823.  
XX  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
OS Synthetic.  
XX  
PN US2003087848-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 02-FEB-2001; 2001US-00776479.  
XX  
PR 03-FEB-2000; 2000US-0179991P.  
XX  
PA (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX  
DR WPI; 2003-657977/62.  
XX  
PT Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 17; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents

CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAAAAAAAAAA 3  
  
RESULT 1061  
AAQ90391  
ID AAQ90391 standard; DNA; 21 BP.  
XX  
AC AAQ90391;  
XX  
DT 08-JAN-1996 (first entry)  
XX  
DE CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).  
XX  
KW CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;  
KW SAED; hybridisation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 21  
FT /\*tag= a  
FT /note= "3' ribonucleoside terminal"  
XX  
PN WO9512808-A1.  
XX  
PD 11-MAY-1995.  
XX  
PF 26-OCT-1994; 94WO-US012270.  
XX  
PR 01-NOV-1993; 93US-00146504.  
XX  
PA (NANO-) NANOGEN INC.  
XX  
PI Heller MJ, Tu E;  
XX  
DR WPI; 1995-185870/24.  
XX  
PT New self-addressable electronic devices - used for multi-step and  
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics  
PT and bio:polymer synthesis.  
XX  
PS Example 1; Page 40; 86pp; English.  
XX  
CC The sequences represented by, AAQ90390-90401 are synthetic DNA probes  
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15  
CC are synthetic DNA probes with 5' amino termini. These sequences were  
CC specific for the polymorphisms of HLA gene dQa. The sequences were used  
CC in the device of the invention. This is a self-addressable electronic  
CC device (SAED) that can be used to carry out multi-step and multiplex  
CC reactions, such as nucleic acid hybridisations. The advantages of this  
CC method are that these reactions can be carried out with complete and  
CC precise electronic control, and that the rate, specificity and  
CC sensitivity of these reactions are greatly improved at micro-locations  
XX  
SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19















PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA WPI; 1995-018287/03.  
DR Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.  
PT Disclosure; Page 8; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAA 2802  
Db 19 TGAATAAAAAAAAAAAAAAAAA 1  
RESULT 1076  
AAQ75751/c  
ID AAQ75751 standard; DNA; 21 BP.  
XX  
AC AAQ75751;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
KW  
XX Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAA 2802  
Db 19 TGAATAAAAAAAAAAAAAAAAA 1  
RESULT 1076  
AAQ75751/c  
ID AAQ75751 standard; DNA; 21 BP.  
XX  
AC AAQ75751;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
KW  
XX Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
SQ

Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAA 2802  
Db 19 TGAATAAAAAAAAAAAAAAAAA 1

RESULT 1077  
AAQ75754/c  
ID AAQ75754 standard; DNA; 21 BP.  
XX  
AC AAQ75754;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
KW  
XX Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAAA 2802  
Db 19 TGAATAAAAAAAAAAAAAAAAA 1

RESULT 1078  
AAQ75759/c  
ID AAQ75759 standard; DNA; 21 BP.  
XX  
AC AAQ75759;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW

XX

RESULT 1081.

AAV35395  
ID AAV35395 standard; DNA; 21 BP.  
XX  
AC AAV35395;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE HIV-1 gag protein DNA primer #8.  
XX  
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;  
KW vaccines; infection; protection; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9822596-A1.  
XX  
PD 28-MAY-1998.  
XX  
PF 19-NOV-1997; 97WO-JP004216.  
XX  
PR 19-NOV-1996; 96JP-00323412.  
XX  
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.  
PA (JAPG ) NIPPON ZEON KK.  
XX  
PI Kojima A, Kurata T, Yasuda A;  
XX WPI; 1998-312481/27.  
DR  
XX  
PT Recombinant vaccinia virus containing fusion HIB gag gene - for  
PT production in host cells of gag protein for use as vaccine.  
XX  
PS Example 1; Page 66; 84pp; Japanese.  
XX  
CC AAV35388-V35414 are primers used in a method which results in a  
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus  
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope  
CC region (30-300 bases in length) of a retroviral gene other than the gag  
CC gene. The gag gene may be altered so as to produce a gag protein modified  
CC from the natural sequence by the addition, deletion or substitution of at  
CC least 1 amino acid residue. The fusion gene is inserted into a region of  
CC a vaccinia virus not essential to its propagation, to give a recombinant  
CC vaccinia virus vector which is used to transform a host cell (such as  
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon  
CC culturing the host cell produces particulate structures containing the  
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag  
CC protein particles may be used in the production of vaccines for  
CC protecting against infection with retroviruses such as HIV  
XX  
SQ Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 3 AAAAAAAAAAAAAAAAAAAAAA 21  
RESULT 1082  
AAV35395/c  
ID AAV35395 standard; DNA; 21 BP.  
XX  
AC AAV35395;  
XX  
DT 13-OCT-1998 (first entry)  
DE HIV-1 gag protein DNA primer #8.  
XX  
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;  
KW vaccines; infection; protection; primer; ss.  
XX

OS Synthetic.  
XX  
PN WO9822596-A1.  
XX  
PD 28-MAY-1998.  
XX  
PF 19-NOV-1997; 97WO-JP004216.  
XX  
PR 19-NOV-1996; 96JP-00323412.  
XX  
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.  
PA (JAPG ) NIPPON ZEON KK.  
XX  
PI Kojima A, Kurata T, Yasuda A;  
XX WPI; 1998-312481/27.  
DR  
XX  
PT Recombinant vaccinia virus containing fusion HIB gag gene - for  
PT production in host cells of gag protein for use as vaccine.  
XX  
PS Example 1; Page 66; 84pp; Japanese.  
XX  
CC AAV35388-V35414 are primers used in a method which results in a  
CC recombinant vaccinia virus comprising of a gag gene from a retrovirus  
CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope  
CC region (30-300 bases in length) of a retroviral gene other than the gag  
CC gene. The gag gene may be altered so as to produce a gag protein modified  
CC from the natural sequence by the addition, deletion or substitution of at  
CC least 1 amino acid residue. The fusion gene is inserted into a region of  
CC a vaccinia virus not essential to its propagation, to give a recombinant  
CC vaccinia virus vector which is used to transform a host cell (such as  
CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon  
CC culturing the host cell produces particulate structures containing the  
CC fusion gag protein. The recombinant vaccinia virus or the fusion gag  
CC protein particles may be used in the production of vaccines for  
CC protecting against infection with retroviruses such as HIV  
XX  
SQ Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 21 TTTTTTTTTTTTTTTTTT 3  
RESULT 1083  
AAQ64724  
ID AAQ64724 standard; cDNA to mRNA; 22 BP.  
XX  
AC AAQ64724;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-JAN-1995 (first entry)  
XX  
DE 2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.  
XX  
KW antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;  
KW RNA cleavage; antiviral therapy; chimeric molecule; PKR;  
KW protein synthesis regulation; phosphorylation; eIF-2alpha;  
KW eukaryotic translation initiation factor; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1..4  
FT /\*tag= a  
FT /label= 2',5'-linked tetraadenylate  
FT /note= "nucleotides linked through phosphodiester bonds  
FT at hydroxyl groups of 2' and 5' carbons"  
FT misc\_feature 4..5



```
FT /tag= b
FT /note= "the 2-5A moiety (*tag = a) and the antisense DNA
FT sequence (*tag = c) are linked by two 1,4-butanediol
FT molecules linked through phosphodiester bonds"
FT 5..22
FT misc_feature
FT /tag= c
FT /note= "antisense region, complementary to oligo dT"
XX
XX WO9409129-A2.
XX
XX
XX PD 28-APR-1994.
XX
XX PF 20-OCT-1993; 93WO-US010103.
XX
XX PR 21-OCT-1992; 92US-00965666.
XX 17-SEP-1993; 93US-00123449.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (CLEV-) CLEVELAND CLINIC RES INST.
XX
XX Torrence P, Silverman R, Maitra R, Lesiak K;
XX
XX WPI; 1994-151315/18.
XX
XX Specific cleavage of RNA, useful partic. for treating viral infection,
XX cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
XX of 2-5A dependent RNase.
XX
XX Example 9; Page 66; 86pp; English.
XX
XX This sequence was used to determine whether 2-5A-antisense chimeric
XX molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711
XX and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense
XX oligonucleotide chimeric molecules, the antisense region targets the
XX chimeric molecule to a particular region of RNA to be specifically
XX cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A
XX RNase. Typical applications are treatment of viral infections (esp. for
XX cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular
XX disorders (e.g. restenosis after angioplasty), genetic disorders,
XX osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1084
AAFL17413
ID AAF17413 standard; DNA; 22 BP.
XX
XX AAF17413;
AC
XX 09-MAR-2001 (first entry)
DT
XX
XX L1 cleavage site related sequence #3.
DE
XX Retrotransposon; genetic defect; cystic fibrosis; ds.
KW
XX Unidentified.
OS
XX US6150160-A.
PN
XX 21-NOV-2000.
XX
XX 28-APR-1997; 97US-00847844.
XX
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```
PR 16-NOV-1995; 95US-0006831P.
PR 15-NOV-1996; 96US-00749805.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Moran JV, Dombroski BA, Kazazian HH, Boeke JD;
XX
XX WPI; 2001-060015/07.
XX
XX DNAC comprising a promoter P and an L1 cassette sequence having a core
XX retrotransposon element, useful for random insertion of a heterologous or
XX homologous DNA sequence into a cell genome and for correcting genetic
XX defects.
XX
XX Disclosure; Fig 14; 87pp; English.
XX
XX The present invention relates to DNA for a promoter and an L1 cassette
XX sequence having a core retrotransposon element. The invention is useful
XX for random insertion of a heterologous or homologous DNA sequence into a
XX cell genome, and for correction of a genetic defect in the cell into
XX which the insertion is made. Genetic defects which may be corrected
XX includes cystic fibrosis, mutations in the dystrophin gene, genetic
XX defects associated with blood clotting and other genetic defects
XX
XX Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.7%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1085
AAT923356
ID AAT923356 standard; DNA; 22 BP.
XX
XX AAT923356;
AC
XX 26-JAN-1998 (first entry)
DT
XX Amino modified oligodeoxyribonucleotide.
DE
XX Amino modified oligodeoxyribonucleotide; oligonucleotide;
XX achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;
XX N-fluoresceinyl-(5-aminomethyl)-1,3-benzenedimethanol;
XX hybridisation probe; PCR primer; nucleic acid sequencing;
XX affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_difference 11
FT /tag= a
FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"
XX
FT misc_difference 12
FT /tag= b
FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"
XX
XX WO9705156-A1.
XX
XX 13-FEB-1997.
XX
XX 26-JUL-1996; 96WO-DK000330.
XX
XX 27-JUL-1995; 95DK-00000863.
XX
XX (BEHR/) BEHRENS C.
XX (PETE/) PETERSEN K H.
XX (EGHO/) EGHOLM M.
XX
```

PA (NIEL/) NIELSEN J.  
PA (DAHL/) DAHL O.  
XX  
PI Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;  
XX WPI; 1997-145615/13.  
DR  
XX New achiral linker reagents - useful for incorporation of multiple amino  
PT gps. or reporter gps. into oligo:nucleotide(s).  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC Achiral linker reagents have been developed for the incorporation of  
CC multiple amino groups into oligonucleotides. The present sequence  
CC represents a modified oligodeoxyribonucleotide. The achiral linker  
CC reagents can be used for incorporation of multiple primary amino groups  
CC or reporter groups into oligonucleotides. They are compatible with  
CC conventional DNA synthesis following the phosphoramidite methodology, and  
CC can be incorporated in good yields. The linker reagents may be used for  
CC labelling of oligonucleotides. They may also be used for preparation of  
CC oligonucleotides, e.g. for use as hybridisation probes, for use as  
CC primers in the polymerase chain reaction or in nucleic acid sequencing  
CC reactions, for production of affinity matrices for purification of DNA  
CC binding proteins or other biomolecules, for production of affinity  
CC matrices for detection of nucleic acid sequences, for cloning recombinant  
CC DNA or for in-vitro mutagenesis  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 8e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTTTT 2186  
Db 1 TTTTTTTTTTNNTTTTTTTTT 21  
  
RESULT 1086  
AAC62450/c  
ID AAC62450 standard; DNA; 23 BP.  
XX  
AC AAC62450;  
XX  
DT 07-FEB-2001 (first entry)  
XX  
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #1.  
XX  
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;  
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;  
KW nucleic acid purification; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 23  
FT /\*tag= a  
XX  
PN WO200058329-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 28-MAR-2000; 2000WO-GB001190.  
XX  
PR 29-MAR-1999; 99GB-00007245.  
XX  
PA (GOLD/) GOLDSBOROUGH A.  
XX  
WPI; 2000-664908/64.  
XX  
PT Detaching nucleic acid molecule comprising unconventional nucleotide  
PT incorporated at predetermined site from a solid support involves cleaving  
PT the nucleic acid molecule at the site of unconventional nucleotide.

XX  
PS Disclosure; Page 16; 47pp; English.  
XX  
CC The present invention is concerned with the cleavage of nucleic acids  
CC from solid supports. This is carried out by adding a non-conventional  
CC nucleotide into the nucleic acid attached to the support, so that it is  
CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
CC released. This is useful in many molecular biological procedures such as  
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-  
CC based assays, mutagenesis procedures, nucleic acid purification and  
CC affinity chromatography. The present sequence is an oligonucleotide used  
CC in assays to demonstrate the methods of the invention  
XX  
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAA 2804  
Db 23 AAAAAAAAAAAAAAAAAAAA 5  
  
RESULT 1087  
AAC62451/c  
ID AAC62451 standard; RNA; 23 BP.  
XX  
AC AAC62451;  
XX  
DT 07-FEB-2001 (first entry)  
XX  
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.  
XX  
KW Nucleic acid cleavage; solid support; affinity chromatography;  
KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.  
XX  
OS Synthetic.  
XX  
PN WO200058329-A1.  
XX  
PD 05-OCT-2000.  
XX  
PF 28-MAR-2000; 2000WO-GB001190.  
XX  
PR 29-MAR-1999; 99GB-00007245.  
XX  
PA (GOLD/) GOLDSBOROUGH A.  
XX  
WPI; 2000-664908/64.  
XX  
PT Detaching nucleic acid molecule comprising unconventional nucleotide  
PT incorporated at predetermined site from a solid support involves cleaving  
PT the nucleic acid molecule at the site of unconventional nucleotide.  
XX  
PS Example 1; Page 32; 47pp; English.  
XX  
CC The present invention is concerned with the cleavage of nucleic acids  
CC from solid supports. This is carried out by adding a non-conventional  
CC nucleotide into the nucleic acid attached to the support, so that it is  
CC recognised and cleaved by a specific DNA glycosylase and the sequence is  
CC released. This is useful in many molecular biological procedures such as  
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-  
CC based assays, mutagenesis procedures, nucleic acid purification and  
CC affinity chromatography. The present sequence is an oligonucleotide used  
CC in assays to demonstrate the methods of the invention  
XX  
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

















PT gene therapy (particularly for regulating gene expression), or in assays  
PT for detecting the presence of ligands or activation of an effector of  
PT RCANA.  
XX  
XX Example 6; Page 75; 126pp; English.  
XX  
CC The present invention relates to regulatable, catalytically active  
CC nucleic acids (RCANAs) which are regulated by polypeptides. These are  
CC useful for regulating gene expression, in assays for detecting the  
CC presence of ligands, for activation of an effector of RCANA, and in gene  
CC therapy. The present sequence is an oligonucleotide substrate used in the  
CC construction of an RCANA  
XX  
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
RESULT 1102  
ADA39569  
ID ADA39569 standard; RNA; 28 BP.  
XX  
AC ADA39569;  
XX  
XX 20-NOV-2003 (first entry)  
XX Substrate RNA related oligonucleotide SEQ ID NO:25.  
DE regulatable catalytically active nucleic acid; RCANA; catalytic domain;  
XX regulation; screening; gene therapy; biological pathway regulation;  
KW regulatory element; metabolic pathway; ribozyme; ss.  
KW  
XX Synthetic.  
OS  
XX WO2003027310-A2.  
PN  
XX 03-APR-2003.  
PD  
XX 24-SEP-2002; 2002WO-US030458.  
PF  
XX 24-SEP-2001; 2001US-0324715P.  
PR  
XX (ARCH-) ARCHEMIX CORP.  
PA  
XX  
PI Wilson C, Cload ST, Keefe AD;  
PI  
XX WPI; 2003-354657/33.  
DR  
XX  
PT Regulating production of a product in a cell, comprises inserting a  
PT regulatable catalytically active nucleic acid into a gene that produces  
PT the product or regulates the production of the product in the cell.  
XX  
XX Example 6; Page 76; 128pp; English.  
PS  
XX The present invention describes a method for regulating production of a  
CC product in a cell. The method comprises inserting a regulatable  
CC catalytically active nucleic acid (RCANA) into a gene that produces the  
CC product or regulates the production of the product in the cell, where the  
CC RCANA comprises a catalytic domain which modifies a transcript to alter  
CC its coding potential and a regulatory domain that recognises an effector  
CC that alters the function of the catalytic domain, and contacting the  
CC regulatory domain with an effector to regulate production of the product.  
CC Also described: (1) regulating a biological pathway in cell; and (2)  
CC screening a population of cells for a cell that produces a bioproduct.  
CC The methods are useful for regulating a biological pathway in cell, or  
CC regulating production of a product in a cell. The RCANAs are useful as  
CC regulatory elements to control the expression of genes in a metabolic

CC pathway, or as regulated selectable markers to increase a selective  
CC pressure favouring or disfavouring production of a targeted bioproduct.  
CC The RCANAs are also useful for in vitro or in vivo sensing or detection,  
CC and in gene therapy. The present sequence represents an RNA substrate  
CC oligonucleotide, which is used in an example from the present invention.  
XX  
SQ Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
RESULT 1103  
AAS11744  
ID AAS11744 standard; DNA; 28 BP.  
XX  
AC AAS11744;  
XX  
XX 24-OCT-2001 (first entry)  
DT Human haemoglobin alpha 2 transcript (extreme 3' end).  
XX  
DE Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.  
XX  
KW Homo sapiens.  
XX  
OS WO200161051-A1.  
PN  
XX 23-AUG-2001.  
PD  
XX 16-FEB-2001; 2001WO-US005305.  
PF  
XX 16-FEB-2000; 2000US-0182983P.  
PR  
XX (SEQU-) SEQUEL GENETICS INC.  
PA  
XX Jarvik JW;  
XX  
PI WPI; 2001-514778/56.  
PI  
XX  
DR Transcript, genetic, and especially nucleic acid sequence analysis  
XX comprises analysis of hybrid peptide products.  
XX  
XX Example 11; Page 30; 48pp; English.  
PS  
XX The invention relates to a method of peptide-based transcript or genetic  
CC analysis comprising: (a) providing multiple polynucleotides (I) derived  
CC from mRNAs from a biological sample, where (I) has homology to a known  
CC reference sequence (II); (b) expressing (I); and (c) assessing a physical  
CC property of the expression products to determine the sequences of (I) by  
CC comparison with the predicted properties of polypeptides encoded by (II).  
CC The method is useful for transcript or genetic analysis, especially  
CC nucleic acid analysis where the method comprises expressing polypeptides  
CC from two or more reading frames and determining the masses to create a  
CC peptide mass signature characteristic of the nucleic acid molecule. The  
CC peptide is considerably smaller than the DNA molecule that encodes it  
CC (individual amino acids averages about 110 Daltons each whereas the  
CC trinucleotides (triplets) that encode them average N Daltons each). Also,  
CC the peptides are much more diverse in composition than nucleic acids, as  
CC they are composed of combinations of 20 different amino acids instead of  
CC combinations of 4 different nucleotides, e.g., two random DNA fragments  
CC of identical composition (e.g., with 10 adenines, 10 thymines, 15  
CC guanines, and 15 cytosines) are extremely unlikely to encode peptides of  
CC identical composition. This means that whereas the two nucleic acids have  
CC identical masses and cannot be distinguished on the basis of mass, the  
CC peptides that they encode will, except in statistically very rare cases,  
CC have different masses and can be readily distinguished in the basis of  
CC mass. The present sequence represents the coding sequence of human

```
CC haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC demonstrate the method of the invention
XX
SQ Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 6 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1104
AAV61015
ID AAV61015 standard; DNA; 28 BP.
XX
AC AAV61015;
XX
DT 03-DEC-1998 (first entry)
XX
DE HS/HIP reverse transcriptase PCR primer #4.
XX
KW Human; heparan sulfate/heparin interacting protein; HIP; diagnosis;
KW blood coagulation; antithrombin-3; bleeding; wound; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9838214-A1.
XX
PD 03-SEP-1998.
XX
PF 27-FEB-1998; 98WO-US003788.
XX
PR 28-FEB-1997; 97US-00810609.
XX
PA (TEXA ) UNIV TEXAS A & M SYSTEM.
XX
PI Carson DD, Hoeoek M, Liu S;
XX
WPI; 1998-495388/42.
XX
PT Use of heparin sulphate/heparin interacting protein - for modulating
PT blood coagulation, e.g. for neutralising heparin, treating diseases
PT involving excessive bleeding or administration to wound sites.
XX
PS Example 1; Page 78; 148pp; English.
XX
CC A method has been developed for identifying a heparin (Hp) component that
CC binds to antithrombin-3 (AT-3). The method comprises: (a) contacting a Hp
CC sample suspected of containing a Hp component that binds to AT-3 with a
CC heparan sulphate (HS)/Hp interacting protein (HIP) to allow binding of
CC the Hp component; and (b) detecting the binding of the Hp component to
CC the HS/HIP. The present sequence represents a primer for reverse
CC transcriptase PCR of heparan sulfate/heparin interacting protein
CC (HS/HIP). Products from the present invention can be used for modulating
CC blood coagulation. They can be used for neutralising heparin, treating
CC diseases characterised by excessive bleeding or administration to wound
CC sites. The HS/HIPs can also be used for the production of antibodies and
CC in diagnostic applications
XX
SQ Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTT 2183
Db 10 CTTTTTTTTTTTTTTTTTTT 28

CC haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC demonstrate the method of the invention
XX
SQ Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTT 2183
Db 10 CTTTTTTTTTTTTTTTTTTT 28

RESULT 1106
```

```
RESULT 1105
AAZ61254
ID AAZ61254 standard; DNA; 28 BP.
XX
AC AAZ61254;
XX
DT 30-MAY-2000 (first entry)
XX
DE Oligo dT primer for honey bee venom PX3.101 cDNA.
XX
KW Protein PX3.101; honey bee; venom; interleukin-8; IL-8; receptor; CXCR1;
KW CXCR2; cyclooxygenase; lipoxigenase; phospholipase; protease;
KW inflammatory disease; gene therapy; cancer; autoimmune disease; pain;
KW chemokine imbalance; rheumatoid arthritis; multiple sclerosis; psoriasis;
KW systemic lupus erythematosus; Crohn's disease; vasculitis; scleroderma;
KW metastatic cancer; Alzheimer's disease; wound healing; aging process;
KW antigen; primer; ss.
XX
OS Apis mellifera.
XX
PN GB2341389-A.
XX
PD 15-MAR-2000.
XX
PF 13-SEP-1999; 99GB-00021605.
XX
PR 14-SEP-1998; 98US-0100172P.
XX
PA (PANP-) PAN PACIFIC PHARM INC.
XX
PI Chi X, Lu Y;
XX
WPI; 2000-185368/17.
XX
PT Isolated nucleic acids encoding the bee venom protein PX3.101 useful for
PT treating autoimmune and inflammatory disorders such as rheumatoid
PT arthritis.
XX
PS Example 3; Page 43; 83pp; English.
XX
CC The present primer was used for cDNA encoding the protein PX3.101, which
CC is a honey bee venom isolated Apis mellifera. PX3.101 inhibits the
CC binding of interleukin-8 (IL-8) to its receptor (e.g. CXCR1 and CXCR2)
CC and inhibits a variety of enzymes (e.g. cyclooxygenases, lipoxigenases,
CC phospholipases and proteases) associated with inflammatory diseases. The
CC nucleic acids may be used for the recombinant production of PX3.101
CC proteins either in vivo (as part of a gene therapy protocol) or in vitro
CC (as a fermentation culture). The nucleic acids may also be used as probes
CC to identify similar sequences in samples. The PX3.101 protein may be used
CC for the treatment of inflammatory diseases, cancers, autoimmune diseases,
CC pain and/or diseases associated with chemokine (especially IL-8)
CC imbalances such as rheumatoid arthritis, multiple sclerosis, psoriasis,
CC systemic lupus erythematosus (SLE), Crohn's disease, vasculitis,
CC scleroderma, metastatic cancer and Alzheimer's disease in humans. It is
CC also disclosed that the proteins may be used to accelerate wound healing,
CC reduce several aging processes and protect against ultraviolet light. The
CC proteins may also be used as antigens in the production of antibodies
CC specific for PX3.101. The antibodies may be used as diagnostic agents to
CC detect PX3.101 protein in samples and to down regulate PX3.101 activity
XX
SQ Sequence 28 BP; 0 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

Query Match          0.7%; Score 19; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTTTT 2183
Db 10 CTTTTTTTTTTTTTTTTTTT 28

RESULT 1106
```

AAI71210  
ID AAI71210 standard; DNA; 28 BP.  
XX  
AC AAI71210;  
XX  
DT 22-JAN-2002 (first entry)  
XX  
DE Single stranded DNA PCR primer SEQ ID NO:5.  
XX  
KW Single stranded DNA primer; PCR primer; amplification; ss.  
XX  
OS Synthetic.  
XX  
PN JP2001204472-A.  
XX  
PD 31-JUL-2001.  
XX  
PF 21-JAN-2000; 2000JP-00012535.  
XX  
PR 21-JAN-2000; 2000JP-00012535.  
XX  
PA (SUME ) SUMITOMO ELECTRIC IND CO.  
XX  
DR WPI; 2001-609513/70.  
XX  
PT New polynucleotide for the amplification of a one-side single-stranded  
PT DNA and the production of a double-stranded cDNA comprises a single-  
PT stranded DNA primer.  
XX  
PS Disclosure; Page 11; 13pp; Japanese.  
XX  
CC The present invention describes a single-stranded DNA primer comprising a  
CC single-stranded DNA having a dtn sequence, which hybridises with the  
CC polyA site of an mRNA at the 3'-terminal, and has a blocking group at the  
CC 5'-terminal in which the other part constitutes an adapter double-  
CC stranded DNA connected to the double-stranded cDNA. The terminal of the  
CC side of the DNA is not connected to the double-stranded cDNA, which  
CC consists of a base sequence having full homology to the single-stranded  
CC DNA corresponding to the 5'-terminal. A method is also described for the  
CC preparation of a double-stranded cDNA in which the above single-stranded  
CC DNA primer is hybridised with the polyA site of an mRNA and said single-  
CC stranded DNA primer is used as the primer to reverse-transcribe said mRNA  
CC and further it is converted to a double-stranded cDNA by a DNA  
CC polymerase. The primer is used for the uniform amplification of DNAs. The  
CC present sequence represents a PCR primer which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 28 BP; 3 A; 3 C; 2 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTTTTTT 2183  
Db 10 CTTTTTTTTTTTTTTTTTTT 28  
  
RESULT 1107  
AAQ79096/c  
ID AAQ79096 standard; DNA; 29 BP.  
XX  
AC AAQ79096;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-AUG-1995 (first entry)  
XX  
DE Tobacco PMT PCR primer P-23.  
XX  
KW Tobacco; transgenic plant; putrescine-N-methyltransferase; PMT; alkaloid;  
KW nicotine; primer; polymerase chain reaction; PCR; Nicotiana tabacum; ss.  
XX  
OS Synthetic.

XX WO9428142-A1.  
PN  
XX  
PD 08-DEC-1994.  
XX  
PF 01-JUN-1994; 94WO-US0006106.  
XX  
PR 01-JUN-1993; 93US-00076681.  
XX  
PA (PHIM ) PHILIP MORRIS PROD INC.  
XX  
XX Wahab SZ, Malik VS;  
PI  
XX  
XX WPI; 1995-022814/03.  
DR  
XX  
PT Recombinant DNA encoding tobacco protein, PMT - useful for producing  
PT transgenic tobacco plants with decreased alkaloid content.  
XX  
PS Disclosure; Page 57; 69pp; English.  
XX  
CC Forward primer P-18 (AAQ79095), based on an N-terminal methionine and  
CC amino acids 1-7 of a CNBr fragment (AAR67579) of tobacco putrescine-N-  
CC methyltransferase (PMT), and reverse primer P-23 (AAQ79096), were used to  
CC amplify RNA derived from tobacco var. Burley 21 root extract. Clone Q7  
CC was obtained.. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 29 BP; 2 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 29 AAAAAAAAAAAAAAAAAA 11  
  
RESULT 1108  
AAQ68614  
ID AAQ68614 standard; cDNA; 29 BP.  
XX  
AC AAQ68614;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-JAN-1995 (first entry)  
XX  
DE tRNAPolyU reverse tRNA primer.  
XX  
KW cDNA; RNA template; reverse-transcriptase; primer; tRNAPolyU;  
KW tRNA template; pUC18; ss.  
XX  
OS Synthetic.  
XX  
PN WO9413689-A1.  
XX  
PD 23-JUN-1994.  
XX  
PF 09-DEC-1993; 93WO-US012029.  
XX  
PR 09-DEC-1992; 92US-00989851.  
XX  
PA (MILL/) MILLER J E.  
XX  
PI Miller JE;  
XX  
DR WPI; 1994-217796/26.  
XX  
PT In vivo cDNA synthesis - by using synthetic polynucleotide(s) which bind  
PT in vivo to RNA templates as primers for reverse transcriptase.  
XX  
PS Example 1; Page 33; 102pp; English.  
XX  
CC DNA encoding the modified tRNA primer, tRNAPolyU (AAQ68616), was obtained

CC using the primer pair given in AAQ68612-13. The DNA was cloned in pUC18.  
CC PCR was used to amplify a promoter-trNA-polyU fragment and to define the  
CC end of the tRNApolyU coding template. A reverse trNA primer (AAQ68614)  
CC was used. The 5' base of this primer was also the last 3' base of the  
CC encoded tRNApolyU template, as shown in AAQ68617. For in vitro production  
CC of tRNApolyU, a DraI-sensitive T7-trNAPolyU cassette was linearized and  
CC used as template for in vitro transcription using oligomers AAQ68612 and  
CC AAQ68515. The trNA primer is used for in vivo cDNA synthesis. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1109  
AAT09934  
ID AAT09934 standard; cDNA; 29 BP.  
XX  
AC AAT09934;  
XX  
DT 07-AUG-1996 (first entry)  
XX  
DE Reverse trNA primer #5.

XX Polymerase chain reaction: PCR; primer; amplify; murine; tRNAproGGG; RT;  
KW DNA polymerase I; bacteriophage T7; RNA polymerase promoter; synthesis;  
KW Moloney Murine Leukaemia Virus; MoMuLV; reverse transcriptase; analysis;  
KW covalently-linked cDNA; subtractive cDNA library; light sensitive cDNA;  
KW cytotoxic sensitive cDNA; cDNA probe; diagnosis; DNA sequencing; ss.  
XX  
OS Synthetic.

XX WO9535369-A1.  
XX 28-DEC-1995.  
XX  
PD 22-JUN-1995; 95WO-US007968.  
XX  
PF 22-JUN-1994; 94US-00264038.  
XX  
PR (MILL/) MILLER J E.  
XX  
PA Miller JE;  
XX  
PI WPI; 1996-058406/06.  
XX

PT Method for synthesising covalently linked complementary DNA - uses  
PT primers which can bind reverse transcriptase and anneal to a distinct  
PT template, allowing synthesis to occur.  
XX  
PS Example 1; Page 43; 140pp; English.

CC This sequence represents a reverse trNA primer and is used to amplify the  
CC sequence represented by AAT09937. The amplified sequence is used in the  
CC method of the invention, along with the sequence amplified by AAT09930  
CC and AAT09931. The sequence amplified by AAT09930 and AAT09931 is a  
CC recombinant tRNAproGGG primer operatively linked to the bacteriophage T7  
CC RNA polymerase promoter which is capable of binding to the Moloney Murine  
CC Leukaemia Virus (MoMuLV) reverse transcriptase (RT) and can then be used  
CC in the method of the invention. The method is for synthesising a  
CC covalently-linked cDNA copy of a plurality of polynucleotide template  
CC molecules. In this method, a polynucleotide template primer molecule  
CC (such as the amplified sequence) is used in a mixture with a RT enzyme or  
CC complex. The mixture is then incubated under conditions which permit the  
CC synthesis of a DNA molecule which comprises regions complementary to the  
CC polynucleotide template molecule. The primers and DNA molecules can be

CC used in the construction of subtractive cDNA libraries, production of  
CC specific cytotoxic or light sensitive cDNA products, and cDNA probes for  
CC analytical, diagnostic or preparative use. Also, they can be used in in  
CC vivo DNA sequencing. The method of cDNA synthesis utilises structure-  
CC specific analogues to the natural target site of the RT enzyme or complex  
XX  
SQ Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1110  
AAQ97396/c  
ID AAQ97396 standard; DNA; 29 BP.

XX  
AC AAQ97396;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-APR-1996 (first entry)  
XX

DE Rat type I steroid 5-alpha reductase cDNA PCR primer.

XX Steroid 5-alpha reductase; sexual development; differentiation; probe;  
KW recombinant; inhibit; prostatic hyperplasia; acne; hirsutism;  
KW male pattern baldness; endometriosis; prostate cancer; testosterone;  
KW dihydroxytestosterone; ss.

OS Rattus sp.

XX US5422262-A.

XX 06-JUN-1995.

XX 18-NOV-1991; 91US-00795859.

XX 30-APR-1990; 90US-00517661.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Andersson S, Russell DW;

XX WPI; 1995-214658/28.

XX Steroid 5 alpha-reductase nucleic acid segments and recombinant vectors -  
PT where the sequences are useful in e.g. analysis of normal and abnormal  
PT sexual differentiation.

XX Example 1; Col 21; 72pp; English.

CC 5-alpha reductase enzymes catalyse the conversion of testosterone to  
CC dihydroxytestosterone. The rat steroid 5-alpha reductase I (SRD5A-I) cDNA  
CC sequence has been isolated and purified using the PCR primer AAQ97396.  
CC The rat enzyme cDNA can be used in the prepn. of genetic constructs for  
CC the large scale production of SRD5A or as probes for enzyme-encoding  
CC sequences from alternative sources. The sequences are also useful in the  
CC analysis of normal and abnormal sexual differentiation, benign prostatic  
CC hyperplasia, male pattern baldness; acne; hirsutism and endometriosis.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX

SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804



Db 29 AAAAAAAAAAAAAAAAAAAA 11

RESULT 1111  
AAT99803/C  
ID AAT99803 standard; DNA; 29 BP.  
XX  
AC AAT99803;  
XX  
DT 20-MAR-1998 (first entry)  
XX  
DE Primer for rat steroid 5alpha-reductase coding sequence.  
XX  
KW Steroid 5alpha-reductase; enzyme; testosterone conversion; inhibitor;  
KW rat; PCR primer; amplify; ss.  
XX  
OS Synthetic.  
OS Rattus sp.  
XX  
PN US5679521-A.  
XX  
PD 21-OCT-1997.  
XX  
PF 01-JUN-1995; 95US-00457616.  
XX  
PR 30-APR-1990; 90US-00517661.  
PR 18-NOV-1991; 91US-00795859.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Russell DW, Andersson S;  
XX  
DR WPI; 1997-525718/48.  
XX  
PT Production of recombinant steroid 5alpha-reductase enzyme - by culturing  
PT cell containing DNA encoding the enzyme.  
XX  
PS Example 1; Col 20; 70pp; English.  
XX  
CC This sequence is a primer for the DNA encoding rat steroid 5alpha-  
CC reductase. The encoded enzyme can be produced by the method of the  
CC invention. The method is for producing a steroid 5alpha-reductase, and  
CC comprises preparing a recombinant host cell containing a DNA segment  
CC encoding a steroid 5alpha-reductase and culturing the cell under  
CC conditions such that the steroid 5alpha-reductase is produced by the  
CC cell. The steroid 5alpha-reductase produced by the method is used for  
CC identifying substances that affect the enzymatic activity of steroid  
CC 5alpha-reductase. Substances identified as inhibiting steroid 5alpha-  
CC reductase activity can be used for inhibiting the conversion of  
CC testosterone  
XX  
SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAA 2804  
Db 29 AAAAAAAAAAAAAAAAAAAA 11

RESULT 1112  
AAI69697  
ID AAI69697 standard; DNA; 29 BP.  
XX  
AC AAI69697;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Hepatitis E virus HEV-T1 sequence related PCR primer #62.  
XX  
KW Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.

XX Unidentified.  
OS  
XX  
PN CN1300771-A.  
XX  
PD 27-JUN-2001.  
XX  
PF 23-DEC-1999; 99CN-00125741.  
XX  
PR 23-DEC-1999; 99CN-00125741.  
XX  
PA (CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.  
XX  
PI Wang Y, Zhang H, Li H;  
XX  
DR WPI; 2001-550442/62.  
XX  
PT Hepatitis E virus gene sequence and its application.  
XX  
PS Example 1; Page 15(Disclosure); 34pp; Chinese.  
XX  
CC The present invention relates to a novel nucleotide sequence and protein  
CC of a new hepatitis E virus HEV-T1 and the application of the nucleotide  
CC sequence and protein in diagnosing, preventing and treating hepatitis.  
CC The present sequence is a PCR primer described in the exemplification of  
CC the invention  
XX  
SQ Sequence 29 BP; 3 A; 3 C; 3 G; 20 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2165 CTTTTTTTTTTTTTTTTT 2183  
Db 11 CTTTTTTTTTTTTTTTTT 29

RESULT 1113  
ADA26182  
ID ADA26182 standard; DNA; 29 BP.  
XX  
AC ADA26182;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:27.  
XX  
KW genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;  
KW characteristic; single nucleotide polymorphism; SNP; genotyping;  
KW chromosome 1; gene; ds.  
XX  
OS Synthetic.  
OS Oryza sativa.  
XX  
PN WO2003070934-A1.  
XX  
PD 28-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-JP001317.  
XX  
PR 25-FEB-2002; 2002JP-00048115.  
XX  
PA (PLAN-) PLANT GENOME CENT CO LTD.  
XX  
PI Minobe Y, Monna L, Kitazawa N, Yoshino R, Suzuki J;  
XX  
DR WPI; 2003-697617/66.  
XX  
PT Judging the genotype of a region around a plant sd-1 gene with  
PT polymorphism-obtained markers isolated by positional cloning, useful in  
PT genotyping for examination of semi-dwarf character of rice.  
XX



CC having at least 2 portions, comprising treatment with nanoparticles that  
CC carry oligonucleotides complementary to at least 2 parts of (I), where  
CC detectable change caused by hybridisation of the oligonucleotide to (I)  
CC is observed. The method is used to detect (or to separate) specific (I),  
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic  
CC analysis etc., and generally to detect analytes other than (I). The  
CC oligonucleotide-derivatised nanoparticles are also useful for preparing  
CC nanostructures useful, for example, as biochips, biofilters, mechanical  
CC devices, separation membranes, chemical sensors, in computers, and for  
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be  
CC produced, allowing their direct use (as probes) in polymerase chain  
CC reaction, i.e. they survive multiple heating/cooling cycles so do not  
CC need to be added after amplification. (I) are detected by simple colour  
CC change, without the need for special equipment, making possible rapid  
CC field testing for e.g. pathogens. AAS63374-AAS63448 represent  
CC oligonucleotide-nanoparticle probes, and related sequences, used in the  
CC method of the invention

XX  
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1116  
AAS10385  
ID AAS10385 standard; DNA; 30 BP.  
XX  
AC AAS10385;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Oligonucleotide-cyclic disulphide linker, c1 #2.  
XX  
KW Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;  
KW DNA isolation; genetic disease; bacterial disease; viral disease;  
KW forensic science; paternity testing; gene therapy; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= a  
FT /note= "A is covalently linked to a cyclic-disulphide  
FT moiety"

XX WO200151665-A2.  
XX  
PD 19-JUL-2001.  
XX  
PF 12-JAN-2001; 2001WO-US001190.  
XX  
PR 13-JAN-2000; 2000US-0176409P.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
PR 12-JAN-2001; 2001US-00760500.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Li Z;  
XX  
DR WPI; 2001-451868/48.  
XX  
XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or  
PT viral diseases, by contacting the nucleic acid with oligonucleotides  
PT attached to nanoparticles and having sequences complementary a portion of  
PT the nucleic acid.

XX  
PS Example 24; Fig 44; 323pp; English.  
XX  
CC The sequence represents a cyclic disulphide linked oligonucleotide which  
CC may be coupled with colloidal gold particles (nanoparticles) and used to  
CC demonstrate the method of the invention. The invention relates to  
CC isolating or detecting a nucleic acid of interest, in a mixture of  
CC nucleic acids, by binding it to 2 or more complementary nucleotides which  
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.  
CC colloidal gold) are used to both isolate and detect (e.g. by linking the  
CC particle to a fluorescent probe) the resultant complex. The methods are  
CC useful for detecting nucleic acids, natural or synthetic, and modified or  
CC unmodified. The methods may also be applied in the diagnosis of genetic,  
CC bacterial and viral diseases, in forensics, in DNA sequencing, for  
CC paternity testing, for cell line authentication, and for monitoring gene  
CC therapy. The methods are further useful in research and analytical  
CC laboratories in DNA sequencing, in the field to detect the presence of  
CC specific pathogens, for quick identification of an infection to assist in  
CC drug prescription, and in homes and health centres for inexpensive first-  
CC line screening. The methods, which are based on observing colour change  
CC with the naked eye, are cheap, fast, simple, robust (reagents are  
CC stable), do not require specialised or expensive equipment, and little or  
CC no instrumentation is required

XX  
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1117  
ABK65048  
ID ABK65048 standard; DNA; 30 BP.  
XX  
AC ABK65048;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Nanoparticle-oligonucleotide #68.  
XX  
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;  
KW ss.  
XX  
OS Synthetic.  
XX  
PN WO200218643-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 10-AUG-2001; 2001WO-US025237.  
XX  
PR 11-AUG-2000; 2000US-0224631P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
DR WPI; 2002-258024/30.  
XX  
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or  
PT bacterial disease, comprises hybridizing nanoparticles with attached  
PT oligonucleotides to nucleic acid and detecting change brought about by  
PT hybridization.

XX PS Example 24; Fig 44; 412pp; English.

XX CC The invention relates to a method of detecting a nucleic acid (NA) having

CC at least 2 portions comprising: (a) providing nanoparticles (NP) with

CC attached oligonucleotides (OGN), where OGN has a sequence complementary

CC to the sequence of NA; (b) contacting NA and NP under conditions

CC effective to allow hybridisation of OGN with NA; and (c) observing a

CC detectable change brought about by hybridisation of OGN with NA. The

CC method is useful for detecting a nucleic acid, separating a selected

CC nucleic acid from others and methods of nanofabrication. Detecting

CC analytes such as nucleic acids and proteins are useful for the diagnosis

CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use

CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.

CC In particular assays using OGN-NP conjugates prepared using linkers

CC comprising a steroid residue attached to a cyclic disulphide have been

CC found to be approximately 10 times more sensitive than assays employing

CC conjugates prepared using alkanethiols or acyclic disulphides as the

CC linker. The OGN-NP conjugates are stable allowing them to be used

CC directly in PCR solutions. Therefore conjugates added as probes to a DNA

CC target to be PCR amplified can be carried through the 30 or 40 heating

CC cooling cycles of the PCR and are still able to detect the amplicons

CC without opening the tubes and causing contamination. ABK64981-ABK65055

CC represent nanoparticle-oligonucleotides of the invention

XX SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1118

ABS64686

ID ABS64686 standard; DNA; 30 BP.

AC ABS64686;

XX 15-NOV-2002 (first entry)

DT Nucleic acid detection method associated polynucleotide #68.

DE Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;

KW nanoparticle; viral RNA detection; bacterial DNA detection;

KW fungal DNA detection; nanoprobe conjugate; ss.

XX Synthetic.

OS WO200246472-A2.

XX 13-JUN-2002.

PD 07-DEC-2001; 2001WO-US046418.

XX 08-DEC-2000; 2000US-0254392P.

PR 08-DEC-2000; 2000US-0254418P.

PR 11-DEC-2000; 2000US-0255235P.

PR 11-DEC-2000; 2000US-0255236P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

PR 09-APR-2001; 2001US-0282640P.

PR 10-AUG-2001; 2001US-00927777.

XX (NANO-) NANOSPHERE INC.

PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

XX Taton TA, Garimella V, Li Z, Park S;

PI WPI; 2002-608256/65.

DR

XX PT Detecting nucleic acid having two portions, by providing nanoparticles

PT having oligonucleotides attached to it, contacting nucleic acid and

PT nanoparticles to allow hybridization, and observing detectable change.

XX Example 24; Fig 44; 442pp; English.

XX The invention describes a method of detecting (M1) a nucleic acid having

CC two portions, involving providing nanoparticles having oligonucleotides

CC attached to it, which has a sequence complementary to sequence of two

CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to

CC allow hybridisation of oligonucleotides with two or more portions of

CC nucleic acid, and observing a detectable change brought about by

CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide

CC conjugates (II) and the aggregate probe are useful for detecting two or

CC more nucleic acids (from a biological source) having at least two

CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated

CC with a disease, synthetic, or structurally-modified natural or synthetic

CC RNA or DNA, or a product of a polymerase chain reaction amplification.

CC (II) is useful for preparing a nanoprobe conjugate for detecting an

CC analyte, and for detecting a nucleic acid bound to an electrode surface.

CC (I) and (II) are useful for fabrication, and for separating a selected

CC nucleic acid having two portions from other nucleic acids. (I), (II) and

CC the aggregate probe are useful for detecting an analyte (especially

CC polyvalent analyte) in a sample. This sequence represents a

CC polynucleotide used to demonstrate the method of the invention

XX SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1119

AAL61658

ID AAL61658 standard; DNA; 30 BP.

XX AAL61658;

AC 22-SEP-2003 (first entry)

DT Oligonucleotide #19 used in the nucleic acid detection method.

DE Nucleic acid detection; fabrication; ss.

KW Unidentified.

OS WO2003035829-A2.

XX 01-MAY-2003.

PD 08-OCT-2002; 2002WO-US032088.

XX 09-OCT-2001; 2001US-0327864P.

PR 07-DEC-2001; 2001US-00008978.

XX (NANO-) NANOSPHERE INC.

PA Park S, Taton TA, Mirkin CA;

XX WPI; 2003-430409/40.

DR Detecting nucleic acid having two portions, by providing nanoparticles

XX having oligonucleotides attached to it, contacting nucleic acid and

PT nanoparticles to allow hybridization, and observing detectable change.

XX Example 24; Fig 44; 467pp; English.



CC The invention relates to a method of detecting a nucleic acid having two  
CC portions. The method involves providing nanoparticles having  
CC oligonucleotides attached to it which has a sequence complementary to  
CC sequence of two portions of nucleic acid, contacting nucleic acid and  
CC nanoparticles to allow hybridisation of oligonucleotides with two or more  
CC portions of nucleic acid and observing a detectable change brought about  
CC by hybridisation. The method and aggregate probes are useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic or structurally modified natural or  
CC synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. The invention is useful for preparing a nanoprobe  
CC conjugate for detecting an analyte and for detecting a nucleic acid bound  
CC to an electrode surface. It is also useful for fabrication and for  
CC separating a selected nucleic acid having two portions from other nucleic  
CC acids. The present sequence is an oligo used to illustrate the method of  
CC the invention  
XX  
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1120  
AAX77343/c  
ID AAX77343 standard; DNA; 30 BP.  
XX  
AC AAX77343;  
XX  
DT 09-AUG-1999 (first entry)  
XX  
DE Sindbis virus mRNA amplifying RT-PCR 3' primer.  
XX  
KW Nucleic acid identification; exogenous protein; gene sorting;  
KW growth factor; membrane receptor; sindbis virus; RT-PCR; primer; ss.  
XX  
OS Synthetic.  
OS Sindbis virus.  
XX  
PN WO9925876-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 17-NOV-1998; 98WO-US024520.  
XX  
PR 17-NOV-1997; 97US-00972218.  
XX  
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.  
XX  
PI Bailey JE, Renner WA, Orberger GH, Koller D;  
XX WPI; 1999-357620/30.  
DR  
XX Isolating genes encoding proteins with selected properties, useful for  
PT identifying therapeutic agents or targets.  
XX  
PS Disclosure; Page 66; 136pp; English.  
XX  
CC The invention relates to the identification of a recombinant nucleic acid  
CC encoding an exogenous protein having a selected property. The method  
CC comprises preparing a population of eukaryotic host cells, culturing the  
CC cells under suitable conditions and identifying cells that contain the  
CC recombinant nucleic acid. The method is used to sort genes according to  
CC the type of proteins they express, and also to identify new ligand/  
CC receptor interactions. Typical applications of the nucleic acid and the  
CC exogenous protein are in isolation of new growth factors, cytokines, of  
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of

CC which may be useful as therapeutic agents or therapeutic targets, e.g.  
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell  
CC proliferation or metabolic processes etc. The protein can also be used to  
CC screen for specific modulators. The nucleic acid can also be used as  
CC sources of therapeutic antisense or ribozyme sequences. The method allows  
CC the protein (rather than a partial DNA sequence) to be isolated and,  
CC since a wide range of cells can be used, they can be expressed with the  
CC correct glycosylation pattern  
XX  
SQ Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAAAAA 12  
  
RESULT 1121  
AAA90394/c  
ID AAA90394 standard; DNA; 30 BP.  
XX  
AC AAA90394;  
XX  
DT 10-JAN-2001 (first entry)  
XX  
DE Sindbis virus 3' RT-PCR primer.  
XX  
KW Nucleic acid identification; exogenous protein; drug screening;  
KW recombinant expression; pSINRep5 vector; mammalian expression system;  
KW reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Sindbis virus.  
OS Synthetic.  
XX  
PN JP2000189173-A.  
XX  
PD 11-JUL-2000.  
XX  
PF 23-AUG-1999; 99JP-00236220.  
XX  
PR 17-NOV-1998; 98US-00193707.  
PR 17-NOV-1998; 98WO-US024520.  
XX  
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.  
XX  
DR WPI; 2000-551637/51.  
XX  
PT Identifying a recombinant nucleic acid to identify and isolate various  
PT cellular proteins, comprises culturing a composition comprising  
PT eukaryotic host cells and identifying a cell comprising recombinant  
PT nucleic acid.  
XX  
PS Example; Page 35; 56pp; Japanese.  
XX  
CC The invention relates to the identification of a recombinant nucleic acid  
CC encoding an exogenous protein having a selected property. The method  
CC comprises preparing populations of eukaryotic host cells, where each cell  
CC comprises an expression vector encoding a different exogenous protein.  
CC The host cells are cultured under suitable conditions and the nucleic  
CC acid which encodes the exogenous protein is identified. The method is  
CC useful for the identification and isolation of proteins with a selected  
CC property. Typical applications of the nucleic acid and the exogenous  
CC protein are in isolation of new growth factors, cytokines, membrane  
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may  
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-  
CC apoptotic or tumour suppressing proteins, regulators of cell  
CC proliferation or of metabolic processes. The protein can also be used to  
CC screen for ligands and specific modulators of activity. The method of the  
CC invention allows the direct cloning of full length cDNAs in one step. It  
CC facilitates direct expression of the protein without the need to perform

CC further procedures such as subcloning and establishment of a cell line  
CC for protein production. The method allows a protein of interest (rather  
CC than a partial DNA sequence) to be isolated and, since a wide range of  
CC cell types can be used, they can be expressed in a correctly folded and  
CC glycosylated form. Sequences AAA90394-A90395 represent Sindbis virus  
CC reverse transcription-PCR (RT-PCR) primers used in the exemplifications  
CC of the invention. This patent is related to WO9925876  
XX  
SQ Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db ||||||  
30 AAAAAAAAAAAAAAAAAAAAAA 12  
  
RESULT 1122  
AAF26221  
ID AAF26221 standard; DNA; 30 BP.  
XX  
AC AAF26221;  
XX  
DT 26-APR-2001 (first entry)  
XX  
DE APC binding protein associated primer ON-AT+ SEQ ID 6.  
XX  
KW APC binding protein; cell proliferation; adenomatous polyposis coli;  
KW tumor cell detection; primer; ss.  
XX  
OS Unidentified.  
XX  
PN DE19933237-A1.  
XX  
PD 18-JAN-2001.  
XX  
PF 15-JUL-1999; 99DE-01033237.  
XX  
PR 15-JUL-1999; 99DE-01033237.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Mueller O;  
XX  
DR WPI; 2001-148321/16.  
XX  
PT Determining proliferative capacity of cells, useful e.g. for detecting  
PT tumor cells, by measuring concentration and subcellular localization of  
PT adenomatous polyposis coli protein.  
XX  
PS Claim 10; Page 12; 26pp; German.  
XX  
CC This invention describes a novel method for determining the proliferative  
CC activity of cells, comprising detecting, in a sample, the concentration  
CC and/or subcellular localization of APC (adenomatous polyposis coli)  
CC protein (I). The invention also describes (1) determining function of (I)  
CC in a sample by detecting presence of the C-terminal, DNA-binding domain  
CC of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting  
CC the DNA-binding domain of (I); (3) purifying, enriching and/or detecting  
CC (I) or its fragments by reaction with a probe; (4) double-stranded DNA  
CC (II) that contains the sequence GGCGCA<sub>2-3G</sub> (S1) and/or GATCCT<sub>2-3GC</sub>  
CC (S2); (5) peptide fragment of (I) containing at least the DNA-binding  
CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340  
CC -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,  
CC one of which is Ab and the other directed against the N-terminal region  
CC (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or  
CC its fragments in a sample consisting of (II), Ab or the set of (7). The  
CC method is used to detect proliferative, especially tumor (precursor),  
CC cells, to detect function of (I) and mutations in (I), and to purify  
CC and/or enrich (I), or its fragments, from a sample. The method allows  
CC simple, rapid and reliable detection of proliferation, without the need

CC for polymerase chain reaction or sequencing  
XX  
SQ Sequence 30 BP; 23 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db ||||||  
7 AAAAAAAAAAAAAAAAAAAAAA 25  
  
RESULT 1123  
AAQ43410/C  
ID AAQ43410 standard; DNA; 31 BP.  
XX  
AC AAQ43410;  
XX  
DT 25-MAR-2003 (revised)  
DT 29-OCT-1993 (first entry)  
XX  
DE Structural production oligonucleotide S-Strand-1.  
XX  
KW Molecular scaffolding; molecule orientation; orient; juxtaposition;  
KW functional artificial components; one; two; three; dimensional;  
KW structure formation; therapeutic; analytical; industrial; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1. .15  
FT /\*tag= a  
FT /note= "exposed/exposable sticky end"  
FT misc\_feature 1  
FT /\*tag= b  
FT /note= "PO4-Cytosine"  
FT misc\_feature 31  
FT /\*tag= c  
FT /note= "Thymine - Teflon based solid support"  
XX  
PN WO9312244-A1.  
XX  
PD 24-JUN-1993.  
XX  
PF 03-DEC-1992; 92WO-US010431.  
XX  
PR 12-DEC-1991; 91US-00805564.  
XX  
PA (UYN Y ) UNIV NEW YORK STATE.  
XX  
PI Seeman NC, Zhang Y;  
XX  
DR WPI; 1993-214185/26.  
XX  
PT Prodn. of structure including double stranded polynucleotide - comprises  
PT cleavage of loop in core structure of 1st polynucleotide with restriction  
PT enzyme and ligation to 2nd polynucleotide, used to orient mols., etc.  
XX  
PS Example; Page 34; 58pp; English.  
XX  
CC The sequence is that of the oligonucleotide S-Strand-1 which can be used  
CC in the formation or modification of one-, two- and three- dimensional  
CC structures. It may be used as molecular scaffolding to orient and  
CC juxtapose other molecules. It has analytical, industrial or therapeutical  
CC potential. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 31 BP; 2 A; 4 C; 2 G; 23 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
OS HEPATITIS VIRUS.  
XX  
PN JP04084887-A.  
XX  
PD 18-MAR-1992.  
XX  
PF 25-JUL-1990; 90JP-00198588.  
XX  
PR 25-JUL-1990; 90JP-00198588.  
XX  
PA (KAGA ) KAGAKU OYOBI KESSEI RYOH.  
XX  
DR WPI; 1992-145501/18.  
XX  
PT Nucleic acid fragment coding peptide of non-A non-B hepatitis virus - for  
PT the early diagnosis of non-A non-B hepatitis by ELISA or agglutination  
PT methods.  
XX  
PS Example 2; Page 7; 12pp; Japanese.  
XX  
CC This sequence represents a primer for the coding sequence for a non-A non  
CC -B hepatitis virus peptide. The protein encoded by the amplified sequence  
CC can be used to prepare an antibody specific for non-A non-B hepatitis  
CC virus. The peptide and antibody can be used in both ELISA and  
CC agglutination methods and is useful in the early diagnosis of non-A non-B  
CC hepatitis  
XX  
SQ Sequence 32 BP; 1 A; 5 C; 5 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 32 AAAAAAAAAAAAAAAAAAAAAA 14  
  
RESULT 1126  
AAT77235/c  
ID AAT77235 standard; DNA; 32 BP.  
XX  
AC AAT77235;  
XX  
DT 12-FEB-1998 (first entry)  
XX  
DE Rat fibroblast growth factor FGF-10 RACE primer X.  
XX  
KW Fibroblast growth factor; rat; human; recombinant DNA; bone disease;  
KW wound healing; cartilage; RACE primer; ss.  
XX  
OS Synthetic.  
OS Rattus rattus.  
XX  
PN WO9720929-A1.  
XX  
PD 12-JUN-1997.  
XX  
PF 06-DEC-1996; 96WO-JP003579.  
XX  
PR 07-DEC-1995; 95JP-00345689.  
PR 28-MAR-1996; 96JP-00103240.  
PR 24-JUL-1996; 96JP-00214378.  
XX  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
XX  
PI Itoh N, Negoro T, Katsumata T, Tagashira S;  
XX  
DR WPI; 1997-319776/29.  
XX  
PT Recombinant fibroblast growth factor FGF-10 and related DNA - useful for  
PT the treatment of bone disease and for wound healing.

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 31 AAAAAAAAAAAAAAAAAAAAAA 13  
  
RESULT 1124  
AAF60568/c  
ID AAF60568 standard; DNA; 32 BP.  
XX  
AC AAF60568;  
XX  
DT 27-APR-2001 (first entry)  
XX  
DE Neuraminidase PCR primer #6.  
XX  
KW PCR primer; virucide; vaccine; gene therapy; neuraminidase; vaccine;  
KW immune response; ss.  
XX  
OS Influenza virus.  
XX  
PN WO200109291-A1.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-GB002933.  
XX  
PR 30-JUL-1999; 99GB-00017981.  
PR 30-JUL-1999; 99US-0146145P.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Brownlee GG, Fodor E, Poon L;  
XX  
DR WPI; 2001-159859/16.  
XX  
PT New negative-sense single stranded RNA virus, e.g. influenza virus,  
PT attenuated by replacing the poly U track with a poly A track, useful as a  
PT vaccine and in gene therapy.  
XX  
PS Example 7; Page 28; 49pp; English.  
XX  
CC The present invention relates to an attenuated influenza virus. The virus  
CC is attenuated by replacement of the poly U track in a genomic nucleic  
CC acid by a poly A track capable of being copied to provide a poly U tail  
CC for mRNA transcribed from the nucleic acid. The attenuated virus is  
CC useful as a vaccine, for immunisation against diseases caused by the  
CC equivalent wild type viruses. The present sequence is a PCR primer used  
CC to generate the virus of the present invention  
XX  
SQ Sequence 32 BP; 1 A; 6 C; 4 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
DB 32 AAAAAAAAAAAAAAAAAAAAAA 14  
  
RESULT 1125  
AAV03988/c  
ID AAV03988 standard; DNA; 32 BP.  
XX  
AC AAV03988;  
XX  
DT 13-MAY-1998 (first entry)  
XX  
DE Primer B for Non-A non-B hepatitis viral peptide coding sequence.  
XX  
KW Non-A non-B hepatitis virus; antibody production; infection diagnosis;  
KW PCR primer; amplify; ss.  
XX

XX Example 1; Page 36; 5lpp; Japanese.

CC The present sequence represents a RACE primer involved in the

CC amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,

CC vectors, containing the DNA, and host cells, containing the vectors, are

CC useful for the recombinant production of FGF-10. The recombinant FGF-10

CC is useful for the treatment of diseases and injury of bone or cartilage,

CC and as a wound healing promoter

XX

SQ Sequence 32 BP; 3 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 32 AAAAAAAAAAAAAAAAAAAAAA 14

RESULT 1127

AAS63424

ID AAS63424 standard; DNA; 32 BP.

XX

AC AAS63424;

DT 29-JAN-2002 (first entry)

XX

DE Oligonucleotide-nanoparticle probe #48.

XX

KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;

KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;

KW ss.

OS Synthetic.

XX

PN WO200173123-A2.

XX

PD 04-OCT-2001.

XX

PF 28-MAR-2001; 2001WO-US010071.

XX

PR 28-MAR-2000; 2000US-0192699P.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

PR 26-JUN-2000; 2000US-0213906P.

PR 08-DEC-2000; 2000US-0254392P.

PR 11-DEC-2000; 2000US-0255235P.

PR 12-JAN-2001; 2001US-00760500.

PR 28-MAR-2001; 2001US-00820279.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Park S, Li Z;

XX

DR WPI; 2001-656926/75.

XX

PT Detecting and separating nucleic acid, useful e.g. for diagnosis,

PT comprises reaction with nanoparticles that carry oligonucleotides

PT complementary to parts of the target.

XX

PS Example 18; Page 148; 404pp; English.

XX

CC The invention relates to a method for detection of nucleic acid (I)

CC having at least 2 portions, comprising treatment with nanoparticles that

CC carry oligonucleotides complementary to at least 2 parts of (I), where

CC detectable change caused by hybridisation of the oligonucleotide to (I)

CC is observed. The method is used to detect (or to separate) specific (I),

CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic

CC analysis etc., and generally to detect analytes other than (I). The

CC oligonucleotide-derivatised nanoparticles are also useful for preparing

CC nanostructures useful, for example, as biochips, biofilters, mechanical

CC devices, separation membranes, chemical sensors, in computers, and for

CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be

CC produced, allowing their direct use (as probes) in polymerase chain

CC reaction, i.e. they survive multiple heating/cooling cycles so do not

CC need to be added after amplification. (I) are detected by simple colour

CC change, without the need for special equipment, making possible rapid

CC field testing for e.g. pathogens. AAS63374-AAS63448 represent

CC oligonucleotide-nanoparticle probes, and related sequences, used in the

CC method of the invention

XX

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1128

AAS10367

ID AAS10367 standard; DNA; 32 BP.

XX

AC AAS10367;

XX

DT 24-OCT-2001 (first entry)

XX

DE Alkanethiol-modified oligonucleotide, SA2012F.

XX

KW Nanoparticle; alkanethiol-modified oligonucleotide; DNA detection;

KW DNA isolation; genetic disease; bacterial disease; viral disease;

KW forensic science; paternity testing; gene therapy; ss; SA2012F.

XX

OS Synthetic.

XX

XX

FH Key Location/Qualifiers

FT misc\_feature 1

FT /\*tag= a

FT /note= "A is covalently linked to a hexythiol moiety"

FT misc\_feature 12

FT /\*tag= b

FT /note= "T is covalently linked to a fluorescein moiety"

PN WO200151665-A2.

XX

PD 19-JUL-2001.

XX

PF 12-JAN-2001; 2001WO-US001190.

XX

PR 13-JAN-2000; 2000US-0176409P.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

PR 12-JAN-2001; 2001US-00760500.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Li Z;

XX

DR WPI; 2001-451868/48.

XX

PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or

PT viral diseases, by contacting the nucleic acid with oligonucleotides

PT attached to nanoparticles and having sequences complementary a portion of

PT the nucleic acid.

XX

PS Example 18; Page 320; 323pp; English.

XX

CC The sequence represents an alkanethiol-modified oligonucleotide which may

CC be coupled with colloidal gold particles (nanoparticles) and used to



CC demonstrate the method of the invention. The invention relates to  
CC isolating or detecting a nucleic acid of interest, in a mixture of  
CC nucleic acids, by binding it to 2 or more complementary nucleotides which  
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.  
CC colloidal gold) are used to both isolate and detect (e.g. by linking the  
CC particle to a fluorescent probe) the resultant complex. The methods are  
CC useful for detecting nucleic acids, natural or synthetic, and modified or  
CC unmodified. The methods may also be applied in the diagnosis of genetic,  
CC bacterial and viral diseases, in forensics, in DNA sequencing, for  
CC paternity testing, for cell line authentication, and for monitoring gene  
CC therapy. The methods are further useful in research and analytical  
CC laboratories in DNA sequencing, in the field to detect the presence of  
CC specific pathogens, for quick identification of an infection to assist in  
CC drug prescription, and in homes and health centres for inexpensive first-  
CC line screening. The methods, which are based on observing colour change  
CC with the naked eye, are cheap, fast, simple, robust (reagents are  
CC stable), do not require specialised or expensive equipment, and little or  
CC no instrumentation is required  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1129  
ABK65031  
ID ABK65031 standard; DNA; 32 BP.  
XX  
AC ABK65031;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Nanoparticle-oligonucleotide #51.  
XX  
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;  
KW ss.  
XX Synthetic.  
XX WO200218643-A2.  
XX  
PD 07-MAR-2002.  
XX  
PF 10-AUG-2001; 2001WO-US025237.  
XX  
PR 11-AUG-2000; 2000US-0224631P.  
PR 08-DEC-2000; 2000US-0254392P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
DR WPI; 2002-258024/30.  
XX  
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or  
PT bacterial disease, comprises hybridizing nanoparticles with attached  
PT oligonucleotides to nucleic acid and detecting change brought about by  
PT hybridization.  
XX  
PS Example 18; Page 162; 412pp; English.  
XX  
CC The invention relates to a method of detecting a nucleic acid (NA) having  
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with

CC attached oligonucleotides (OGN), where OGN has a sequence complementary  
CC to the sequence of NA; (b) contacting NA and NP under conditions  
CC effective to allow hybridisation of OGN with NA; and (c) observing a  
CC detectable change brought about by hybridisation of OGN with NA. The  
CC method is useful for detecting a nucleic acid, separating a selected  
CC nucleic acid from others and methods of nanofabrication. Detecting  
CC analytes such as nucleic acids and proteins are useful for the diagnosis  
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use  
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.  
CC In particular assays using OGN-NP conjugates prepared using linkers  
CC comprising a steroid residue attached to a cyclic disulphide have been  
CC found to be approximately 10 times more sensitive than assays employing  
CC conjugates prepared using alkanethiols or acyclic disulphides as the  
CC linker. The OGN-NP conjugates are stable allowing them to be used  
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA  
CC target to be PCR amplified can be carried through the 30 or 40 heating  
CC cooling cycles of the PCR and are still able to detect the amplicons  
CC without opening the tubes and causing contamination. ABK64981-ABK65055  
CC represent nanoparticle-oligonucleotides of the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1130  
ABS64669  
ID ABS64669 standard; DNA; 32 BP.  
XX  
AC ABS64669;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Nucleic acid detection method associated polynucleotide #51.  
XX  
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;  
KW nanoparticle; viral RNA detection; bacterial DNA detection;  
KW fungal DNA detection; nanoprobe conjugate; ss.  
XX Synthetic.  
XX WO200246472-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 07-DEC-2001; 2001WO-US046418.  
XX  
PR 08-DEC-2000; 2000US-0254392P.  
PR 08-DEC-2000; 2000US-0254418P.  
PR 11-DEC-2000; 2000US-0255235P.  
PR 11-DEC-2000; 2000US-0255236P.  
PR 12-JAN-2001; 2001US-00760500.  
PR 28-MAR-2001; 2001US-00820279.  
PR 09-APR-2001; 2001US-0282640P.  
PR 10-AUG-2001; 2001US-00927777.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA, Garimella V, Li Z, Park S;  
XX  
DR WPI; 2002-608256/65.  
XX  
XX Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change.  
XX

PS Example 18; Page 436; 442pp; English.

XX The invention describes a method of detecting (M1) a nucleic acid having

CC two portions, involving providing nanoparticles having oligonucleotides

CC attached to it, which has a sequence complementary to sequence of two

CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to

CC allow hybridisation of oligonucleotides with two or more portions of

CC nucleic acid, and observing a detectable change brought about by

CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide

CC conjugates (II) and the aggregate probe are useful for detecting two or

CC more nucleic acids (from a biological source) having at least two

CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated

CC with a disease, synthetic, or structurally-modified natural or synthetic

CC RNA or DNA, or a product of a polymerase chain reaction amplification.

CC (II) is useful for preparing a nanoprobe conjugate for detecting an

CC analyte, and for detecting a nucleic acid bound to an electrode surface.

CC (I) and (II) are useful for fabrication, and for separating a selected

CC nucleic acid having two portions from other nucleic acids. (I), (II) and

CC the aggregate probe are useful for detecting an analyte (especially

CC polyvalent analyte) in a sample. This sequence represents a

CC polynucleotide used to demonstrate the method of the invention

XX

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1131

ACD27316

ID ACD27316 standard; DNA; 32 BP.

XX

AC ACD27316;

XX

DT 15-OCT-2003 (first entry)

XX

DE Nanotechnology nucleic acid detection method associated #50.

XX

KW Nanotechnology; ss; nucleic acid detection; nanoparticle;

KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;

KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;

KW sexually transmitted disease; inherited disorder; forensic;

KW paternity testing; cell line authentication.

XX

OS Synthetic.

XX

PN US2002155461-A1.

XX

PD 24-OCT-2002.

XX

PF 12-OCT-2001; 2001US-00976378.

XX

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX

DR WPI; 2003-228115/22.

XX

PT Detecting nucleic acids having 2 portions e.g. for detecting disease,

PT comprises use of nanoparticles which have oligonucleotides attached to

PT them that are complementary to portions of the nucleic acid sequence.

XX

PS Example 18; Page 40; 130pp; English.

XX

CC This invention relates to a novel method for detecting a nucleic acid

CC having 2 portions. The method comprises providing nanoparticles having

CC oligonucleotides attached, where the oligonucleotide on each nanoparticle

CC has a sequence complementary to a sequence of 2 portions of nucleic acid.

CC The nucleic acid and nanoparticle are contacted to allow hybridisation of

CC the oligonucleotide on the nanoparticle with two or more portions of

CC nucleic acid and observing a detectable change brought about by the

CC hybridisation. The method of the invention is useful for separating a

CC selected nucleic acid having 2 portions, from other nucleic acids, and

CC for detecting nucleic acids having 2 portions. The method of the

CC invention is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.

CC Preferably, the method is useful for detecting nucleic acids for

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency

CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr

CC virus), bacterial diseases, sexually transmitted diseases, inherited

CC disorders, in forensics, in DNA sequencing, for paternity testing, for

CC cell line authentication, for monitoring gene therapy, etc. This method

CC involves detecting nucleic acids based on observing a colour change with

CC the naked eye so is cheap, fast, simple and robust, and does not require

CC specialised expensive equipment. The present sequence represents an

CC oligonucleotide used to demonstrate the method of the invention

XX

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1132

AAL61641

ID AAL61641 standard; DNA; 32 BP.

XX

AC AAL61641;

XX

DT 22-SEP-2003 (first entry)

XX

DE Thiol-modified oligo #2 used in the nucleic acid detection method.

XX

KW Nucleic acid detection; fabrication; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT misc\_feature 1 /\*tag= a

FT /\*note= "Linked to HS(CH2)6 group"

FT misc\_feature 32

FT /\*tag= b

FT /\*note= "Linked to (CH2)6-F (fluorescein)"

PN WO2003035829-A2.

XX

PD 01-MAY-2003.

XX

PF 08-OCT-2002; 2002WO-US032088.

XX

PR 09-OCT-2001; 2001US-0327864P.

PR 07-DEC-2001; 2001US-00008978.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Park S, Taton TA, Mirkin CA;

XX

DR WPI; 2003-430409/40.

XX Detecting nucleic acid having two portions, by providing nanoparticles

PT having oligonucleotides attached to it, contacting nucleic acid and

PT nanoparticles to allow hybridization, and observing detectable change.

XX

PS Example 18; Page 167; 467pp; English.

XX

CC The invention relates to a method of detecting a nucleic acid having two

CC portions. The method involves providing nanoparticles having

CC oligonucleotides attached to it which has a sequence complementary to

CC sequence of two portions of nucleic acid, contacting nucleic acid and

CC nanoparticles to allow hybridisation of oligonucleotides with two or more

CC portions of nucleic acid and observing a detectable change brought about

CC by hybridisation. The method and aggregate probes are useful for

CC detecting two or more nucleic acids (from a biological source) having at

CC least two portions such as viral RNA, bacterial or fungal DNA, a gene

CC associated with a disease, synthetic or structurally modified natural or

CC synthetic RNA or DNA, or a product of a polymerase chain reaction

CC amplification. The invention is useful for preparing a nanoprobe

CC conjugate for detecting an analyte and for detecting a nucleic acid bound

CC to an electrode surface. It is also useful for fabrication and for

CC separating a selected nucleic acid having two portions from other nucleic

CC acids. The present sequence is an oligo used to illustrate the method of

CC the invention

XX

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1133

ABX79177

ID ABX79177 standard; DNA; 32 BP.

XX

AC ABX79177;

XX

DT 15-APR-2003 (first entry)

XX

DE Fluorescein-labelled alkanethiol-modified oligonucleotide #2.

XX

KW Nanoparticle; ss; nucleic acid detection; viral disease;

KW human immunodeficiency virus infection; hepatitis virus infection;

KW herpes virus infection; cytomegalovirus infection; forensic science;

KW Epstein-Barr virus infection; bacterial disease; gene therapy;

KW sexually transmitted disease; inherited disorder; DNA sequencing;

KW paternity testing; cell line authentication.

XX

OS Synthetic.

OS

XX US2002155462-A1.

XX

PD 24-OCT-2002.

XX

PF 12-OCT-2001; 2001US-00976577.

XX

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX WPI; 2003-198491/19.

DR Detecting nucleic acids having at least 2 portions comprises use of

XX nanoparticles which have oligonucleotides attached to them that are

PT complementary to portions of the nucleic acid sequence.

PT

XX

PS Example 18; Page 40; 130pp; English.

XX

CC The invention relates to detecting a nucleic acid (NA) having at least 2

CC portions, comprising providing a type of nanoparticles (NP) having

CC attached to oligonucleotides (O) (O) on each NP has a sequence

CC complementary to sequence of at least 2 portions of NA, contacting NA

CC and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,

CC and observing a detectable change brought about by hybridisation of (O)

CC on NP with NA. The nanoparticle is useful for separating a selected

CC nucleic acid having at least 2 portions, from other nucleic acids, and

CC for detecting nucleic acids having at least 2 portions. The method of

CC using NP is useful for detecting any type of nucleic acids which may be

CC used for diagnosis of disease and in sequencing of nucleic acids.

CC Preferably, the method is useful for detecting nucleic acids for

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency

CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr

CC virus), bacterial diseases, sexually transmitted diseases, inherited

CC disorders, in forensics, in DNA sequencing, for paternity testing, for

CC cell line authentication and for monitoring gene therapy. The method is

CC useful in research and analytical laboratories in DNA sequencing and in

CC the field to detect the presence of specific pathogens. Detecting nucleic

CC acids based on observing a colour change with the naked eye is cheap,

CC fast, simple and robust, and do not require specialised expensive

CC equipment. The present sequence is a fluorescein labelled oligonucleotide

CC used to demonstrate the method of the invention

XX

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1134

ABX92173

ID ABX92173 standard; DNA; 32 BP.

XX

AC ABX92173;

XX

DT 12-MAY-2003 (first entry)

XX

DE Nanoparticle-associated oligonucleotide SEQ ID 51.

XX

KW Nonparticle; nucleic acid detection; hybridisation; diagnosis;

KW sequencing; viral infection; human immunodeficiency virus; HIV;

KW hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;

KW bacterial infection; sexually transmitted disease; inherited disorder;

KW forensic; paternity testing; cell line authentication; gene therapy; ss.

XX

OS Synthetic.

OS

XX US2002155458-A1.

XX

PD 24-OCT-2002.

XX

PF 28-SEP-2001; 2001US-00967409.

XX

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.



PR 26-JUN-2000; 2000US-00603830.  
XX (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
XX WPI; 2003-182627/18.  
XX  
PT Detecting nucleic acids having at least two portions involves use of  
PT nanoparticles which have oligonucleotides attached to them that are  
PT complementary to portions of the nucleic acid sequence.  
XX  
PS Example 18; Page 59; 130pp; English.  
XX  
CC This invention describes a novel method of detecting nucleic acid having  
CC at least two portions. The method involves providing nanoparticles  
CC attached to oligonucleotides, where the oligonucleotide on each  
CC nanoparticle have a sequence complementary to a sequence of at least two  
CC portions of nucleic acid, contacting nucleic acid and nanoparticle to  
CC allow hybridisation of the oligonucleotide on the nanoparticle with two  
CC or more portions of nucleic acid and observing a detectable change  
CC brought about by hybridisation of the oligonucleotide nanoparticle with  
CC nucleic acid. The method is useful for separating a selected nucleic acid  
CC having at least two portions, from other nucleic acids and for detecting  
CC nucleic acids having at least two portions. The method is useful for  
CC detecting any type of nucleic acids which may be used for diagnosis of  
CC disease and in sequencing of nucleic acids. Preferably, the method is  
CC useful for detecting nucleic acids for diagnosis and/or monitoring of  
CC viral infections (human immunodeficiency virus (HIV), hepatitis virus,  
CC herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial  
CC diseases, sexually transmitted diseases, inherited disorders, in  
CC forensics, in DNA sequencing, for paternity testing, for cell line  
CC authentication, and for monitoring gene therapy. The method is useful in  
CC research and analytical laboratories in DNA sequencing, in the field to  
CC detect the presence of specific pathogens. Detecting nucleic acids based  
CC on observing a colour change with the naked eye is cheap, fast, simple  
CC and robust and does not require specialised expensive equipment. ABX92123  
CC -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the  
CC method of the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 1135  
ACD27251  
ID ACD27251 standard; DNA; 32 BP.  
XX  
XX ACD27251;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #50.  
XX  
KW Nanotechnology; ss; nucleic acid detection; nanoparticle;  
KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;  
KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;  
KW sexually transmitted disease; inherited disorder; forensic;  
KW paternity testing; cell line authentication.  
XX  
OS Synthetic.  
XX  
PN US2002155459-A1.  
XX  
PD 24-OCT-2002.

XX 11-OCT-2001; 2001US-00975062.  
PF  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
XX (NANO-) NANOSPHERE INC.  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
XX WPI; 2003-228114/22.  
XX  
PT Detecting nucleic acids having 2 portions e.g. for detecting disease,  
PT comprises use of nanoparticles which have oligonucleotides attached to  
PT them that are complementary to portions of the nucleic acid sequence.  
XX  
PS Example 18; Page 40; 129pp; English.  
XX  
CC This invention relates to a novel method for detecting a nucleic acid  
CC having 2 portions. The method comprises providing nanoparticles having  
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle  
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.  
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of  
CC the oligonucleotide on the nanoparticle with two or more portions of  
CC nucleic acid and observing a detectable change brought about by the  
CC hybridisation. The method of the invention is useful for separating a  
CC selected nucleic acid having 2 portions, from other nucleic acids, and  
CC for detecting nucleic acids having 2 portions. The method of the  
CC invention is useful for detecting any type of nucleic acids which may be  
CC used for diagnosis of disease and in sequencing of nucleic acids.  
CC Preferably, the method is useful for detecting nucleic acids for  
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency  
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr  
CC virus), bacterial diseases, sexually transmitted diseases, inherited  
CC disorders, in forensics, in DNA sequencing, for paternity testing, for  
CC cell line authentication, for monitoring gene therapy, etc. This method  
CC involves detecting nucleic acids based on observing a colour change with  
CC the naked eye so is cheap, fast, simple and robust, and does not require  
CC specialised expensive equipment. The present sequence represents an  
CC oligonucleotide used to demonstrate the method of the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
  
RESULT 1136  
ACD27121  
ID ACD27121 standard; DNA; 32 BP.  
XX  
XX ACD27121;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method oligonucleotide #50.  
XX  
KW Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;  
KW DNA sequencing; paternity testing; cell line authentication.  
XX  
OS Synthetic.  
XX  
PN US2002164605-A1.



XX 07-NOV-2002.  
PD  
XX  
XX  
PF 28-SEP-2001; 2001US-00966312.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
XX WPI; 2003-247253/24.  
XX  
PT Detecting nucleic acid having two portions, by providing nanoparticles  
PT having oligonucleotides attached to it, contacting nucleic acid and  
PT nanoparticles to allow hybridization, and observing detectable change,  
PT useful in forensics.  
XX  
PS Example 18; Page 40; 130pp; English.  
XX  
CC This invention relates to a novel method for detecting nucleic acid  
CC sequences having two portions. The method involves providing  
CC nanoparticles having oligonucleotides attached to them, which has a  
CC sequence complementary to sequence of two portions of nucleic acid,  
CC contacting nucleic acid and nanoparticles, to allow hybridisation of  
CC oligonucleotides with two or more portions of nucleic acid, and observing  
CC a detectable change brought about by hybridisation. The method of the  
CC invention and the aggregate probes are useful for detecting two or more  
CC nucleic acids (from a biological source) having at least two portions,  
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with  
CC a disease, synthetic, or structurally- modified natural or synthetic RNA  
CC or DNA, or a product of a polymerase chain reaction amplification.  
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the  
CC invention are useful for nanofabrication, and for separating a selected  
CC nucleic acid having two portions from other nucleic acids. The method of  
CC the invention is useful in forensics, DNA sequencing, for paternity  
CC testing, cell line authentication, and monitoring gene therapy.  
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates  
CC of the invention improve the sensitivity of the nucleic acid detection  
CC assay. The present sequence represents an oligonucleotide used to  
CC demonstrate the method of the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1137  
ACD27381  
ID ACD27381 standard; DNA; 32 BP.  
XX  
AC ACD27381;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #50.  
XX  
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;  
KW pathogen detection.  
XX  
OS Synthetic.

XX US2002182611-A1.  
XX  
XX 05-DEC-2002.  
XX  
PF 28-SEP-2001; 2001US-00966491.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
XX WPI; 2003-596264/56.  
XX  
PT Detection of nucleic acid for, e.g. research and analytical laboratories  
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid  
PT with nanoparticles having oligonucleotides.  
XX  
PS Example 18; Page 40; 109pp; English.  
XX  
CC This invention relates to a novel method for detecting a nucleic acid by  
CC contacting a nucleic acid with at least two types of nanoparticles having  
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides  
CC on the nanoparticles, and observing a detectable change. The  
CC oligonucleotides on each nanoparticle have a sequence complementary to  
CC its respective portion of the sequence of the nucleic acid to be  
CC detected. The method of the invention may be used for the detection of a  
CC nucleic acid used in, e.g. research and analytical laboratories in DNA  
CC sequencing, in the field to detect the presence of specific pathogens, in  
CC the doctor's office for quick identification of an infection to assist in  
CC prescribing a drug for treatment, and in homes and health centres for  
CC inexpensive first-line screening. The method of the invention detects  
CC nucleic acids based on observing a colour change with the naked eye. This  
CC method is cheap, fast, simple, robust and does not require specialised or  
CC expensive equipment. The present sequence represents an oligonucleotide  
CC used to demonstrate the method of the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1138  
ACD27186  
ID ACD27186 standard; DNA; 32 BP.  
XX  
AC ACD27186;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method associated #50.  
XX  
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.  
XX  
OS Synthetic.  
XX  
PN US2002182613-A1.  
XX  
PD 05-DEC-2002.

PF 12-OCT-2001; 2001US-00976971.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-596265/56.  
XX  
PT Detection of nucleic acid for, e.g. research and analytical laboratories  
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid  
PT with nanoparticles having oligonucleotides.  
XX  
PS Example 18; Page 40; 107pp; English.  
XX  
CC This invention relates to a novel method for detecting a nucleic acid by  
CC contacting nucleic acid with at least two types of nanoparticles having  
CC oligonucleotides, allowing hybridisation of the oligonucleotides on the  
CC nanoparticles, and observing a detectable change. The oligonucleotides on  
CC each nanoparticle have a sequence complementary to its respective portion  
CC of the sequence of the nucleic acid. The method of the invention may be  
CC used for the detection of a nucleic acid used in, e.g. research and  
CC analytical laboratories in DNA sequencing, in the field to detect the  
CC presence of specific pathogens, in the doctor's office for quick  
CC identification of an infection, to assist in prescribing a drug for  
CC treatment, and in homes and health centres for inexpensive first-line  
CC screening. The inventive method of detecting nucleic acids based on  
CC observing a colour change with the naked eye are cheap, fast, simple,  
CC robust (the reagents are stable), do not require specialised or expensive  
CC equipment, and little or no instrumentation is required. The present  
CC sequence represents an oligonucleotide used to demonstrate the method of  
CC the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1139  
ACD27056  
ID ACD27056 standard; DNA; 32 BP.  
XX  
AC ACD27056;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method oligonucleotide #50.  
XX  
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
XX  
OS Synthetic.  
XX  
PN US2003044805-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 15-OCT-2001; 2001US-00981344.  
XX  
PR 29-JUL-1996; 96US-0031809P.  
PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX  
DR WPI; 2003-521746/49.  
XX  
PT Detection of nucleic acid having -2 portions used to prepare biomaterials  
PT and in nanofabrication methods, comprises providing nanoparticles,  
PT contacting nucleic acid and nanoparticles, and observing change.  
XX  
PS Example 18; Page 40; 130pp; English.  
XX  
CC This invention relates to a novel method for detecting nucleic acids. The  
CC method comprises providing nanoparticles with oligonucleotides attached  
CC to them, which have a sequence complementary to a sequence of two  
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles  
CC to allow hybridisation of the oligonucleotides with two or more portions  
CC of the nucleic acid, and observing a detectable change brought about by  
CC the hybridisation. The nucleic acid to be detected must have at least two  
CC portions and the distances between these are chosen so that when the  
CC nanoparticle-oligonucleotide conjugate binds the target sequence a  
CC detectable change occurs. The method of the invention is useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic, or structurally- modified natural  
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
CC and for detecting a nucleic acid bound to an electrode surface.  
CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
CC nanofabrication and for separating a selected nucleic acid having two  
CC portions from other nucleic acids. Diagnostic assays employing  
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
CC nucleic acid detection methods and can be used to detect nucleic acids  
CC that are present in only small amounts in a sample. The invention also  
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These  
CC conjugates are stable with tailored hybridisation abilities. The present  
CC sequence represents an oligonucleotide used to demonstrate the method of  
CC the invention  
XX  
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19  
  
RESULT 1140  
ACH00060  
ID ACH00060 standard; DNA; 32 BP.  
XX  
AC ACH00060;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Nanotechnology nucleic acid detection method oligonucleotide #50.  
XX  
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.  
XX  
OS Synthetic.  
XX  
PN US2003049631-A1.  
XX

PD 13-MAR-2003.  
XX 10-OCT-2001; 2001US-00974500.  
PF 29-JUL-1996; 96US-0031809P.  
XX 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX (NANO-) NANOSPHERE INC.  
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
PI Taton TA;  
XX WPI; 2003-634854/60.  
DR Detection of nucleic acid having at least two portions, by contacting  
XX nucleic acid and nanoparticles under conditions, which allows  
PT hybridization of oligonucleotides on nanoparticles with at least two  
PT portions of nucleic acid.  
XX Example 18; Page 40; 108pp; English.  
PS This invention relates to a novel method for detecting nucleic acids. The  
XX method comprises providing nanoparticles with oligonucleotides attached  
CC to them, which have a sequence complementary to a sequence of two  
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles  
CC to allow hybridisation of the oligonucleotides with two or more portions  
CC of the nucleic acid, and observing a detectable change brought about by  
CC the hybridisation. The nucleic acid to be detected must have at least two  
CC portions and the distances between these are chosen so that when the  
CC nanoparticle-oligonucleotide conjugate binds the target sequence a  
CC detectable change occurs. The method of the invention is useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic, or structurally- modified natural  
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention  
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,  
CC and for detecting a nucleic acid bound to an electrode surface.  
CC Nanoparticles and nanoparticle conjugates of the invention are useful for  
CC nanofabrication and for separating a selected nucleic acid having two  
CC portions from other nucleic acids. Diagnostic assays employing  
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of  
CC nucleic acid detection methods and can be used to detect nucleic acids  
CC that are present in only small amounts in a sample. The invention also  
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These  
CC conjugates are stable with tailored hybridisation abilities. The present  
CC sequence represents an oligonucleotide used to demonstrate the method of  
CC the invention  
XX SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
DB 1 AAAAAAAAAAAAAAAAAA 19  
RESULT 1141  
ADA06155  
ID ADA06155 standard; DNA; 32 BP.  
XX AC ADA06155;  
XX DT 06-NOV-2003 (first entry)  
XX DE Nanoparticle labelled oligonucleotides, spacer DNA #1.

XX ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;  
KW nanostructure; viral disease; human immunodeficiency virus infection;  
KW hepatitis virus infection; herpes virus infection;  
KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;  
KW sexually transmitted disease; inherited disorders; paternity testing;  
XX cell line authentication; gene therapy.  
OS Synthetic.  
XX US2003068622-A1.  
PN 10-APR-2003.  
XX 12-OCT-2001; 2001US-00976863.  
PF 29-JUL-1996; 96US-0031809P.  
XX 21-JUL-1997; 97WO-US012783.  
PR 29-JAN-1999; 99US-00240755.  
PR 25-JUN-1999; 99US-00344667.  
PR 26-APR-2000; 2000US-0200161P.  
PR 26-JUN-2000; 2000US-00603830.  
XX (NANO-) NANOSPHERE INC.  
PA Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;  
XX Taton TA;  
PI WPI; 2003-576420/54.  
XX Detecting nucleic acids having at least 2 portions comprises use of  
XX nanoparticles which have oligonucleotides attached to them that are  
PT complementary to portions of the target nucleic acid sequence.  
PT Example 18; Page 40; 130pp; English.  
XX The invention relates to detecting a nucleic acid (NA) having at least 2  
PS portions comprising providing a type of nanoparticles (NP, e.g. colloidal  
XX gold) having oligonucleotides (O) attached (where (O) on each NP has a  
CC sequence complementary to sequence of at least two portions of NA),  
CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more  
CC portions of NA, and observing a detectable change brought about by  
CC hybridization of (O) on NP with NA. Also included are aggregate probes,  
CC core probes, substrate having NP attached to it, a metallic or  
CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures  
CC comprising nanoparticles and methods of nanofabrication utilising  
CC nanoparticles and satellite probes. The methods, probes nucleic acids,  
CC nanoparticles and oligonucleotides are useful for separating a selected  
CC nucleic acid having at least two portions, from other nucleic acids, and  
CC for detecting nucleic acids having at least two portions, for detecting  
CC NA having at least two portions. The method is useful for disease and in  
CC type of nucleic acids which may be used for diagnosis of disease and in  
CC sequencing of nucleic acids. Preferably, the method is useful for  
CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases  
CC (human immunodeficiency virus, hepatitis virus, herpes virus,  
CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually  
CC transmitted diseases, inherited disorders, in forensics, in DNA  
CC sequencing, for paternity testing, for cell line authentication, for  
CC monitoring gene therapy, etc. The method is useful in research and  
CC analytical laboratories in DNA sequencing, in the field to detect the  
CC presence of specific pathogens, etc. Detecting nucleic acids based on  
CC observing a colour change with the naked eye is cheap, fast, simple and  
CC robust, and do not require specialised expensive equipment. The present  
CC sequence is a spacer oligonucleotide used to illustrate the method of the  
CC invention.  
XX SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
Query Match 0.7%; Score 19; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804



Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1142

ACD26991

ID ACD26991 standard; DNA; 32 BP.

XX ACD26991;

AC

XX 15-OCT-2003 (first entry)

DT

XX Nanotechnology nucleic acid detection method oligonucleotide #50.

DE

XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

KW

XX Synthetic.

OS

XX US2003049630-A1.

PN

XX 13-MAR-2003.

PD

XX 20-SEP-2001; 2001US-00957318.

XX

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX

PA (NANO-) NANOSPHERE INC.

XX

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX

DR WPI; 2003-615795/58.

XX

PT Detecting nucleic acid having two portions, by providing nanoparticles

PT having oligonucleotides attached to it, contacting nucleic acid and

PT nanoparticles to allow hybridization, and observing detectable change.

XX

PS Example 18; Page 40 ; 129pp; English.

XX

CC This invention relates to a novel method for detecting nucleic acids. The

CC method comprises providing nanoparticles with oligonucleotides attached

CC to them, which have a sequence complementary to a sequence of two

CC portions of nucleic acid, contacting the nucleic acid and nanoparticles

CC to allow hybridisation of the oligonucleotides with two or more portions

CC of the nucleic acid, and observing a detectable change brought about by

CC the hybridisation. The nucleic acid to be detected must have at least two

CC portions and the distances between these are chosen so that when the

CC nanoparticle-oligonucleotide conjugate binds the target sequence a

CC detectable change occurs. The method of the invention is useful for

CC detecting two or more nucleic acids (from a biological source) having at

CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene

CC or synthetic RNA or DNA, or a product of a polymerase chain reaction

CC amplification. Nanoparticle-oligonucleotide conjugates of the invention

CC are useful for preparing a nanoprobe conjugate for detecting an analyte,

CC and for detecting a nucleic acid bound to an electrode surface.

CC Nanoparticles and nanoparticle conjugates of the invention are useful for

CC nanofabrication and for separating a selected nucleic acid having two

CC portions from other nucleic acids. Diagnostic assays employing

CC nanoparticle-oligonucleotide conjugates improve the sensitivity of

CC nucleic acid detection methods and can be used to detect nucleic acids

CC that are present in only small amounts in a sample. The present sequence

CC represents an oligonucleotide used to demonstrate the method of the

XX invention

SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1143

ADE71592

ID ADE71592 standard; DNA; 32 BP.

XX

AC ADE71592;

XX

DT 29-JAN-2004 (first entry)

XX

DE Magneto-gold nanoparticle probe #2.

XX

KW Magneto-gold nanoparticle; probe; ss; core nanoparticle;

KW non-alloying gold shell; shell nanoparticle; gold salt.

XX

OS Synthetic.

XX

PN US2003129608-A1.

XX

PD 10-JUL-2003.

XX

PF 22-MAY-2002; 2002US-00153483.

XX

PR 25-MAY-2001; 2001US-0293861P.

PR 28-DEC-2001; 2001US-00034451.

PR 28-DEC-2001; 2001WO-US050825.

XX

PA (MIRK/) MIRKIN C A.

PA (CAOY/) CAO Y.

PA (JINR/) JIN R.

XX

PI Mirkin CA, Cao Y, Jin R;

XX

DR WPI; 2004-031299/03.

XX

PT Core/shell nanoparticle for detecting target molecules, e.g. nucleic

PT acids, comprises inner metal-containing nanoparticle core, outer non-

PT alloying gold shell, and oligonucleotides attached to gold shell.

XX

PS Example 5; Page 8; 21pp; English.

XX

CC The invention relates to a core/shell nanoparticle comprising an inner

CC metal-containing nanoparticle core and an outer non-alloying gold shell

CC surrounding the nanoparticle core. Oligonucleotides may be attached to

CC the gold shell. The invention also relates to preparation of core/shell

CC nanoparticles by treating inner metal-containing nanoparticle cores

CC simultaneously with a solution containing gold salt and a solution

CC containing a reducing agent to produce a non-alloying gold shell

CC surrounding the nanoparticle cores, and isolating the core/shell

CC nanoparticles. Detection of target analytes, e.g. a nucleic acid, bound

CC to a surface comprises contacting the surface with a solution comprising

CC a core/shell nanoparticle receptor conjugate under conditions effective

CC to allow binding of nanoparticle conjugates with the bound nucleic acid,

CC subjecting the nanoparticle conjugate to an external magnetic field to

CC accelerate movement of the nanoparticle conjugate to the surface, to

CC promote binding interaction between the nanoparticle conjugate and target

CC analyte, removing any nanoparticle conjugates that have not bound with

CC the target analyte and observing a detectable change brought about by a

CC binding interaction of the target analyte with the nanoparticle

CC conjugates. The invention is used for detecting target molecules such as

CC nucleic acids, peptides and proteins. The optical properties of

CC core/shell nanoparticles form a new calorimetric channel for nanoparticle

CC -based DNA detection. This sequence represents a magneto-gold

XX nanoparticle probe used in the scope of the invention.

SQ Sequence 32 BP; 24 A; 4 C; 0 G; 4 T; 0 U; 0 Other;



```
Query Match          0.7%; Score 19; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 19: Conservative 0; Mismatches 0; Indels
```

RESULT 1144  
ABQ80395  
IN ABO80395 standard; DNA; 33 BP.

AC AB080395:

06-NOV-2003 (first entry)

Probe APC 1-MUT.

XX  
KW Probe; target; nanoparticle; detection; DNA sequencing; pathogen;  
XX infection; screening; colour change; ss.

OS Homo sapiens.

Key	Location/Qualifiers
modified_base	1
	/*tag= a
	/note= "Gold-S'-A."

AA PN WO2003048769-A1.

12-JUN-2003.

27-NOV-2002: 2002WO-US038069.

30-NOV-2001: 2001US-0334644P.

XX  
P  
(NANO-) NANOSPHERE INC.

XX  
PI  
storhoff J.T. Fritz BM, Herrmann M;

XX  
WPT: 2003-617993/58

XX Detecting target polynucleotide in a sample, by amplifying target,  
PT hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle  
PT detection system, and determining amount of signal generated due to  
PT binding.

Example 1: page 35: 74pp; English.

The sequences given in ABQ80394-99 represent probes and targets which were used in the method of the invention for detecting a target polynucleotide in a sample. The method comprises amplifying the target, hybridizing the target to oligonucleotides bound to nanoparticles in a nanoparticle detection system, determining the amount of signal generated as a result of binding, optionally repeating the above steps, and detecting the presence of the target oligonucleotide by analysing for the amount of signal produced after at least one amplification cycle. The method is useful for detecting target polynucleotide in a sample, and for determining the quantity of target polynucleotide in a sample. The method is useful in research and analytical laboratories in DNA sequencing, in the field to detect the presence of specific pathogens, in the doctor's office for quick identification of an infection to assist in prescribing a drug for treatment, and in homes and health centres for inexpensive first-line screening. The method is based on observing colour change with the naked eye, hence the method is cheap, fast, simple, robust, do not require specialized or expensive equipment, and little or no instrumentation is required.

XX  
CC

Query Match	0.7%;	Score 19;	DB 1;	Length 33;
Best Local Similarity	100.0%;	Pred. No. 2e+03;		

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1146  
ADC60749/c  
ID ADC60749 standard; DNA; 33 BP.  
XX  
AC ADC60749;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Termitomyces albuminosus acidic peroxidase-related RT-PCR primer.  
XX  
KW acidic peroxidase; TAP; organochlorine compound;  
KW waste water purification; Western blotting; ss; PCR; RT-PCR; primer.  
XX

OS Termitomyces albuminosus.  
XX  
PN JP2003070473-A.  
XX  
PD 11-MAR-2003.  
XX  
PF 03-SEP-2001; 2001JP-00266069.  
XX  
PR 03-SEP-2001; 2001JP-00266069.  
XX  
PA (KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN.  
PA (RIKA ) RIKAGAKU KENKYUSHO.  
XX  
DR WPI; 2003-590855/56.  
XX  
PT New protein with acidic peroxidase activity, derived from Termitomyces  
PT albuminosus ATTC42010, useful in the analysis of organochlorine compounds  
PT during waste water purification processes.  
XX

PS Example 2; SEQ ID NO 3; 12pp; Japanese.  
XX

CC The invention relates to a novel acidic peroxidase protein (TAP) obtained  
CC from Termitomyces albuminosus ATTC42010. The polypeptide of the invention  
CC may be useful in the analysis of organochlorine compounds during waste  
CC water purification processes and in Western blotting techniques. The  
CC polypeptide has enhanced activity under acidic pH relative to  
CC conventional peroxidases. The current sequence is that of the  
CC Termitomyces albuminosus acidic peroxidase-related RT-PCR primer of the  
CC invention.  
XX

SQ Sequence 33 BP; 2 A; 5 C; 1 G; 25 T; 0 U; 0 Other;  
XX

Query Match 0.7%; Score 19; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 33 AAAAAAAAAAAAAAAAAAAAAA 15

RESULT 1147  
ABK15694/c  
ID ABK15694 standard; DNA; 33 BP.  
XX  
AC ABK15694;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human activating GTPase negative regulator 11.66 PCR primer #1.  
XX  
KW Human; ss; activating GTPase negative regulator 11.66; PCR; primer;  
KW malignant tumour; haemopathy; human immunodeficiency virus infection;  
KW HIV; immunological disease; inflammation; cytostatic; haemostatic;  
KW virucide; immunomodulatory; antiinflammatory.

XX Homo sapiens.  
OS  
XX  
PN WO200211511-A1.  
XX  
PD 14-FEB-2002.  
XX  
PF 19-JUN-2001; 2001WO-CN001008.  
XX  
PR 21-JUN-2000; 2000CN-00116684.  
XX  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-172120/22.  
XX

PT GTPase negative regulator 11.66 polypeptide and encoding polynucleotide,  
PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX

PS Example 4; Page 13; 36pp; Chinese.  
XX

CC The invention relates to an isolated polypeptide of activating GTPase  
CC negative regulator 11.66, its fragment, analogue or derivative and the  
CC nucleic acid encoding it. Also included are vectors expressing the  
CC protein, a host cell comprising the vector, the isolation of modulators  
CC of the protein and an antibody which recognises the protein. The protein  
CC and nucleic acid are used in diagnosis and treatment of a malignant  
CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,  
CC immunological diseases and various inflammations. The present sequence is  
CC a PCR primer used to clone the cDNA encoding activating GTPase negative  
CC regulator 11.66  
XX

SQ Sequence 33 BP; 3 A; 5 C; 2 G; 23 T; 0 U; 0 Other;  
XX

Query Match 0.7%; Score 19; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 33 AAAAAAAAAAAAAAAAAAAAAA 15

RESULT 1148  
AAA75564/c  
ID AAA75564 standard; DNA; 34 BP.  
XX  
AC AAA75564;  
XX  
DT 22-JAN-2001 (first entry)  
XX  
DE PCR primer for DNA encoding zeocin selective marker gene fragment.  
XX  
KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;  
KW tumourigenesis; leukaemia; hematopoiesis; B cell tumour; PCR primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200053761-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-US006067.  
XX  
PR 09-MAR-1999; 99US-00264908.  
PR 11-MAR-1999; 99US-00265992.  
PR 01-JUL-1999; 99US-0142013P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
XX  
DR WPI; 2000-565600/52.  
XX  
XX New human cytokine, designated zalphall1 ligand, useful for stimulating  
PT the proliferation and/or development of hematopoietic cells in vitro and  
PT in vivo, and for treating tumorigenesis.  
XX  
XX Example 6; Page 213; 256pp; English.  
PS  
XX The present PCR primer was used to amplify DNA encoding a fragment of  
CC zeocin selective marker. The amplified fragment was used to construct a  
CC vector for expression of zalphall1 ligand polypeptide. Zalphall1 ligand is  
CC a cytokine. The zalphall1 ligand is useful for stimulating the  
CC proliferation and development of haematopoietic cells in vitro and in  
CC vivo. Zalphall1 ligand polynucleotides can be used as primers or probes  
CC for cloning the zalphall1 gene. The zalphall1 ligand is useful for treating  
CC tumorigenesis. A zalphall1 ligand-saporin fusion toxin may be used for  
CC treating leukaemias and lymphomas. Antagonists against zalphall1 ligand  
CC are useful as research reagents for characterizing ligand-receptor  
CC interaction. Antagonists are also useful for inhibiting expansion,  
CC proliferation, activation and differentiation of cells involved in  
CC regulating hematopoiesis. The zalphall1 ligand may also be used to  
CC stimulate an immune response against B cell tumour, a virus, a parasite  
CC or a bacterium. The zalphall1 polypeptides, polynucleotides, antagonists,  
CC agonists and antibodies are also useful for the detection, diagnosis,  
CC prevention, and treatment of diseases associated with a zalphall1 ligand  
CC genetic defect  
XX  
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 34 AAAAAAAAAAAAAAAAAA 16  
  
RESULT 1149  
AAD09727/c  
ID AAD09727 standard; DNA; 34 BP.  
XX  
AC AAD09727;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
XX ZC18698 primer, to synthesise human activated CD3+ selected cell cDNA.  
DE  
XX Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;  
KW cancer; inflammation; gene therapy; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200146422-A1.  
PN  
XX  
XX 28-JUN-2001.  
PD  
XX  
XX 22-DEC-2000; 2000WO-US035308.  
PF  
XX  
XX 23-DEC-1999; 99US-00471767.  
PR  
XX 01-DEC-2000; 2000US-0250841P.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Presnell SR, Kindsvogel W;  
PI  
XX WPI; 2001-408648/43.  
XX  
XX Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.  
PT  
XX

PS Example 4B; Page 145; 167pp; English.  
XX  
CC The patent discloses novel human cytokine, ZCYTO18 protein and its  
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells  
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in  
CC K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in  
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer  
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It is  
CC is useful for increasing platelets in a patient or injured tissue. It is  
CC also used in gene therapy. The present sequence is a PCR primer, ZC18698  
CC used to synthesise a cDNA strand from human activated CD3+ selected  
CC cells. This primer is used for the identification of human ZCYTO18  
CC message in activated T-cell library  
XX  
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 34 AAAAAAAAAAAAAAAAAA 16  
  
RESULT 1150  
AAS20662/c  
ID AAS20662 standard; DNA; 34 BP.  
XX  
AC AAS20662;  
XX  
DT 09-APR-2002 (first entry)  
XX  
XX Primer ZC18698 used to create XhoI site into human zalphall1 Ligand cDNA.  
DE  
XX Cytokine; zalphall1 Ligand; zalphall1 receptor; NK cell progenitor;  
KW natural killer cell proliferation; T-cell proliferation;  
KW B-cell proliferation; anti-tumour response; immune system;  
KW immunostimulant; cytostatic; human; primer; ss.  
XX  
XX Synthetic.  
XX  
XX US6307024-B1.  
PN  
XX 23-OCT-2001.  
PD  
XX  
XX 09-MAR-2000; 2000US-00522217.  
PF  
XX  
XX 09-MAR-1999; 99US-0123547P.  
PR  
XX 11-MAR-1999; 99US-0123904P.  
PR  
XX 01-JUL-1999; 99US-0142013P.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
PI  
XX WPI; 2002-040208/05.  
DR  
XX  
XX New zalphall1 ligand polypeptides and polynucleotides, useful for  
PT stimulating proliferation, activation, differentiation and/or induction  
PT of inhibition of specialized cell function, or for stimulating an  
PT antigenic response.  
XX  
XX Example 6; Col 135; 105pp; English.  
PS  
XX The present invention relates to the isolation of a novel cytokine,  
CC zalphall1 ligand and the polynucleotide encoding it. The invention also  
CC gives the sequence for the zalphall1 receptor and the polynucleotide  
CC encoding it. The zalphall1 ligand polypeptide stimulates proliferation of  
CC natural killer (NK) cells or NK cell progenitors, the activation of NK  
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with  
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and

CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The  
CC zalphall1 Ligand polypeptide is also useful in preparing antibodies that  
CC bind to zalphall1 Ligand epitopes. The zalphall1 Ligand polynucleotides can  
CC be used as probes or primers to clone regions of a zalphall1 Ligand gene,  
CC and in gene therapy. Zalphall1 Ligand may also be used to identify  
CC inhibitors of its activity, to enhance the generation of anti-tumour  
CC responses with or without the infusion of donor lymphocytes, and to  
CC activate or stimulate the immune system. The present sequence represents  
CC a primer used in the methods of the present invention  
XX  
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | |  
Db 34 AAAAAAAAAAAAAAAAAAAAAA 16

RESULT 1151  
ADD68172/c  
ID ADD68172 standard; DNA; 34 BP.  
XX  
AC ADD68172;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE PCR primer relating to the invention ZC18698 SEQ ID NO:30.

XX ss; PCR; primer; zcytor17; antiinflammatory; dermatological;  
KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicemia;  
KW toxic shock syndrome; infectious disease.  
XX  
OS Synthetic.

XX WO2003060090-A2.  
XX  
XX 24-JUL-2003.

XX 21-JAN-2003; 2003WO-US001984.  
XX  
XX 18-JAN-2002; 2002US-0350325P.  
PR 25-APR-2002; 2002US-0375323P.  
PR 19-DEC-2002; 2002US-0435315P.

XX (ZYMO ) ZYMOGENETICS INC.

XX PI Sprecher CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;  
PI Novak JE, Gross JA, Dillon SR;  
XX  
DR WPI; 2003-618179/58.

XX New zcytor17 ligand polypeptides, useful for treating inflammatory  
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's  
PT disease, atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia.  
XX

PS Example 6; SEQ ID NO 30; 372pp; English.

XX The invention relates to a novel isolated zcytor17 ligand polypeptide. A  
CC polypeptide of the invention has antiinflammatory, dermatological, a  
CC immunosuppressive, and antimicrobial activity, and may have a use in a  
CC vaccine. The polypeptide is useful for treating inflammatory diseases,  
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicemia, toxic  
CC shock syndrome or infectious diseases. The present sequence is used in  
CC the exemplification of the invention.

XX Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | |  
Db 34 AAAAAAAAAAAAAAAAAAAAAA 16

RESULT 1152  
AAX14632/c  
ID AAX14632 standard; DNA; 35 BP.  
XX  
AC AAX14632;  
XX

DT 24-MAR-1999 (first entry)

XX Triple helix forming nucleotides 4791-4725 of the n-myc gene.

DE Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.

XX Homo sapiens.

XX US5861244-A.

XX 19-JAN-1999.

XX 22-DEC-1993; 93US-00173489.

XX 29-OCT-1992; 92US-00968436.

XX (PROF-) PROFILE DIAGNOSTIC SCI INC.

XX Hepburn AG, Wang C;

XX WPI; 1999-130384/11.

XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.

XX Disclosure; Col 13-14; 168pp; English.

XX The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus

XX Sequence 35 BP; 1 A; 4 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
| | | | |  
Db 35 GAAAAAAAAAAAAAAAAAAAAA 17

RESULT 1153  
ABZ46327/c  
ID ABZ46327 standard; DNA; 41 BP.  
XX



CC medications a patient needs to take before finding an effective therapy  
XX  
SQ Sequence 41 BP; 3 A; 2 C; 3 G; 33 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 19; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 40 AAAAAAAAAAAAAAAAAAAAAA 22  
  
RESULT 1154  
ABZ48839/c  
ID ABZ48839 standard; DNA; 41 BP.  
XX  
AC ABZ48839;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #5622.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;  
KW drug evaluation; drug screening; genotyping; genetic profiling;  
KW therapeutic customisation; adverse reaction; clinical trial;  
KW drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,G)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKE ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.  
XX  
PS Claim 23; Page 175; 2785pp; English.  
XX  
CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur

AC ABZ46327;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #3111.  
XX  
KW Human; drug metabolising enzyme; gene; drug metabolism; chromosome 15;  
KW polymorphic site; drug evaluation; drug screening; genotyping;  
KW genetic profiling; therapeutic customisation; adverse reaction;  
KW clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT variation replace(21,G)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
XX  
PN WO200252044-A2.  
XX  
PD 04-JUL-2002.  
XX  
PF 27-DEC-2001; 2001WO-JP011592.  
XX  
PR 27-DEC-2000; 2000JP-00399443.  
PR 02-MAY-2001; 2001JP-00135256.  
PR 27-AUG-2001; 2001JP-00256862.  
XX  
PA (RIKE ) RIKEN KK.  
XX  
PI Nakamura Y, Sekine A, Iida A, Saito S;  
XX  
DR WPI; 2002-583571/62.  
XX  
PT Identifying individuals having a polymorphism, useful for determining the effectiveness or side effect of a drug or treatment protocol, comprises detecting at least one polymorphism in the drug metabolizing enzyme nucleic acid.  
XX  
PS Claim 23; Page 116; 2785pp; English.  
XX  
CC Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes encoding enzymes associated with drug metabolism. The invention relates to methods and compositions for identifying individuals who have at least one polymorphism in such drug metabolising enzyme-encoding genes. The polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50887 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients. This would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety. Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different



(BIOW-) BLOWNDOWN GENE DEV INC SHANGHAI.

Mao Y, Xie Y;

WPI; 2001-550164/61.

New human polypeptide FD 17 for diagnosing and treating malignant tumor, hemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and inflammations.

Example 2; Page 11; 36pp; Chinese.

The present invention describes the human FD 17 protein (I). (I) has cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic activities. The polynucleotide encoding (I) can be used in gene therapy. (I) and the polynucleotide encoding it are applicable in the diagnosis and treatment of malignant tumour, haemopathy, human immunodeficiency virus (HIV) infection, immunological diseases and various inflammations. The present sequence represents a PCR primer for human FD 17, which is used in an example from the present invention

SQ Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;  
Query Match            0.7%; Score 18.8; DB 1; Length 24;  
Best Local Similarity   90.9%; Pred. NO. 1.1e+03;  
Matches         20; Conservative      0; Mismatches    2; Indels          0; Gaps            0;

QY        2163 TCCTTTTTCCTTTTTTTTTTTTTTT 2184  
Db        | ||||| |||||||  
          2 TTCTTTTCCTTTTTTTTTTTTTTT 23

RESULT 1159  
ABK13715  
ID ABK13715 standard; DNA; 24 BP.  
XX  
AC ABK13715;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.  
XX Human; transcriptional activation subunit 14; malignant neoplasm;  
KW haematopathy; cytotstatic; HIV infection; human immunodeficiency virus;  
KW immunological disease; inflammation; virucide; immunomodulatory;  
KW antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.  
XX Homo sapiens.  
OS WO200194403-A1.  
PN  
PD 13-DEC-2001.  
XX  
PF 14-MAY-2001; 2001WO-CN000753.  
XX  
PR 16-MAY-2000; 2000CN-00115720.  
XX  
PA (SHAN-) SHANGHAI BLOWNDOWN GENE DEV INC.  
XX Mao Y, Xie Y;  
PI WPI; 2002-090139/12.  
XX Human transcriptional activation subunit 14 and encoding polynucleotide,  
PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX Example 2; Page 17; 36pp; Chinese.  
PS The present invention relates to the isolation of human transcriptional  
CC activation subunit 14, and the polynucleotide encoding it. Also described









PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
XX WPI; 2000-679677/66.  
DR  
XX Identifying extendible primers for use in identification, or  
XX classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
PT  
XX Claim 14; Page 50; 66pp; English.  
PS  
XX The present invention provides a method for identifying a set of  
XX extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 4 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2173 TTTTCTTTTCTTTTAACTTTGAAAG 2197  
Db 1 TTTTCTTTTCTTTTAACTTTTCCAG 25  
RESULT 1168  
ACI00608/c  
ID ACI00608 standard; DNA; 25 BP.  
XX  
AC ACI00608;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 599.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
XX WPI; 2003-567953/53.  
DR  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 599; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC compounds. The nucleic acid probes are specifically designed for analysis

CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 2 A; 7 C; 7 G; 9 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1269 AAGACCGGACACCCCATGGGACCAG 1293  
Db 25 AAGACAGGACACCTCAAGGGACCTG 1  
RESULT 1169  
ACI61005/c  
ID ACI61005 standard; DNA; 25 BP.  
XX  
AC ACI61005;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 60996.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
XX WPI; 2003-567953/53.  
DR  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 60996; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis

CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 1.3e+03;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 572 GTGAGCGCCCGCAGGGATGCCTACC 596  
Db 25 GTGAGCGACCGCAGGGCTACCTTCC 1

RESULT 1170  
AAA88688  
ID AAA88688 standard; DNA; 26 BP.

XX  
AC AAA88688;

DT 05-FEB-2001 (first entry)

DE Oligo-dT-XhoI primer.

XX Sweetgum; angiosperm; cytochrome P450-1; conifer; loblolly pine;  
KW transgenic plant; lignin; paper; pulping; PCR primer; ss.

XX Synthetic.

PN WO200058489-A2.

PD 05-OCT-2000.

PF 24-MAR-2000; 2000WO-US008083.

PR 26-MAR-1999; 99US-00277248.

XX (INTO ) INT PAPER CO.

XX Chiang VL, Carraway DT;

XX WPI; 2000-647240/62.

PT Use of angiosperm coniferyl aldehyde 5-hydroxylase which catalyzes 5-  
PT hydroxylation of coniferyl aldehyde, for modifying lignin biosynthesis in  
PT gymnosperms, involves expressing the enzyme in a gymnosperm plant.

XX Example 3; Page 23; 123pp; English.

CC The present sequence is that of an oligo-dT primer including a 5' XhoI  
CC site. The primer was used with a gene-specific primer to amplify sweetgum  
CC cytochrome P450-1 cDNA (see AAA88681). An aim of the invention is to  
CC identify, sequence and clone specific genes such as P450-1 from an  
CC angiosperm that are involved in production of syringyl lignin, and to  
CC then introduce such genes into the genome of a gymnosperm, such as  
CC loblolly pine, to induce production of syringyl lignin and thereby  
CC provide enhanced pulpability to the wood structure

XX Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.6; DB 1; Length 26;  
Best Local Similarity 84.0%; Pred. No. 1.4e+03;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2161 TCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 2 TGTGCAGTT TTTT TTTT TTTT TTTT TTTT TTTT 26

RESULT 1171  
AAQ75596  
ID AAQ75596 standard; DNA; 20 BP.

XX  
AC AAQ75596;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 8.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2188  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 1172  
ABZ85312  
ID ABZ85312 standard; DNA; 20 BP.

XX  
AC ABZ85312;

DT 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

DE Human; antisense; lung dysfunction; nasal airway dysfunction;

XX Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;







schultz782-3.rng

RESULT 1179











PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 8.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGAAAAA AAAA AAAA AAAA AAAA 2802  
Db 20 TGGAAAAA AAAA AAAA AAAA AAAA 1  
  
RESULT 1191  
AAQ75588/c  
ID AAQ75588 standard; DNA; 20 BP.  
XX  
AC AAQ75588;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 8.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAA AAAA AAAA AAAA AAAA 2803  
Db 20 TGTAAAAA AAAA AAAA AAAA AAAA 1  
  
RESULT 1192  
AAQ75601  
ID AAQ75601 standard; DNA; 20 BP.  
XX  
AC AAQ75601;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 8.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTT TTTT TTTT TTTT TTTT 2185  
Db 1 TTTTTTTT TTTT TTTT TTTT TTTT 20  
  
RESULT 1193  
AAQ75564  
ID AAQ75564 standard; DNA; 20 BP.  
XX  
AC AAQ75564;



```
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
XX
DE
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
PD
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTAA 2188
Db 1 TTTTTTTTTTTTTTTTGAA 20

RESULT 1194
AAQ75564/c
ID AAQ75564 standard; DNA; 20 BP.
XX
AC AAQ75564;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
PD
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAATAAAAAAAAAA 2802
Db 20 TTCAAAAAAATAAAAAAAAAA 1

RESULT 1195
AAQ75600
ID AAQ75600 standard; DNA; 20 BP.
XX
AC AAQ75600;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
PF 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.  
Synthetic.

JP06303997-A.  
01-NOV-1994.

16-APR-1993; 93JP-00112515.  
16-APR-1993; 93JP-00112515.

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA  
by digestion with restriction enzymes.

Disclosure; Page 7; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plurality of labelled reverse transcription primers (GENSEQ files AAQ75547- and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0;

QY 2170 TTTT TTTTTTTTTTTTAAAC 2189  
Dn 1 TTTT TTTTTTTTTTTTATC 20

RESULT 1213  
AAQ75726/c  
ID AAQ75726 standard; DNA; 21 BP.  
XX AC AAQ75726;  
XX DT  
XX DT  
XX DT  
DE Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS JP06303997-A.  
XX PN  
XX PD  
XX PF  
XX PR  
XX PR  
XX PA  
XX DR  
XX WPI; 1995-018287/03.  
PT Analysis of cDNA and gene expression - by amplification of mRNA





XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2802  
Db 20 TTTAAAAA 1  
RESULT 1217  
AAQ75730/c  
ID AAQ75730 standard; DNA; 21 BP.  
XX  
XX AAQ75730;  
XX  
XX 04-AUG-1995 (first entry)  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
XX  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
XX Synthetic.  
XX  
XX JP06303997-A.  
XX  
XX 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2782 ATTGAAAA 2801  
Db 20 ATTAAAAA 1  
RESULT 1218  
AAQ75763  
ID AAQ75763 standard; DNA; 21 BP.  
XX  
XX AAQ75763;  
XX  
XX 04-AUG-1995 (first entry)  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2170 TTTTAAAA 2189  
Db 1 TTTTAAAA 20  
RESULT 1219  
AAQ75728/c  
ID AAQ75728 standard; DNA; 21 BP.  
XX  
XX AAQ75728;  
XX  
XX 04-AUG-1995 (first entry)  
XX







XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAATAAAAAAAAAA 2804  
Db 20 GACAAAAAATAAAAAAAAAA 1  
RESULT 1225  
AAQ75702  
ID AAQ75702 standard; DNA; 21 BP.  
XX AC AAQ75702;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-00112515.  
XX PR 16-APR-1993; 93JP-00112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX PS Disclosure; Page 6; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2170 TTTT TTTT TTTT TTTT TTTT AAC 2189  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT ACC 20  
RESULT 1226  
AAQ75661/c  
ID AAQ75661 standard; DNA; 21 BP.  
XX AC AAQ75661;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-00112515.  
XX PR 16-APR-1993; 93JP-00112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX PS Disclosure; Page 6; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAAAAAATAAAAAAAAAA 2803  
Db 20 TGCAAAAAAATAAAAAAAAAA 1  
RESULT 1227  
AAQ75675  
ID AAQ75675 standard; DNA; 21 BP.  
XX AC AAQ75675;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-00112515.  
XX PR 16-APR-1993; 93JP-00112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX

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PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          0.7%; Score 18.4; DB 1; Length 21;
    Best Local Similarity 95.0%; Pred. No. 9.1e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2168 TTTT-----TTTTTTTATA 2187
Db      1 TTTT-----TTTTTTTATA 20

RESULT 1228
AAQ75771
ID   AAQ75771 standard; DNA; 21 BP.
XX
AC   AAQ75771;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          0.7%; Score 18.4; DB 1; Length 21;
    Best Local Similarity 95.0%; Pred. No. 9.1e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2168 TTTT-----TTTTTTTATA 2187
Db      1 TTTT-----TTTTTTTATA 20

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XX PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 6; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2169 TTTTTTTTTTTTTTTTTTAA 2188  
Db 1 TTTTTTTTTTTTTTTTGAA 20  
RESULT 1231  
AAQ75627/c  
ID AAQ75627 standard; DNA; 21 BP.  
XX AAQ75627;  
AC  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 6; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTCAAAAAAAAAAAAAAAA 2802  
Db 20 TTCAAAAAAAAAAAAAAAA 1  
RESULT 1232  
AAQ75693/c  
ID AAQ75693 standard; DNA; 21 BP.  
XX AAQ75693;  
AC  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAAAAAAAAAAAAAAA 2803  
Db 20 TGTAAAAAAAAAAAAAAA 1  
RESULT 1233  
AAQ75739/c  
ID AAQ75739 standard; DNA; 21 BP.  
XX AAQ75739;  
AC  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGAAAAAATAAAAAAAAAA 2802  
Db 20 TCGAAAAAATAAAAAAAAAA 1  
  
RESULT 1234  
AAQ75778  
ID AAQ75778 standard; DNA; 21 BP.  
XX  
AC AAQ75778;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.

XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20  
  
RESULT 1235  
AAQ75778/c  
ID AAQ75778 standard; DNA; 21 BP.  
XX  
AC AAQ75778;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAATAAAAAAAAAA 2804  
Db 21 GAAGAAAAAATAAAAAAAAAA 2









XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
XX  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20  
  
RESULT 1245  
AAQ75682/c  
ID AAQ75682 standard; DNA; 21 BP.  
XX  
AC AAQ75682;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20  
  
RESULT 1245  
AAQ75682/c  
ID AAQ75682 standard; DNA; 21 BP.  
XX  
AC AAQ75682;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 21 GAATAA AAAAAA AAAAAA AAAAAA 2  
  
RESULT 1246  
AAQ75678  
ID AAQ75678 standard; DNA; 21 BP.  
XX  
AC AAQ75678;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2168 TTTT TTTT TTTT TTTT TTTT TTTT 2187  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20  
  
RESULT 1247  
AAQ75694/c  
ID AAQ75694 standard; DNA; 21 BP.  
XX  
AC AAQ75694;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.



















QY 2784 TGAAGAAAAAAGAAAAAAGAAAAA 2803  
Db 20 TGTAAAAAAGAAAAAAGAAAAA 1

RESULT 1267  
AAQ75782/c  
ID AAQ75782 standard; DNA; 21 BP.  
XX AC AAQ75782;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-00112515.  
XX PR 16-APR-1993; 93JP-00112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX PS Disclosure; Page 9; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAGAAAAAAGAAAAA 2804  
Db 20 GAGAAAAAAGAAAAAAGAAAAA 1

RESULT 1268  
AAQ75662/c  
ID AAQ75662 standard; DNA; 21 BP.  
XX AC AAQ75662;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.

PN JP06303997-A.  
XX 01-NOV-1994.  
PD 16-APR-1993; 93JP-00112515.  
PF 16-APR-1993; 93JP-00112515.  
PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX PS Disclosure; Page 6; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAGAAAAAAGAAAAAAGAAAAA 2803  
Db 20 TGCAGAAAAAAGAAAAAAGAAAAA 1

RESULT 1269  
AAQ75679  
ID AAQ75679 standard; DNA; 21 BP.  
XX AC AAQ75679;  
XX DT 04-AUG-1995 (first entry)  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX OS Synthetic.  
XX PN JP06303997-A.  
XX PD 01-NOV-1994.  
XX PF 16-APR-1993; 93JP-00112515.  
XX PR 16-APR-1993; 93JP-00112515.  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX DR WPI; 1995-018287/03.  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX PS Disclosure; Page 7; 11pp; Japanese.  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse







XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTTAAAC 2189  
Db 1 TTTTTTTTTTTTTTTTATC 20  
RESULT 1276  
AAQ75683/c  
ID AAQ75683 standard; DNA; 21 BP.  
XX AAQ75683;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 GATAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1277  
AAQ75696  
ID AAQ75696 standard; DNA; 21 BP.  
XX AAQ75696;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2171 TTTTTTTTTTTTTTTTAACT 2190  
Db 1 TTTTTTTTTTTTTTTTACT 20  
RESULT 1278  
AAQ75647  
ID AAQ75647 standard; DNA; 21 BP.  
XX AAQ75647;  
XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 1lpp; Japanese.  
XX

A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
SQ

Query Match 0.7%; Score 18.4; DB 1; Length 21;  
Best Local Similarity 95.0%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 2785 GAAAAAAAAAAAAAAA 2804  
Db 20 GACAAAAAAAAAAAAAAA 1

RESULT 1280  
ABA93238  
ID ABA93238 standard; DNA; 22 BP.  
XX  
AC ABA93238;  
XX  
DT 18-APR-2002 (first entry)  
XX  
DE PolyA adaptor oligonucleotide SEQ ID NO:1.  
XX  
KW Detection; comparative detection; adaptor; ss.  
OS Synthetic.  
XX  
PN JP2001333800-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 30-MAY-2000; 2000JP-00160324.  
XX  
PR 30-MAY-2000; 2000JP-00160324.  
XX  
PA (UNIT-) UNITECH CO LTD.  
XX  
DR WPI; 2002-135950/18.  
XX  
PT Comparative detection of the amounts of RNA and DNA.  
XX  
PS Disclosure; Page 9; 9pp; Japanese.  
XX

The present invention describes a method for the comparative detection of  
CC the amount of an RNA. The method comprises: (a) cDNAs obtained by  
CC transcribing respectively from at least two tissue RNAs are respectively  
CC fragmented by using a same restriction enzyme; (b) each different adaptor  
CC and a common adaptor are added to each of the cDNA fragments derived from  
CC the same or different tissues by the step (a); (c) the resultant adaptor-  
CC added cDNAs are mixed together; (d) an adaptor primer having the common  
CC sequence to said different adaptor and a gene-specific adaptor are used  
CC to amplify said adaptor-added cDNAs containing no region derived from  
CC polyadenylic acid of the mRNA before the addition of the adaptor among  
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
CC from the measured result; (g) each different adaptor and a common adaptor  
CC are added to each of the genomic DNA fragments derived from a same or  
CC different individuals; (h) the resultant adaptor-added genomic DNAs are  
CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
CC an adaptor primer having the common sequence to the different adaptor and  
CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts



CC of the genomic DNAs are measured between the individuals. The method is  
CC used for the detection of the amounts of RNA and DNA. The present  
CC sequence represents an oligonucleotide which is used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 22;  
Best Local Similarity 95.0%; Pred. No. 1e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAAGAAAAAAGAAAAA 2803  
Db 3 TCAAGAAAAAAGAAAAA 22  
  
RESULT 1281  
ABK12409  
ID ABK12409 standard; DNA; 24 BP.  
XX  
AC ABK12409;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.  
XX  
KW Polypeptide-laminin B210.67; embryo development teratogenesis;  
KW cytotstatic; reverse transcriptase-PCR; RT-PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN CN1328013-A.  
XX  
PD 26-DEC-2001.  
XX  
PF 14-JUN-2000; 2000CN-00116514.  
XX  
PR 14-JUN-2000; 2000CN-00116514.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
WPI; 2002-270054/32.  
XX  
PT Polypeptide-laminin B210.67, useful for treating diseases such as embryo  
PT development teratogenesis.  
XX  
PS Example 2; Page 18 (disclosure); 33pp; Chinese.  
XX  
CC The present invention relates to the isolation of polypeptide-laminin  
CC B210.67, and the polynucleotide encoding it. Also described is the  
CC process for preparing the protein by DNA recombination. The polypeptide  
CC is useful for treating diseases such as embryo development teratogenesis.  
CC The present sequence for reverse transcriptase (RT)-PCR primer #1 is used  
CC with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-  
CC laminin B210.67  
XX  
SQ Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 24;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGAGAAAAAAGAAAAA 2802  
Db 5 TTAAGAAAAAAGAAAAA 24  
  
RESULT 1282  
AAL47515  
ID AAL47515 standard; DNA; 24 BP.  
XX

AC AAL47515;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human cyclophilin-40-12-54 coding sequence PCR primer #2.  
XX  
KW Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1331162-A.  
XX  
PD 16-JAN-2002.  
XX  
PF 28-JUN-2000; 2000CN-00116823.  
XX  
PR 28-JUN-2000; 2000CN-00116823.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
WPI; 2002-305482/35.  
XX  
PT Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.  
XX  
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC cyclophilin-40-12.54. The sequences can be used in the treatment of  
CC immunopathy and cancer. The present sequence is a PCR primer for the  
CC coding sequence of the invention  
XX  
SQ Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 24;  
Best Local Similarity 95.0%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2168 TTTTTCCTTTTTCCTTTT 2187  
Db 1 TTTTTCCTTTTTCCTTTT 20  
  
RESULT 1283  
AAF74925/C  
ID AAF74925 standard; DNA; 25 BP.  
XX  
AC AAF74925;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:22.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
WPI; 2001-244776/25.  
XX

XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 25;  
Best Local Similarity 95.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTGTGTTTTTTTTTTT 2185  
Db 20 TTTTGTGTTTTTTTTTTT 1  
  
RESULT 1284  
AAF74930/c  
ID AAF74930 standard; DNA; 25 BP.  
XX  
AC AAF74930;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:27.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and

CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 25;  
Best Local Similarity 95.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTGTGTTTTTTTTTTT 2185  
Db 20 TTTTGTGTTTTTTTTTTT 1  
  
RESULT 1285  
AAA62140  
ID AAA62140 standard; DNA; 26 BP.  
XX  
AC AAA62140;  
XX  
DT 06-AUG-2003 (revised)  
DT 10-NOV-2000 (first entry)  
XX  
DE A. auriculiformis (RT-) PCR primer.  
XX  
KW PCR primer; RT-PCR primer; plant genetic marker; plant breeding; ss.  
XX  
OS Acacia auriculiformis.  
XX  
PN AU9960643-A.  
XX  
PD 01-JUN-2000.  
XX  
PF 24-NOV-1999; 99AU-00060643.  
XX  
PR 25-NOV-1998; 98JP-00333469.  
XX  
PA (REAS-) RES ASSOC REFORESTATION TROPICAL FOREST.  
XX  
PI Hibino T, Koshiyama J;  
XX  
DR WPI; 2000-412598/36.  
XX  
PT Method for obtaining plant DNA fragments useful as novel genetic markers,  
PT comprising digesting plant DNA, subjecting fragments to genome  
PT subtraction and screening the polymorphic fragments.  
XX  
PS Example 1; Page 13; 21pp; English.  
XX  
CC The present sequence is a primer for Acacia auriculiformis. This sequence  
CC was used in RT-PCR reactions to produce cDNA from A. auriculiformis RNA.  
CC The resulting cDNA was amplified via PCR using the present sequence and  
CC another PCR primer (see AAA62141). The PCR product was used as an  
CC expression probe. The expression probe was used to obtain desired DNA  
CC fragments. The plant genetic fragments obtained by this method may be  
CC useful as markers in plant breeding. In addition, genes encoding the DNA  
CC fragments or their promoter regions may be used to modify expression.  
CC (Updated on 06-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 26 BP; 1 A; 4 C; 5 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 26;  
Best Local Similarity 95.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2162 CTCCTTTTGTGTTTTTTTTT 2181  
Db 7 CCCCTTTTGTGTTTTTTTTT 26  
  
RESULT 1286

AAC93128  
ID AAC93128 standard; DNA; 26 BP.  
XX  
AC AAC93128;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Stephania tetrandra S. moore RNA reverse transcriptase primer Noti-dt.  
XX  
KW Stephania tetrandra S. Moore; IL-6; interleukin-6; hepatotropic;  
KW antiinflammatory; hepatocirrhosis; hepatitis; alcoholism; primer; ss.  
XX  
OS Unidentified.  
XX  
PN US6162437-A.  
XX  
PD 19-DEC-2000.  
XX  
PF 25-NOV-1997; 97US-00978321.  
XX  
PR 05-JUN-1995; 95WO-KR0000073.  
PR 06-DEC-1996; 96US-00750462.  
XX  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
XX  
PI Lee J, Kim Y, Kang H, Pyun K, Choi I;  
XX  
DR WPI; 2001-146043/15.  
XX  
PT Treatment of hepatocirrhosis comprises administering an extract of the  
PT root of Stephania tetrandra in an amount effective to inhibit production  
PT of interleukin-6.  
XX  
PS Example 4; Col 9; 27pp; English.  
XX  
CC The present sequence was used in an example to illustrate a method for  
CC treating hepatocirrhosis. The method comprises administering an extract  
CC of the root of Stephania tetrandra in an amount effective to inhibit  
CC production of interleukin-6 (IL-6). Hepatocirrhosis is often associated  
CC with chronic hepatitis or chronic alcoholism  
XX  
SQ Sequence 26 BP; 0 A; 4 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 26;  
Best Local Similarity 95.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2164 CCTTTTCTTTTCTTTTCTTTTCTTTT 2183  
Db 7 CGTTTCTTTTCTTTTCTTTTCTTTT 26  
  
RESULT 1287  
AAQ36362  
ID AAQ36362 standard; DNA; 28 BP.  
XX  
AC AAQ36362;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-JUN-1993 (first entry)  
XX  
DE GL6anti, targetted to human beta globin sequence.  
XX  
KW Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;  
KW triplex; target; duplex; promoter; coding domain; ss.  
XX  
OS Synthetic.  
XX  
PN US5176996-A.  
XX  
PD 05-JAN-1993.  
XX  
PF 22-DEC-1989; 89US-00453532.

XX 20-DEC-1988; 88US-00287359.  
PR (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PA Hogan ME, Kessler DJ;  
XX  
PI WPI; 1993-035718/04.  
XX  
DR Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -  
XX which bind to target sequence in duplex DNA forming colinear triplex by  
PT binding to major groove.  
PT  
XX  
PS Example 13; Col 36; 29pp; English.  
XX  
CC The beta globin gene encodes on of the proteins comprising human adult  
CC haemoglobin. . Mutation in this gene is responsible for beta thalassemia  
CC and sickle cell anaemia. Expression of the gene may be prevented by the  
CC formation of a triplex between the duplex target DNA sequence and an anti  
CC parallel or parallel synthetic oligonucleotide. The triplex  
CC oligonucleotides are designed to inhibit the beta globin gene in  
CC thalasseemics and in patients with sickle cell anaemia, to be replaced by  
CC the naturally occurring delta protein. Two classes of triplex  
CC oligonucleotides may be used, targetted against the 5' enhancer or the  
CC promoter/coding domain, in this case from base 874 to 900 (numbering is  
CC relative to the principal mRNA start site). A suitable antiparallel  
CC oligonucleotide is GL6anti. See also AAQ36219-361. (Updated on 25-MAR-  
CC 2003 to correct PF field.)  
XX  
SQ Sequence 28 BP; 0 A; 0 C; 6 G; 22 T; 0 U; 0 Other;  
  
Query Match 0.7%; Score 18.4; DB 1; Length 28;  
Best Local Similarity 95.0%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTCTTTTCTTTTCTTTTCTTTT 2185  
Db 9 TTTTCTTTTCTTTTCTTTTCTTTT 28  
  
RESULT 1288  
AAD33514/C  
ID AAD33514 standard; DNA; 28 BP.  
XX  
AC AAD33514;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS19-28-0003 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.





Cucurbita maxima.  
WO200009722-A2.

24-FEB-2000.

10-AUG-1999; 99WO-US018066.

10-AUG-1998; 98US-0096111P.

07-JUN-1999; 99US-0137977P.

(MONS ) MONSANTO CO.

Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;  
Piller KJ, Rao S, Ream JE;

WPI; 2000-224351/19.

Obtaining transgenic plant useful for controlling seed germination and  
seedling growth comprises transgene comprising a sequence expressing  
altered levels of an essential hormone.

Example 17; Page 262; 267pp; English.

The present primer was used to reverse transcribe cDNA encoding a C-20  
oxidase. The amplification describes methods for the inhibition and control of  
gibberellic acid levels. Gibberellic acid levels may be inhibited or  
controlled by use of a chimeric expression construct expressing a RNA or  
protein which suppresses the gibberellin biosynthetic pathway sequence,  
diverts substrate from the pathway, or degrades pathway substrates or  
products. The methods uses copaly diphosphate synthase, 3beta-  
hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a  
2beta,3beta-hydroxylase polynucleotides to achieve this. The method is  
used to control seed germination and seedling growth especially to  
regulate gene products of gibberellin biosynthetic pathway and  
restoration of normal seed germination, in transgenic plants. The plants  
produced are gibberellin deficient, and have shortened hypocotyl and/or  
epicotyl phenotypes compared to normal plants

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTNTTTTTTTTTTTTA 2187  
Db 1 TTTTNTTTTTTTTTTTTV 19

RESULT 1293  
AAZ99489/C  
ID AAZ99489 standard; DNA; 19 BP.  
XX AC AAZ99489;  
XX DT 03-JUL-2000 (first entry)  
XX DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.  
KW Gibberellic acid; copaly diphosphate synthase; 3beta-hydroxylase;  
KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;  
KW seed germination; seedling growth; gibberellin biosynthetic pathway;  
KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.  
XX OS Cucurbita maxima.  
XX PN WO200009722-A2.  
PD 24-FEB-2000.  
XX



PI Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;  
XX  
XX  
XX WPI; 2001-514526/56.  
XX  
XX New polynucleotides regulated by fatty lesion development and their  
PT encoded polypeptides, useful for preventing, treating or ameliorating  
PT atherosclerosis, as well as for immune or hyperproliferative disorders.  
PT  
XX  
XX Example 1; Page 79; 188pp; English.  
PS

New polynucleotides regulated by fatty lesion development and their encoded polypeptides, useful for preventing, treating or ameliorating atherosclerosis, as well as for immune or hyperproliferative disorders.

Example 1; Page 79; 188pp; English.

The present invention relates to an isolated nucleic acid regulated by fatty lesion development, which comprises any of 55 polynucleotide sequences from Oryctolagus cuniculus. The polynucleotide, polypeptide or antibody is useful for preventing, treating, modulating or ameliorating a medical condition, particularly atherosclerosis. The invention is used as a marker or detector of nervous system disorder or disease (e.g. Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The invention may also be useful for treating deficiencies or disorders of the immune system (e.g. lymphopaenia, leukocyte adhesion deficiency syndrome or haemoglobinuria, anaemia), hyperproliferative disorders (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex), coagulation disorders, blood platelet disorders and autoimmune disorders (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease). The polynucleotide sequence is also used in gene therapy. The present sequence is a 3' sequencing primer used in the identification and characterisation of polynucleotides up-regulated by fatty lesion development

sequence 19 BP: 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Name				
Best Local Similarity	94.7%	Pred. No. 7.7e+02;		
Matches 18: Conservative		1; Mismatches	0; Indels	Gaps 0;

```

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2803
          :|||||
Dh      19 BAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 1296  
AAH211968  
ID AAH21968 standard; DNA; 19 BP.  
XX  
AC AAH21968;  
XX  
DT 16-AUG-2001 (first entry)  
XX  
DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.  
XX  
KW Mouse; human; total gene expression analysis; TOGA; DST; EST;  
KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;  
KW central nervous system; antidepressant; gene therapy; diagnosis;  
KW neuropsychiatric disorder; schizophrenia; bipolar disorder;  
KW addiction-related behaviour; chromosome identification; immune response;  
KW PCR primer; probe; ss.

DR  
WFI, 2001-2003, 34.  
XX

PT New neuroleptic-regulated polynucleotides expressed in the cere-



XX New neuroleptic-regulated polynucleotides expressed in the central  
PT nervous system for diagnosing and treating neuropsychiatric disorders  
PT such as schizophrenia, bipolar disorder and addiction-related behavior.  
XX  
PS Example 1; Page 87; 210pp; English.  
XX  
CC The present invention describes isolated neuroleptic-regulated nucleic  
CC acid molecules. (I) have neuroleptic, antimanic and antidepressant  
CC activities, and can be used in gene therapy. (I), polypeptides (II)  
CC encoded by (I), or a host cell (III) comprising (I), are useful for  
CC preventing, treating, modulating or ameliorating a medical condition such  
CC as a neuropsychiatric disorder. (I) are useful as diagnostic agents for  
CC diagnosing a pathological condition or susceptibility to a pathological  
CC condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar  
CC disorder or addiction-related behaviour. (I) are useful for detecting the  
CC presence of a nucleic acid encoding a protein in a mammalian tissue  
CC sample. (I) can be used as probes and primers, for chromosome  
CC identification, to control gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy to treat the above mentioned  
CC disorders, identifying individuals from minute biological samples, as an  
CC alternative to restriction fragment length polymorphism (RFLP) and as  
CC polymorphic markers for forensic purposes. (I) is also useful as  
CC molecular weight markers on Southern gels, diagnostic probes for the  
CC presence of specific mRNA in a particular cell type, as a probe to  
CC subtract-out known sequences in the process of discovering novel  
CC polynucleotides, for selecting and making oligomers for attachment to a  
CC gene chip or other support, to raise anti-DNA antibodies using DNA  
CC immunisation technique, and as an antigen to elicit an immune response.  
CC AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA...AAAAA 2803  
Db 19 BAAAAA...AAAAA 1

RESULT 1298  
AAF76617  
ID AAF76617 standard; DNA; 19 BP.  
XX  
AC AAF76617;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.  
XX  
KW Spearmint; peppermint; (-)-limonene-6-hydroxylase;  
KW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.  
XX  
OS Mentha spicata.  
XX  
PN US6194185-B1.  
XX  
PD 27-FEB-2001.  
XX  
PF 14-APR-1999; 99US-00292768.  
XX  
PR 24-JUN-1997; 97US-00881784.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Croteau RB, Lupien SL, Karp F;  
XX  
DR WPI; 2001-243405/25.  
XX  
PT Novel isolated limonene hydroxylase encoding nucleic acid molecule,

PT useful for altering production of limonene-6-hydroxylase or limonene-3-  
PT hydroxylase in suitable host cell.  
XX  
PS Example 4; Col 55; 57pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)  
CC -limonene-6-hydroxylase. Also provided are a number of probes and PCR  
CC primers which were used to isolate the sequences. These are useful in the  
CC production of transgenic plants with altered flavour and aroma  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT...TTTTT 2184  
Db 1 TTTT...TTTTT 19

RESULT 1299  
AAF76617/C  
ID AAF76617 standard; DNA; 19 BP.  
XX  
AC AAF76617;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.  
XX  
KW Spearmint; peppermint; (-)-limonene-6-hydroxylase;  
KW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.  
XX  
OS Mentha spicata.  
XX  
PN US6194185-B1.  
XX  
PD 27-FEB-2001.  
XX  
PF 14-APR-1999; 99US-00292768.  
XX  
PR 24-JUN-1997; 97US-00881784.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Croteau RB, Lupien SL, Karp F;  
XX  
DR WPI; 2001-243405/25.  
XX  
PT Novel isolated limonene hydroxylase encoding nucleic acid molecule,  
PT useful for altering production of limonene-6-hydroxylase or limonene-3-  
PT hydroxylase in suitable host cell.

Example 4; Col 55; 57pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)  
CC -limonene-6-hydroxylase. Also provided are a number of probes and PCR  
CC primers which were used to isolate the sequences. These are useful in the  
CC production of transgenic plants with altered flavour and aroma  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA...AAAAA 2803  
Db 19 DAAAAA...AAAAA 1





RESULT 1302  
ABK71509  
ID ABK71509 standard; DNA; 19 BP.  
XX  
AC ABK71509;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE CNS related 3' sequencing primer.  
XX  
KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;  
KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;  
KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;  
KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;  
KW addiction; multiple sclerosis; depression; manic-depressive disorder;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200226936-A2.  
XX  
PD 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001WO-US030695.  
PF  
XX 29-SEP-2000; 2000US-0236790P.  
PR 18-JAN-2001; 2001US-0263084P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;  
XX WPI; 2002-383271/41.  
DR  
XX New polynucleotide useful in gene therapy for preventing, treating  
PT modulating or ameliorating a medical condition such as psychoses or a  
PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a  
PT mammal.  
XX  
PS Example 1; Page 40; 254pp; English.  
XX  
CC This invention relates to the cDNA sequences of novel isolated  
CC polynucleotides associated with psychoses or other neuropsychiatric  
CC disorders. The sequences of the invention may act as blockers of D<sub>2</sub>  
CC receptors in the meso-limbic dopamine system. The nucleotide sequences of  
CC the invention and the polypeptides encoded by them are useful in the  
CC manufacture of a medicament useful for preventing, treating, modulating  
CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An  
CC antibody that binds the proteins of the invention is useful for  
CC preventing, treating, modulating or ameliorating neurological disorders  
CC such as psychoses or other neuropsychiatric disorders in a subject. The  
CC sequences are also useful for diagnosing neurological disorders or a  
CC susceptibility to a neurological disorder such as psychoses and other  
CC neuro psychiatric disorders in a subject by determining the presence or  
CC absence of mutation in the nucleotide sequence of apolipoprotein D or by  
CC determining the alteration (increase or decrease) in the expression of  
CC apolipoprotein D. The sequences of the invention are useful in treating  
CC deficiencies or disorders of the central nervous system or peripheral  
CC nervous system by activating or inhibiting the proliferation,  
CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells  
CC or glial cells. The sequences are useful as a marker or detector of a  
CC particular nervous system disease or disorder such as Alzheimer's  
CC disease, Pick's disease, Binswanger's disease, other senile dementia,  
CC Parkinson's disease, obsessive compulsive disorders, epilepsy,  
CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and  
CC manic-depressive disorder. The present sequence represents an  
CC oligonucleotide primer used in the identification of the cDNA sequences  
CC of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
Query Match 0.6%; Score 18.2; DB 1; Length 19;

Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2169 TTTTTTTTTTTTTTTTTTA 2187  
Db 1 TTTTTTTTTTTTTTTTTTV 19  
RESULT 1303  
ABK71509/c  
ID ABK71509 standard; DNA; 19 BP.  
XX  
AC ABK71509;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE CNS related 3' sequencing primer.  
XX  
KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;  
KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;  
KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;  
KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;  
KW addiction; multiple sclerosis; depression; manic-depressive disorder;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200226936-A2.  
XX  
PD 04-APR-2002.  
XX  
XX 01-OCT-2001; 2001WO-US030695.  
PF  
XX 29-SEP-2000; 2000US-0236790P.  
PR 18-JAN-2001; 2001US-0263084P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;  
XX WPI; 2002-383271/41.  
DR  
XX New polynucleotide useful in gene therapy for preventing, treating  
PT modulating or ameliorating a medical condition such as psychoses or a  
PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a  
PT mammal.  
XX  
PS Example 1; Page 40; 254pp; English.  
XX  
CC This invention relates to the cDNA sequences of novel isolated  
CC polynucleotides associated with psychoses or other neuropsychiatric  
CC disorders. The sequences of the invention may act as blockers of D<sub>2</sub>  
CC receptors in the meso-limbic dopamine system. The nucleotide sequences of  
CC the invention and the polypeptides encoded by them are useful in the  
CC manufacture of a medicament useful for preventing, treating, modulating  
CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An  
CC antibody that binds the proteins of the invention is useful for  
CC preventing, treating, modulating or ameliorating neurological disorders  
CC such as psychoses or other neuropsychiatric disorders in a subject. The  
CC sequences are also useful for diagnosing neurological disorders or a  
CC susceptibility to a neurological disorder such as psychoses and other  
CC neuro psychiatric disorders in a subject by determining the presence or  
CC absence of mutation in the nucleotide sequence of apolipoprotein D or by  
CC determining the alteration (increase or decrease) in the expression of  
CC apolipoprotein D. The sequences of the invention are useful in treating  
CC deficiencies or disorders of the central nervous system or peripheral  
CC nervous system by activating or inhibiting the proliferation,  
CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells  
CC or glial cells. The sequences are useful as a marker or detector of a  
CC particular nervous system disease or disorder such as Alzheimer's  
CC disease, Pick's disease, Binswanger's disease, other senile dementia,  
CC Parkinson's disease, obsessive compulsive disorders, epilepsy,  
CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and  
CC manic-depressive disorder. The present sequence represents an  
CC oligonucleotide primer used in the identification of the cDNA sequences  
CC of the invention  
XX

CC manic-depressive disorder. The present sequence represents an  
CC oligonucleotide primer used in the identification of the cDNA sequences  
CC of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2803  
Db :|||||  
19 BAAAAAAAAAAAAAAAAA 1  
  
RESULT 1304  
ABQ73231  
ID ABQ73231 standard; DNA; 19 BP.  
XX  
AC ABQ73231;  
DT 27-SEP-2002 (first entry)  
XX  
DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.  
XX  
KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;  
KW TOGA primer; ss.  
XX  
OS Oryctolagus cuniculus.  
OS Synthetic.  
XX  
PN WO200242420-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 21-NOV-2001; 2001WO-US044072.  
XX  
PR 21-NOV-2000; 2000US-0252216P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
PI Leonardi A, Sartani A, Glass JR, Hasel KW;  
XX WPI; 2002-575233/61.  
DR  
XX  
XX New polynucleotides related to regulated genes characteristic of  
PT atherosclerosis, useful for diagnosing, preventing, treating, modulating  
PT or ameliorating atherosclerosis in a mammalian subject.  
XX  
PS Disclosure; Page 28; 130pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I) and its  
CC complements, and degenerate variants, comprising a sequence selected from  
CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag  
CC (DST) corresponding to mRNAs whose expression is regulated by  
CC proliferative lesion development caused by mechanically induced intimal  
CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions  
CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic  
CC activity and can be used in gene therapy. (I) can be used for diagnosing  
CC a medical condition (e.g. atherosclerosis) in a subject which involves  
CC determining the presence or absence of a mutation in (I) and diagnosing  
CC the medical condition based on the presence or absence of the mutation.  
CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility  
CC to atherosclerosis in a subject which involves detecting an alteration  
CC (an increase or decrease) in amount of expression of (I). (I) is also  
CC useful for diagnosing or monitoring the effects of treating a subject  
CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also  
CC be used for preventing, treating, modulating, or ameliorating a medical  
CC condition such as atherosclerosis in a mammalian subject. The present  
CC sequence represents a TOGA primer which is used in the exemplification of  
XX the present invention  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2169 TTTTTTTTTTTTTTTT 2187  
Db :|||||  
1 TTTTTTTTTTTTTTTT 19  
  
RESULT 1305  
ABQ73231/C  
ID ABQ73231 standard; DNA; 19 BP.  
XX  
AC ABQ73231;  
DT 27-SEP-2002 (first entry)  
XX  
DE Rabbit atherosclerosis related TOGA primer SEQ ID NO:26.  
XX  
KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;  
KW TOGA primer; ss.  
XX  
OS Oryctolagus cuniculus.  
OS Synthetic.  
XX  
PN WO200242420-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 21-NOV-2001; 2001WO-US044072.  
XX  
PR 21-NOV-2000; 2000US-0252216P.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX  
PI Leonardi A, Sartani A, Glass JR, Hasel KW;  
XX WPI; 2002-575233/61.  
DR  
XX  
XX New polynucleotides related to regulated genes characteristic of  
PT atherosclerosis, useful for diagnosing, preventing, treating, modulating  
PT or ameliorating atherosclerosis in a mammalian subject.  
XX  
PS Disclosure; Page 28; 130pp; English.  
XX  
CC The present invention describes an isolated polynucleotide (I) and its  
CC complements, and degenerate variants, comprising a sequence selected from  
CC those given in ABQ73206 to ABQ73222 (NS), which is a digital sequence tag  
CC (DST) corresponding to mRNAs whose expression is regulated by  
CC proliferative lesion development caused by mechanically induced intimal  
CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions  
CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic  
CC activity and can be used in gene therapy. (I) can be used for diagnosing  
CC a medical condition (e.g. atherosclerosis) in a subject which involves  
CC determining the presence or absence of a mutation in (I) and diagnosing  
CC the medical condition based on the presence or absence of the mutation.  
CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility  
CC to atherosclerosis in a subject which involves detecting an alteration  
CC (an increase or decrease) in amount of expression of (I). (I) is also  
CC useful for diagnosing or monitoring the effects of treating a subject  
CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also  
CC be used for preventing, treating, modulating, or ameliorating a medical  
CC condition such as atherosclerosis in a mammalian subject. The present  
CC sequence represents a TOGA primer which is used in the exemplification of  
XX the present invention  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;







transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.

Cucurbita pepo.

US2002053095-A1.

02-MAY-2002.

10-AUG-1999; 99US-00371307.

10-AUG-1999; 99US-00371307.

(BROW/) BROWN S M.

Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ; Pillar KJ, Rao S, Ream JE;

WPI; 2002-489107/52.

Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.

Example 19; Page 104; 155pp; English.

The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA. This primer is used in the exemplification of the invention

Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
:|||||  
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1310  
ABZ68389  
ID ABZ68389 standard; DNA; 19 BP.  
XX  
AC ABZ68389;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE Reverse transcription primer used to produce yeast cDNA.  
XX  
KW Histone acetyltransferase; histone deacetylase; gene expression profile;  
KW chromatin-associated protein; gene expression; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003000715-A1.  
XX  
PD 03-JAN-2003.  
XX









PN WO200261045-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 01-FEB-2002; 2002WO-US002666.  
XX  
PR 01-FEB-2001; 2001US-00775217.  
XX  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
PA (QUAN/) QUAN J.  
XX  
PI Quan J, Hilbush BS, Hasel KWPD, Sutcliffe GJ, Chang HW;  
PI Callahan MA;  
XX  
DR WPI; 2003-092784/08.  
XX  
PT Simplified TOGA method for simultaneous sequence-specific identification  
PT of multiple mRNA molecules in mRNA population, useful for determining  
PT tissue-specific patterns of gene expression or mechanisms of drug  
PT interaction.  
XX  
PS Disclosure; Page 39; 93pp; English.  
XX  
CC The present invention relates to a novel simplified TOGA (RTM) method for  
CC simultaneous sequence-specific identification of multiple mRNA molecules  
CC in a RNA population. The method involves characterising each of the  
CC sequence-specific polymerase chain reaction (PCR) products by partial  
CC sequence and length. The method is useful for determining tissue-specific  
CC patterns of gene expression or mechanisms of drug interaction. It is also  
CC useful for drug screening, studying physiological processes, genomic  
CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.  
CC The present sequence is a primer used to illustrate the method of the  
CC invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1318  
ADC21495  
ID ADC21495 standard; DNA; 19 BP.  
XX  
AC ADC21495;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human PRDI-BF1 RT-PCR primer.  
XX  
KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;  
KW multiple myeloma cell; human; PRDI-BF1;  
KW positive regulatory domain I-binding factor-1; MHC;  
KW major histocompatibility complex Class I; cytostatic; vaccine; ss;  
KW primer; PCR.  
XX  
OS Homo sapiens.  
XX  
PN WO2003029282-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 24-SEP-2002; 2002WO-EP010701.  
XX  
PR 29-SEP-2001; 2001DE-01048236.  
XX  
PA (IMMU-) IMMUGENICS AG.

PI Theobald M, Lotz C;  
XX WPI; 2003-354724/33.  
DR  
XX  
PT New tumor-associated oligopeptide, useful particularly for treating  
PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also  
PT derivatives and related nucleic acid.  
XX  
PS Disclosure; Page 22; 64pp; German.  
XX  
CC This invention describes a novel tumor-associated oligopeptide that is  
CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes  
CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple  
CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive  
CC regulatory domain I-binding factor-1) which is able to induce an MHC  
CC (major histocompatibility complex) Class I allele variant A2-restricted  
CC immune response of CD8+ CTL against tumor cells. The products of the  
CC invention have cytostatic activity and can be used in a vaccine. The  
CC peptide of the invention, also related retro-inverse and pseudopeptides,  
CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies  
CC and T cell receptors specific for PRDI-BF1 peptides are useful for  
CC treating diseases associated with PRDI-BF1, particularly tumors. The  
CC products of the invention are also useful as diagnostic, therapeutic and  
CC prophylactic agents for detecting, modifying, generating, expanding  
CC and/or regulating activation and functional status of T cells, and for  
CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell  
CC receptors and their functional equivalents. This sequence represents an  
CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the  
CC invention.  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 7.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2169 TTTTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTTTT 19  
  
RESULT 1319  
ADC21495/C  
ID ADC21495 standard; DNA; 19 BP.  
XX  
AC ADC21495;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human PRDI-BF1 RT-PCR primer.  
XX  
KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;  
KW multiple myeloma cell; human; PRDI-BF1;  
KW positive regulatory domain I-binding factor-1; MHC;  
KW major histocompatibility complex Class I; cytostatic; vaccine; ss;  
KW primer; PCR.  
XX  
OS Homo sapiens.  
XX  
PN WO2003029282-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 24-SEP-2002; 2002WO-EP010701.  
XX  
PR 29-SEP-2001; 2001DE-01048236.  
XX  
PA (IMMU-) IMMUGENICS AG.  
XX  
PI Theobald M, Lotz C;  
XX WPI; 2003-354724/33.  
XX



CC and second primers and to give short fragment of amplified DNA and (iv)  
CC labelling them to make their differentiation. Differentiation of  
CC informations of known and unknown genes readily provides information of  
CC unknown gene and simultaneous monitoring of signals derived from minor  
CC genes. Furthermore, labelling of DNAs according to functions of known  
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 8.7e+02;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db :|||||  
19 BAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1322  
AAQ45360  
ID AAQ45360 standard; DNA; 23 BP.  
XX  
AC AAQ45360;  
XX  
DT 25-MAR-2003 (revised)  
DT 09-OCT-1994 (first entry)  
XX  
DE Human protein-tyrosine-phosphatase-1D cDNA primer.  
XX  
KW Protein-tyrosine-phosphatase; enzyme; disease diagnosis; DNA primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9408017-A1.  
XX  
PD 14-APR-1994.  
XX  
PF 06-OCT-1993; 93WO-EP002728.  
XX  
PR 06-OCT-1992; 92US-00956315.  
PR 16-FEB-1993; 93US-00018129.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
PI Ullrich A, Vogel W;  
XX  
DR WPI; 1994-135583/16.  
XX  
PT New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for  
PT diagnosis and treatment of diseases associated with abnormal PTP-ID  
PT levels.  
XX  
PS Disclosure; Page 48; 99pp; English.  
XX  
CC This DNA primer is used in the PCR-based amplification of protein-  
CC tyrosine-phosphatase-1B cDNA. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT 2184  
Db ||| |||||  
1 CTCGAGTT TTTT TTTT TTTT TTTT 23  
  
RESULT 1323  
AAT37316  
ID AAT37316 standard; DNA; 23 BP.

XX  
AC AAT37316;  
XX  
DT 06-FEB-1997 (first entry)  
XX  
DE RT-PCR Primer for aromatic acyl transferase sequence.  
XX  
KW Aromatic acyl transferase; transformation; anthocyanin pigment; plants;  
KW acylation; colour; tone; colouration; colour change; Gentiana triflora;  
KW Petunia hybrida; Perilla ocimoides; Scenecio cruentus;  
KW Lavandula angustifolia; ss.  
XX  
OS Synthetic.  
XX  
PN WO9625500-A1.  
XX  
PD 22-AUG-1996.  
XX  
PF 16-FEB-1996; 96WO-JP000348.  
XX  
PR 17-FEB-1995; 95JP-00067159.  
PR 29-JUN-1995; 95JP-00196915.  
PR 30-JAN-1996; 96JP-00046534.  
XX  
PA (SUNR ) SUNTORY LTD.  
XX  
PI Ashikari T, Tanaka Y, Fujiwara H, Nakao M, Fukui Y, Yonekura K;  
PI Mizutani M, Kusumi T;  
XX  
DR WPI; 1996-393401/39.  
XX  
PT DNA coding for aromatic acyl transferase - for transforming plants which  
PT produce anthocyanin pigments and thus altering colour tone, e.g. of  
PT flowers.  
XX  
PS Example 2; Page 21; 94pp; Japanese.  
XX  
CC Vectors containing DNA fragments encoding proteins of plant origin with  
CC aromatic acyl transferase activity may be used to transform plants which  
CC produce anthocyanin pigments. The aromatic acyl transferase acylates the  
CC pigments in the flower resulting in colour tone changes and allowing new  
CC colourations to be produced. Six specific DNA sequences encoding aromatic  
CC acyl transferase from different plants are described in AAT37308-T37313.  
CC This primer was used to reverse transcribe aromatic acyl transferase RNA  
CC to produce a cDNA ready for cloning into expression vectors  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT 2184  
Db ||| |||||  
1 CTCGAGTT TTTT TTTT TTTT TTTT 23  
  
RESULT 1324  
AAZ28229  
ID AAZ28229 standard; DNA; 23 BP.  
XX  
AC AAZ28229;  
XX  
DT 20-DEC-1999 (first entry)  
XX  
DE Second round PCR primer #5 for amplifying gene trapped cDNA.  
XX  
KW Gene trapping; splicing; integration; mutation; genome; intron; exon;  
KW splice acceptor; identification; reverse transcription; ss.  
XX  
OS Synthetic.  
XX  
PN WO9950426-A1.

XX PD 07-OCT-1999.  
XX PF 26-MAR-1999; 99WO-US006474.  
XX PF 27-MAR-1998; 98US-0079729P.  
XX PR 08-APR-1998; 98US-00057328.  
XX PR 14-APR-1998; 98US-0081727P.  
XX PA (LEXI-) LEXICON GENETICS INC.  
XX PI Zambrowicz B, Friedrich GA, Sands AT;  
XX PI WPI; 1999-591324/50.  
XX DR New gene trapping vectors, useful for identifying, activating or mutating  
XX PT genes in eukaryotic cells.  
XX PT  
XX PS Example 2; Page 53; 74pp; English.  
XX CC This sequence represents a PCR primer, #5, used in a second round of PCR  
XX CC amplification of a cDNA. The cDNA had previously been amplified by a  
XX CC first round of PCR from cDNA produced by reverse transcription of RNA  
XX CC which had been generated after 3' gene trapping. The amplified cDNA was  
XX CC then sequenced to obtain the gene trapped sequence. Such gene trapping  
XX CC can be used to acquire novel sequence information from the trapped exons,  
XX CC useful to identify new genes and in screening e.g., to identify the  
XX CC genetic basis of diseases (such as cancer) or phenotypes, especially in  
XX CC the analysis of single nucleotide polymorphisms. The vector can also be  
XX CC introduced into a cell to activate expression of a naturally occurring  
XX CC cellular gene, useful to study gene function. They can be used to produce  
XX CC mutated cells or animals, and are useful in screening, for example, to  
XX CC identify mutations associated with tumorigenic phenotypes. They can also  
XX CC be used to create cDNA libraries of cells, useful for large scale genetic  
XX CC analysis of the genome and to identify novel and mutated genes. The  
XX CC vectors are more efficient (e.g., their use identified 13-fold more  
XX CC genes) than conventional 3' gene trap vectors that rely on gene trapping  
XX CC as detected by antibiotic selection. Use of vectors incorporating 5' gene  
XX CC trap cassettes increase the probability of identifying the 5' ends of  
XX CC gene open reading frames, important because these are difficult to obtain  
XX CC by conventional methods, and often code for the signal sequence in  
XX CC secreted and transmembrane proteins, an important group for potential  
XX CC drug targets  
XX SQ Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1999 CTAGCTTCTTCAGAGATCAAGTC 2021  
Db 1 CCAGAGTCTTCAGAGATCAAGTC 23  
RESULT 1325  
AAA29299  
ID AAA29299 standard; DNA; 23 BP.  
XX  
AC AAA29299;  
XX  
DT 12-SEP-2000 (first entry)  
XX  
DE Second round primer Btk-i for 3' gene trapped cDNA from ES cells.  
XX  
KW Splice acceptor; vector; gene trap; gene discovery; cloning; analysis;  
KW shuttling; gene activation; over-expression; primer; 3' gene trap;  
KW embryonic stem cell; ES; ss.  
XX  
OS Synthetic.  
XX  
PN WO200031236-A2.  
XX

PD 02-JUN-2000.  
XX  
XX PF 19-NOV-1999; 99WO-US027366.  
XX  
XX PR 20-NOV-1998; 98US-0109302P.  
XX PR 25-MAR-1999; 99US-00276533.  
XX  
XX PA (LEXI-) LEXICON GENETICS INC.  
XX  
XX PI Zambrowicz B, Friedrich GA, Lilleberg S, Sands AT;  
XX PI WPI; 2000-400053/34.  
XX  
XX PT Recombinant vectors for use in, for example, gene discovery, gene cloning  
XX PT and gene mutation.  
XX  
XX PS Example 2; Page 62; 78pp; English.  
XX  
XX CC A 3' gene trapping vector was constructed containing the murine  
XX CC phosphoglycerate kinase (PGK) gene promoter, the first exon of the murine  
XX CC btk gene (nucleotides 40043-40250) and a splice donor (SD) sequence. The  
XX CC PGKbtkSD vector lacks a 3' polyadenylation signal. Any transcript  
XX CC produced by the cassette cannot be properly processed, and therefore  
XX CC identified by 3' RACE, unless it is spliced to a 3' exon that can be  
XX CC polyadenylated. The btk vector was introduced into embryonic stem cells  
XX CC and G418 resistant cells were subsequently isolated and subjected to RNA  
XX CC isolation, reverse transcription, PCR and sequencing to obtain the gene  
XX CC trapped sequences. The claimed genetically engineered vectors comprise 5'  
XX CC and 3' gene trap cassettes. The vectors incorporate structural elements  
XX CC which, after integration into the host cell genome, enhance the number of  
XX CC cellular genes that can be identified and mutated. A 5' gene trap  
XX CC cassette comprises a splice acceptor (SA), an exon sequence (Ex1) located  
XX CC 3' to the SA, which encodes a marker enabling the identification of a  
XX CC cell expressing the exon and a polyadenylation sequence defining the 3'  
XX CC end of Ex1. The vectors may be used for gene discovery, gene cloning,  
XX CC gene mutation, gene regulation, shuttling nucleic acid sequences  
XX CC throughout the genome and gene activation and over expression. The  
XX CC vectors can be used to trap genes with a high level of efficiency  
XX CC regardless of whether the genes are normally expressed in the cell type  
XX CC into which the vector is incorporated. Cells harboring the vectors can be  
XX CC screened using automated gene identification assays such as 3' RACE.  
XX CC Using these vectors, it is possible to produce large numbers of mutations  
XX CC and rapidly identify the mutated or trapped genes  
XX SQ Sequence 23 BP; 7 A; 6 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1999 CTAGCTTCTTCAGAGATCAAGTC 2021  
Db 1 CCAGAGTCTTCAGAGATCAAGTC 23  
RESULT 1326  
ABA97431  
ID ABA97431 standard; DNA; 23 BP.  
XX  
AC ABA97431;  
XX  
DT 21-MAR-2002 (first entry)  
XX  
DE Glycosyltransferase genes PCR primer #2.  
XX  
KW Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200192509-A1.  
XX  
PD 06-DEC-2001.  
XX



PF 01-JUN-2001; 2001WO-JP004675.  
XX  
PR 02-JUN-2000; 2000JP-00170436.  
XX  
XX (ITFL-) INT FLOWER DEV PTY LTD.  
XX  
XX Mizutani M, Sakakibara K, Tanaka Y, Kusumi T, Ono E;  
PI  
XX WPI; 2002-114345/15.  
DR  
XX  
XX New gene encoding protein that transfers a sugar to the 3' position of  
PT anthocyanin for changing flower color.  
PT  
XX  
XX Example 3; Page 13; 50pp; Japanese.  
PS  
XX The present invention provides the genes and proteins of  
CC glycosyltransferases from Gentiana triflora, Senesio cruentus and  
CC Clitoria ternatea. The protein transfers a sugar to the 3' position of  
CC anthocyanin, and can be used for changing the colour of flowers. The  
CC present sequence is a PCR primer used to isolate glycosyltransferase  
CC coding sequences of the invention  
XX  
XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.2e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2162 CTCCTTTTTTTTTTTTTTTTTTTT 2184  
Db 1 CTCGAGTTTTTTTTTTTTTTTTTTT 23  
RESULT 1327  
ABA97997/C  
ID ABA97997 standard; DNA; 24 BP.  
XX  
AC ABA97997;  
XX  
DT 26-APR-2002 (first entry)  
DE Human mitochondria carrier protein 13 PCR primer SEQ ID NO 4.  
XX Human; mitochondria carrier protein 13; malignant tumour; blood disease;  
KW HIV; infection; immunity disease; inflammation; PCR primer; ss.  
KW Homo sapiens.  
OS  
XX  
XX CN1323810-A.  
PN  
XX 28-NOV-2001.  
PD  
XX 16-MAY-2000; 2000CN-00115695.  
PF  
XX 16-MAY-2000; 2000CN-00115695.  
PR (SHAN-) SHANGHAI BODE GENE DEV CO LTD.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-148830/20.  
DR  
XX New polypeptide-human mitochondria carrier protein 13 and polynucleotide  
PT for coding same.  
PT  
XX Example 2; Page 17 (Disclosure); 33pp; Chinese.  
PS  
XX The invention relates to human mitochondria carrier protein 13,  
CC polynucleotide for coding this polypeptide through DNA recombination  
CC technique. This invention also discloses the method for this polypeptide  
CC to cure several diseases, such as malignant tumour, blood disease, HIV  
CC infection and immunity disease and various inflammations etc. This  
CC invention further discloses an antagonist against this polypeptide and

CC its therapeutic action, and the application of polynucleotide for coding  
CC this new human mitochondria carrier protein 13. The present sequence is  
CC that of a PCR primer, useful to the invention  
XX  
SQ Sequence 24 BP; 5 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 1.4e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2777 TTGAATTTGAAAAAATAAAAAA 2799  
Db 23 TGAAAAATTTAAAAAATAAAAAA 1  
RESULT 1328  
AAI72268/C  
ID AAI72268 standard; DNA; 25 BP.  
XX  
AC AAI72268;  
XX 15-APR-2002 (first entry)  
DT  
XX P4 primer used in differential display s-AFLP analysis.  
DE Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;  
XX collagen 1 alpha 2; 7013; 7018; amplification; mammal; dog; cat;  
KW bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;  
KW remission; relapse; polymerase chain reaction; amplify; primer; ss.  
XX  
OS Synthetic.  
XX WO200198539-A2.  
PN  
XX 27-DEC-2001.  
PD  
XX 21-JUN-2001; 2001WO-US019980.  
PF  
XX 21-JUN-2000; 2000US-0215727P.  
PR 27-OCT-2000; 2000US-0243976P.  
XX  
XX (HITB ) HITACHI CHEM CO LTD.  
PA (HITB ) HITACHI CHEM RES CENT INC.  
PA (HITA ) HITACHI LTD.  
XX Mitsuhashi M, Kambara H, Matsunaga H, Kawamura M;  
PI  
XX WPI; 2002-098233/13.  
DR  
XX Identifying lung cancer/metastasis of solid tumor in patient by isolating  
XX blood or non-lung tissue, or bone marrow from patient and identifying  
XX presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.  
PS Example 1; Page 6; 29pp; English.  
XX  
XX The sequences given in AAI72265-69 are oligonucleotides which were used  
CC in the method of the invention for identifying lung cancer or metastasis  
CC of a solid tumour. The method comprises isolating blood (or non-lung  
CC tissue in the case of identifying lung cancer, or bone marrow in case of  
CC identifying metastasis) from a patient, and identifying the presence of  
CC at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or  
CC 7018. These oligos lead to the amplification of cDNA's which were more  
CC abundant in lung cancer RNA than in normal blood. The method is useful  
CC for identifying lung cancer in a mammal e.g., human, dog or cat, and  
CC identifying metastasis of solid tumour in a patient, where the solid  
CC tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The  
CC method is useful for identifying presence of lung cancer cells in the  
CC blood or bone marrow, and also for identifying metastasis and thus for  
CC identifying lung cancer cells in an organ such as liver or brain. The  
CC method is useful to identify the presence of lung cancer cells at a very  
CC early stage in the disease, or after remission or to identify a relapse  
XX  
SQ Sequence 25 BP; 0 A; 3 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2785 GAAAAAAAAAAAAAAAAAAAA 2803  
Db 24 BAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1329  
ACF79235/c  
ID ACF79235 standard; DNA; 25 BP.  
XX  
AC ACF79235;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Calix(a)arene-oligonucleotide hybrid.  
XX  
KW Calix(4)arene; triplex; gene therapy; DNA sensor; ss.  
XX  
OS Synthetic.

Key Location/Qualifiers  
FT stem\_loop 1..25  
FT /\*tag= a  
FT modified\_base 13  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= calix(4)arene nucleoside"

WO2003059925-A1.  
24-JUL-2003.  
19-JUN-2002; 2002WO-KR001160.  
15-JAN-2002; 2002KR-00002316.  
(POST-) POSTECH FOUND.

Kim BH, Kim SJ;  
WPI; 2003-627375/59.

New calix(4)arene-nucleoside hybrid useful in gene therapy has at least one nucleoside attached to a calix(4)arene group through amide bonding, and is derived from a calix(4)arene having amino groups.  
Claim 7; Page 20; 16pp; English.

The present sequence is that of a calix(4)arene-oligonucleotide hybrid of the invention, which includes a calix(4)arene-nucleoside (preferably thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions as a DNA hairpin structure mimic. It effectively recognises DNA or RNA through triplex formation by bonding between the calix(4)arene-containing cavity and a biologically active substance. The hybrid has a certain level of both rigidity and flexibility, is stable in vivo, has high cell permeability and can be mass-produced. It can be used as a DNA sensor or for gene therapy

Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1330  
AAC96079/c  
ID AAC96079 standard; DNA; 25 BP.  
XX  
AC AAC96079;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #46.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure; gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or classification of a nucleic acid of an organism, allele or gene such as class 1/2 HLA comprises identifying all possible nucleotide sequences of specific length.  
XX  
PS Claim 14; Page 45; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of extendible primers which can be used in the identification, typing and classification of genes. This can then be used to predict protein sequence and structure, in organ donation to match the organ with the receiver, and to identify bacteria in a sample. The method can be used to type the human leukocyte antigen genes (HLA) and 16s rRNA genes in particular  
XX  
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18.2; DB 1; Length 25;  
Best Local Similarity 87.0%; Pred. No. 1.5e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2776 GTTAGAATTGAAAAAAAAAAAAA 2798  
Db 23 GTTAAAACTCAAAAAAAAAAAAAA 1

RESULT 1331  
AAT27193  
ID AAT27193 standard; DNA; 25 BP.  
XX  
AC AAT27193;  
XX  
DT 20-NOV-1996 (first entry)  
XX

Stem loop oligonucleotide targeted to p53 chromosomal binding site.  
DE  
XX  
KW Stem loop; target; secondary structure; parallel binding domain; antiparallel; replication inhibitor; cell growth inhibitor; p53;  
KW detection; stable; strong affinity; nuclease resistant;  
KW Watson-Crick bonding; Hoogsteen bonding; ss.  
XX  
OS Synthetic.











CC when cleaved. The present sequence is a puromycin linker described in the  
 CC exemplification of the invention

SX Sequence 28 BP; 20 A; 2 C; 4 G; 0 T; 2 U; 0 Other;

SS Query Match 0.6%; Score 18.2; DB 1; Length 28;  
 Best Local Similarity 87.0%; Pred. No. 1.9e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2167 TTTT TTTT TTTT TTTT TTTT TTTT AAC 2189  
 Db ||||| ||||| ||||| ||||| ||||| |||||  
 28 TTTT TTTT TTTT TTTT TTTT TTTT GCATC 6

RESULT 1342  
 AAT70113/c

ID AAT70113 standard; DNA; 28 BP.

XX AC AAT70113;

XX DT 24-SEP-1997 (first entry)

XX DE PolyAB primer 2.

XX KW primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
 KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
 XX Synthetic.

OS WO9640998-A1.

PV 19-DEC-1996.

PF 05-JUN-1996; 96WO-US008582.

PR 07-JUN-1995; 95US-00481687.

PA (PION-) PIONEER HI-BRED INT INC.

PI Wang X, Duvick JP, Briggs SP;

PI WPI; 1997-087067/08.

PT Method for prodn. of cDNA libraries with anchored ends - useful for  
 PT subtractive cloning of sequences of interest.

PS Claim 1; Page 28; 56pp; English.

CC The invention provides a PCR-based method for generating a full-length  
 CC cDNA library with anchored ends. The method uses lock-docking primers  
 CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
 CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
 CC second primer, polyGH (H = A, C or T) locks onto the polyc tail added by  
 CC terminal deoxynucleotidyl transferase (TdR). In the final step, AAT70112-  
 CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to  
 CC amplify the first strand and produce a cDNA library with anchored ends.  
 CC cDNA libraries produced may be used to identify new (unique) nucleotide  
 CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
 CC method produces discreet sized PCR products which would not necessarily  
 CC require further subcloning/screening. The method also produces full-  
 CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
 CC clones, as produced by previously known methods. Other methods such as  
 CC PCR and RACE require a knowledge of the target sequence to be amplified,  
 CC by using the PCSUB method no previous knowledge is necessary

SX Sequence 28 BP; 18 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

QY 2165 CT TTTT TTTT TTTT TTTT TTTT TTTT TTA 2187  
 ||||| ||||| ||||| ||||| ||||| |||||

Query Match 0.6%; Score 18.2; DB 1; Length 28;  
 Best Local Similarity 87.0%; Pred. No. 1.9e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0

```
Db      28 CTTTTTTTTTTTTTTTTTGGCTA 6
RESULT 1343
ABK52626
ID      ABK52626 standard; DNA; 28 BP.
XX
AC      ABK52626;
XX
DT      27-AUG-2002 (first entry)
XX
DE      Minority genome method VIH-MUT-12 DNA sequence.
XX
KW      Minority genome method; viral quasi-species; majority genome;
KW      genetic diagnosis; viral infection; human immune deficiency virus;
KW      hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS      Unidentified.
XX
FH      Key      Location/Qualifiers
FT      misc_difference 1
FT      /*tag= a
FT      /label= unknown
FT      /note= "C6 aminolinker sequence"
XX
PN      WO200183815-A1.
XX
PD      08-NOV-2001.
XX
PF      27-APR-2001; 2001WO-ES000165.
XX
PR      27-APR-2000; 2000ES-00001068.
XX
PA      (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PI      Arias Esteban A, Baranowski E, Briones Llorente C;
PI      Domingo Solans E, Escarmis Homs C, Gomez Castilla J;
PI      Martin Ruiz- Jarabo C, Parro Garcia V;
XX
DR      WPI; 2002-147445/19.
XX
PT      Detecting minority genomes in viral quasi-species, useful for identifying
PT      mutants responsible for drug resistance and to individualize therapy.
XX
PS      Example 2; Page 55; 107pp; Spanish.
XX
CC      The present invention relates to a new method for detecting minority
CC      genomes, present at less than 50%, in a population of nucleic acids of a
CC      viral quasi-species and having at least one mutation with respect to the
CC      majority genome. The invention can be used for genetic diagnosis of viral
CC      infections, especially human immune deficiency virus and hepatitis B or
CC      C, particularly to detect memory minority genomes that are implicated in
CC      failure of antiviral therapy, so the method may make possible design of
CC      therapies customised for individual patients. The present nucleic acid
CC      sequence represents the VIH-MUT-12 DNA sequence that was used in the
CC      methods of the invention
XX
SQ      Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;
Query Match      0.6%; Score 18.2; DB 1; Length 28;
Best Local Similarity 87.0%; Pred. No. 1.9e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      2166 TTTTTTTTTTTTTTTTTTTTAA 2188
      |||||
Db      2 TTTTTTTTTTTTGTGTAA 24
RESULT 1344
AAD41903
ID      AAD41903 standard; RNA; 28 BP.
XX
AC      AAD41903;
```

```
XX      30-OCT-2002 (first entry)
DT
XX
DE      ON-41 oligonucleotide used in the exemplification of the invention.
XX
KW      Antisense therapy; infection; cardiovascular disorder; immune reaction;
KW      gene therapy; virucide; cytostatic; antibacterial; antiinflammatory;
KW      cancer; cardiant; ss.
XX
OS      Unidentified.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT      given as N in the sequence shown as SEQ ID NO: 50 in the
FT      sequence listing"
FT      modified_base 2
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
FT      modified_base 3
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT      given as N in the sequence shown as SEQ ID NO: 50 in the
FT      sequence listing"
FT      modified_base 4
FT      /*tag= d
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
FT      modified_base 5
FT      /*tag= e
FT      /mod_base= OTHER
FT      /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT      given as N in the sequence shown as SEQ ID NO: 50 in the
FT      sequence listing"
FT      modified_base 11
FT      /*tag= f
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
FT      modified_base 12
FT      /*tag= g
FT      /mod_base= OTHER
FT      /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT      given as N in the sequence shown as SEQ ID NO: 50 in the
FT      sequence listing"
FT      modified_base 14
FT      /*tag= h
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
FT      modified_base 15
FT      /*tag= i
FT      /mod_base= OTHER
FT      /note= "5-(1-propynyl)-2'-deoxyuridine; This base is
FT      given as N in the sequence shown as SEQ ID NO: 50 in the
FT      sequence listing"
FT      modified_base 16
FT      /*tag= j
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
FT      modified_base 17
FT      /*tag= k
FT      /mod_base= OTHER
FT      /note= "5-methyl-2'-deoxycytidine; This base is given as
FT      N in the sequence shown as SEQ ID NO: 50 in the sequence
FT      listing"
```





RESULT 1347  
AAQ34110  
ID AAQ34110 standard; DNA; 18 BP.  
XX AC AAQ34110;  
XX DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX DE Sequence of a microsatellite from clone TGLA60B.  
XX KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KW genetic mapping; traits; amplification; ss.  
XX OS Bos taurus.  
XX PN WO9213102-A1.  
XX PD 06-AUG-1992.  
XX PF 15-JAN-1992; 92WO-US000340.  
XX PR 15-JAN-1991; 91US-00642342.  
XX PA (GENM-) GENMARK.  
XX PI Georges M, Massey JM;  
XX DR WPI; 1992-284684/34.  
XX PT Polymorphic bovine DNA markers - used in genetic identification, gene  
XX mapping, and selective breeding.  
PS Table 7; Page 375; 517pp; English.  
XX CC The sequence is that of a bovine microsatellite sequence obt'd. by  
CC screening a library of bovine MboI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MboI sites, the frequency of (TG)n >9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved in the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1348  
AAQ34110/c  
ID AAQ34110 standard; DNA; 18 BP.  
XX AC AAQ34110;  
XX DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)  
XX DE Sequence of a microsatellite from clone TGLA60B.



XX Solid phase immunoassay using oligo:nucleotide as label - also new  
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for  
PT diagnosing hepatitis C or E virus infection.  
XX  
PS Example; Page 12; 34pp; English.  
XX  
CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
CC They are used in a method for detecting an antigen in a subject. The  
CC method involves binding the antigen to a solid support and then reacting  
CC it with an immunoreactive ligand (L) bound to an oligo; removing any  
CC unreacted L, and then detecting the presence of the oligo. A similar  
CC method can be used to detect Abs, in which case the ligand is an oligo-  
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab  
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which  
CC can be covalently attached by the 5'- terminus to the N- or C-terminal of  
CC a synthetic peptide. In the example, peptide AAR62941 was coupled to  
CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to  
CC contain HEV Abs were immobilised on plastic tubes or wells, then  
CC incubated for 30-60 mins with the peptide-oligo product. The vessels were  
CC washed; bound oligo was released with 0.2M glycine and amplified in a  
CC separate tube using as primers AAQ75025 and AAQ75026 in 30 cycles of PCR.  
CC The amplification product - AAQ75031 - was treated with uracil DNA  
CC glycosylase to remove the U18 fragment, and the product captured by  
CC immobilised oligo-dT. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 1351  
AAT94667  
ID AAT94667 standard; DNA; 18 BP.  
XX  
AC AAT94667;  
XX  
DT 27-MAR-1998 (first entry)  
XX  
DE Anchored poly(T) oligonucleotide polyT-AnchA.  
XX  
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;  
KW snapdragon; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9732023-A1.  
XX  
PD 04-SEP-1997.  
XX  
PF 28-FEB-1997; 97WO-AU000124.  
XX  
PR 01-MAR-1996; 96AU-00008386.  
XX  
PA (FLOR-) FLORIGENE LTD.  
XX  
PI Brugliera F, Holton TA, Michael MZ;  
XX  
DR WPI; 1997-448691/41.  
XX  
PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and  
PT corresponding DNA, used in the manipulation of pigmentation in plants.  
XX  
OS Synthetic.  
XX  
PN WO9732023-A1.  
XX  
PD 04-SEP-1997.  
XX  
PF 28-FEB-1997; 97WO-AU000124.  
XX  
PR 01-MAR-1996; 96AU-00008386.  
XX  
PA (FLOR-) FLORIGENE LTD.  
XX  
PI Brugliera F, Holton TA, Michael MZ;  
XX  
DR WPI; 1997-448691/41.  
XX  
PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and  
PT corresponding DNA, used in the manipulation of pigmentation in plants.  
XX  
PS Example 15; Page 59; 234pp; English.  
XX  
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC  
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream

CC region of a polyadenylation sequence. They were used to prime cDNA  
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and  
CC were also utilised in the PCR amplification of plant cytochrome P450  
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding  
CC flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential  
CC display approach. This can be used to manipulate the pigmentation of  
CC transgenic plants  
XX  
SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2170 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 18  
  
RESULT 1352  
AAT94668/c  
ID AAT94668 standard; DNA; 18 BP.  
XX  
AC AAT94668;  
XX  
DT 27-MAR-1998 (first entry)  
XX  
DE Anchored poly(T) oligonucleotide polyT-AnchC.  
XX  
KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;  
KW snapdragon; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9732023-A1.  
XX  
PD 04-SEP-1997.  
XX  
PF 28-FEB-1997; 97WO-AU000124.  
XX  
PR 01-MAR-1996; 96AU-00008386.  
XX  
PA (FLOR-) FLORIGENE LTD.  
XX  
PI Brugliera F, Holton TA, Michael MZ;  
XX  
DR WPI; 1997-448691/41.  
XX  
PT Novel flavonoid 3'-hydroxylase(s) from flowering plants - and  
PT corresponding DNA, used in the manipulation of pigmentation in plants.  
XX  
PS Example 15; Page 59; 234pp; English.  
XX  
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC  
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream  
CC region of a polyadenylation sequence. They were used to prime cDNA  
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and  
CC were also utilised in the PCR amplification of plant cytochrome P450  
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding  
CC flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential  
CC display approach. This can be used to manipulate the pigmentation of  
CC transgenic plants  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1



```
RESULT 1353
AAV37712
ID AAV37712 standard; cDNA; 18 BP.
XX
AC AAV37712;
XX
XX 25-MAR-2003 (revised)
DT 07-SEP-1998 (first entry)
XX
DE Human protein AQ2_1i 3'-portion and polyA tail.
XX
XX Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
KW bone marrow; thymus; AE648_1i; AK438_1i; AK609_1i; AM1060_1i;
KW AQ2_1i; K433_1i; L256_1i; prevent; treat; ameliorate; medical; ds.
XX
XX Homo sapiens.
OS
XX WO9820130-A2.
PN
XX 14-MAY-1998.
PD
XX 31-OCT-1997; 97WO-US019857.
XX
XX 01-NOV-1996; 96US-00742973.
PR
XX 29-OCT-1997; 97US-00960024.
XX
XX (GEMY ) GENETICS INST INC.
PA
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agostino MJ;
PI
XX WPI; 1998-286946/25.
DR
XX New secreted proteins and associated polynucleotides - obtained from
PT murine adult spleen, human foetal kidney, human ovary, murine bone marrow
PT and murine adult thymus.
XX
XX Disclosure; Page 58; 75pp; English.
PS
XX
XX The present invention describes novel proteins isolated from cDNA clones:
CC AE648_1i; AE693_1i; AK438_1i; AK609_1i; AM1060_1i; AQ2_1i; K433_1i; or
CC L256_1i, deposited as ATCC 98237. The present sequence represents the 3'-
CC portion of AQ2_1i isolated from a human ovary cDNA library. The proteins
CC from the present invention may be administered in a composition to
CC prevent, treat or ameliorate a medical condition. The proteins may
CC exhibit biological activities such as nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating or
CC suppressing activity, haematopoiesis regulating activity, tissue growth
CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC haemostatic and thrombotic activity, receptor/ligand activity, anti-
CC inflammatory activity, cadherin/tumour invasion suppressor activity,
CC tumour inhibition activity and other activities. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
XX Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
Db 1 GAAAAAAAAAAAAAAAAA 18

RESULT 1354
AAV21970
ID AAV21970 standard; DNA; 18 BP.
XX
XX AAV21970;
AC
XX 14-JUL-1998 (first entry)
DT
```

```
XX Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
DE
XX Nuclease resistant; bacterial infection; antibiotic; target;
KW veterinary medicine; treatment; human; industrial process;
KW bacterial control; ss.
XX
OS Synthetic.
XX WO9803533-A1.
PN
XX 29-JAN-1998.
PD
XX 23-JUL-1997; 97WO-US012961.
XX
XX 24-JUL-1996; 96US-00685575.
PR
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
PA
XX Arrow A, Dale RMK, Thompson TL;
PI
XX WPI; 1998-120687/11.
DR
XX Treating bacterial infections in humans or animals with
XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
PT with antibiotics.
PT
XX Claim 49; Page 87; 163pp; English.
PS
XX This antisense oligonucleotide is nuclease resistant and can be used in
XX the treatment of animals, including humans, having a bacterial infection.
CC The treatment comprises administration of such nuclease resistant
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,
CC and formulated with a carrier. A compound comprising this nuclease
CC resistant oligonucleotide can be covalently linked to an antibiotic. The
CC method is used to treat infections by a wide variety of Gram-positive and
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
CC The methods are particularly used in immuno-compromised individuals (e.g.
CC patients with acquired immunodeficiency syndrome or those receiving
CC chemotherapy or radiation therapy), optionally in combination with, or
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from
CC therapeutic use, the oligonucleotides can be used to control bacteria in
CC laboratory cultures, foods, beverages and industrial processes. The
CC oligonucleotides are specific for bacteria, without affecting metabolism
CC in mammalian cells. They may also activate RNase H and have a general,
CC non-specific immune-stimulating effect. The oligonucleotides can be
CC administered orally, intranasally, rectally, topically or by injection,
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that
CC enhances cellular uptake
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1355
AAV21970/c
ID AAV21970 standard; DNA; 18 BP.
XX
XX AAV21970;
AC
XX 14-JUL-1998 (first entry)
DT
XX Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
DE
XX Nuclease resistant; bacterial infection; antibiotic; target;
KW
```

KW veterinary medicine; treatment; human; industrial process;  
KW bacterial control; ss.

OS Synthetic.

XX WO9803533-A1.

PN 29-JAN-1998.

XX 23-JUL-1997; 97WO-US012961.

PF 24-JUL-1996; 96US-00685575.

XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.

PA Arrow A, Dale RMK, Thompson TL;

PI WPI; 1998-120687/11.

DR Treating bacterial infections in humans or animals with  
XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial  
PT nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)  
PT with antibiotics.

XX Claim 49; Page 87; 163pp; English.

CC This antisense oligonucleotide is nuclease resistant and can be used in  
CC the treatment of animals, including humans, having a bacterial infection.  
CC The treatment comprises administration of such nuclease resistant  
CC oligonucleotides, targeted to a nucleic acid or protein of the bacterium,  
CC and formulated with a carrier. A compound comprising this nuclease  
CC resistant oligonucleotide can be covalently linked to an antibiotic. The  
CC method is used to treat infections by a wide variety of Gram-positive and  
CC Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.  
CC The methods are particularly used in immuno-compromised individuals (e.g.  
CC patients with acquired immunodeficiency syndrome or those receiving  
CC chemotherapy or radiation therapy), optionally in combination with, or  
CC fused to, antiviral or other antimicrobial oligonucleotides. Apart from  
CC therapeutic use, the oligonucleotides can be used to control bacteria in  
CC laboratory cultures, foods, beverages and industrial processes. The  
CC oligonucleotides are specific for bacteria, without affecting metabolism  
CC in mammalian cells. They may also activate RNase H and have a general,  
CC non-specific immune-stimulating effect. The oligonucleotides can be  
CC administered orally, intranasally, rectally, topically or by injection,  
CC optionally coupled to an agent (e.g. carbohydrate or polyamine) that  
CC enhances cellular uptake.

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1356

AAX19943

ID AAX19943 standard; DNA; 18 BP.

XX AAX19943;

AC 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:3 from JP11075880.

DE Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.

XX

PD 23-MAR-1999.

XX

PF 10-JUL-1998; 98JP-00195719.

XX

PR 14-JUL-1997; 97JP-00205378.

XX

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX

DR WPI; 1999-257710/22.

XX

PT Labelling of an oligonucleotide - useful for detecting genes.

XX

PS Example 1; Page 7; 10pp; Japanese.

XX

CC A method has been developed for labelling an oligonucleotide having a  
CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
CC adenine and thymine or uracil or guanine and cytosine, and n is an  
CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
CC sequence is added and extended using a labelled body of the nucleotide  
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to  
CC 3' exonuclease activity. The method can be used for detecting a gene. The  
CC method can detect a gene in a sensitivity up to ten times higher than  
CC prior art methods. The present sequence represents a primer used in an  
CC example from the present invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTTTTTT 18

RESULT 1357

AAX19943/c

ID AAX19943 standard; DNA; 18 BP.

XX

AC AAX19943;

XX

DT 14-JUN-1999 (first entry)

XX

DE Primer SEQ ID NO:3 from JP11075880.

XX

KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX

OS Synthetic.

XX

PN JP11075880-A.

XX

PD 23-MAR-1999.

XX

PF 10-JUL-1998; 98JP-00195719.

XX

PR 14-JUL-1997; 97JP-00205378.

XX

PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX

DR WPI; 1999-257710/22.

XX

PT Labelling of an oligonucleotide - useful for detecting genes.

XX

PS Example 1; Page 7; 10pp; Japanese.

XX

CC A method has been developed for labelling an oligonucleotide having a  
CC repeated sequence of (XY)<sub>n</sub> (where X and Y consists of a combination of  
CC adenine and thymine or uracil or guanine and cytosine, and n is an  
CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
CC sequence is added and extended using a labelled body of the nucleotide  
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to

CC 3' exonuclease activity. The method can be used for detecting a gene. The  
CC method can detect a gene in a sensitivity up to ten times higher than  
CC prior art methods. The present sequence represents a primer used in an  
CC example from the present invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1358  
AA19942  
ID AAX19942 standard; DNA; 18 BP.

XX  
AC AAX19942;

XX 14-JUN-1999 (first entry)

XX Primer SEQ ID NO:2 from JP11075880.

XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.

XX Synthetic.

XX JP11075880-A.

XX 23-MAR-1999.

XX 10-JUL-1998; 98JP-00195719.

XX 14-JUL-1997; 97JP-00205378.

XX (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

XX WPI; 1999-257710/22.

XX Labelling of an oligonucleotide - useful for detecting genes.

XX Example 1; Page 7; 10pp; Japanese.

XX A method has been developed for labelling an oligonucleotide having a  
CC repeated sequence of (XY)n (where X and Y consists of a combination of  
CC adenine and thymine or uracil or guanine and cytosine, and n is an  
CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
CC sequence is added and extended using a labelled body of the nucleotide  
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to  
CC 3' exonuclease activity. The method can be used for detecting a gene. The  
CC method can detect a gene in a sensitivity up to ten times higher than  
CC prior art methods. The present sequence represents a primer used in an  
CC example from the present invention

XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1359

AA19942/c

ID AAX19942 standard; DNA; 18 BP.

XX

AC AAX19942;

XX 14-JUN-1999 (first entry)  
DT Primer SEQ ID NO:2 from JP11075880.  
XX  
DE Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.  
XX  
KW Synthetic.  
XX  
OS JP11075880-A.  
XX  
PN 23-MAR-1999.  
XX  
PD 10-JUL-1998; 98JP-00195719.  
XX  
PF 14-JUL-1997; 97JP-00205378.  
XX  
PR (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
XX  
PA WPI; 1999-257710/22.  
XX  
DR Labelling of an oligonucleotide - useful for detecting genes.  
XX  
PT Example 1; Page 7; 10pp; Japanese.  
XX  
PS A method has been developed for labelling an oligonucleotide having a  
XX repeated sequence of (XY)n (where X and Y consists of a combination of  
CC adenine and thymine or uracil or guanine and cytosine, and n is an  
CC integer of 1 or more ) at the 3'-terminal side in which the repeated  
CC sequence is added and extended using a labelled body of the nucleotide  
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to  
CC 3' exonuclease activity. The method can be used for detecting a gene. The  
CC method can detect a gene in a sensitivity up to ten times higher than  
CC prior art methods. The present sequence represents a primer used in an  
CC example from the present invention

XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 18 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 1360  
AA18372  
ID AAX18372 standard; DNA; 18 BP.

XX AAX18372;

XX 11-MAY-1999 (first entry)

XX RT-PCR primer of the invention SEQ ID 13.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.

XX JP11032765-A.

XX 09-FEB-1999.

XX 18-JUL-1997; 97JP-00208312.

XX 18-JUL-1997; 97JP-00208312.

XX (TAKI ) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.





Thu Jun 10 13:10:09 2004

CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87160-Z87164 represent  
CC oligoarabinonucleotides containing beta-D-arabinose used in an  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1363  
AAZ87161/c  
ID AAZ87161 standard; RNA; 18 BP.  
XX  
AC AAZ87161;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Oligoarabinonucleotide SEQ ID NO:2.  
XX  
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;  
KW reverse transcription; viral replication; RNase H cleavage;  
KW triple helix formation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Ribose moiety replaced by beta-D-arabinose"  
XX  
PN WO9967378-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 17-JUN-1999; 99WO-CA000571.  
XX  
PR 19-JUN-1998; 98CA-02241361.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
XX  
DR WPI; 2000-160584/14.  
XX  
PT Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX  
PS Example 1; Page 29; 91pp; English.  
XX  
CC The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss

CC RNA, but not complementary ss DNA, so may be useful for targeting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87160-Z87164 represent  
CC oligoarabinonucleotides containing beta-D-arabinose used in an  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTT 1  
  
RESULT 1364  
AAZ87162  
ID AAZ87162 standard; RNA; 18 BP.  
XX  
AC AAZ87162;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Oligoarabinonucleotide SEQ ID NO:3.  
XX  
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;  
KW reverse transcription; viral replication; RNase H cleavage;  
KW triple helix formation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Ribose moiety replaced by beta-D-arabinose"  
XX  
PN WO9967378-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 17-JUN-1999; 99WO-CA000571.  
XX  
PR 19-JUN-1998; 98CA-02241361.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
XX  
DR WPI; 2000-160584/14.  
XX  
PT Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX  
PS Example 1; Page 29; 91pp; English.  
XX  
CC The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if

CC any non-specific binding to cellular or serum proteins. They target ss  
CC RNA, but not complementary ss DNA, so may be useful for targetting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87160-Z87164 represent  
CC oligoarabinonucleotides containing beta-D-arabinose used in an  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 0.0%; Pred. No. 7.3e+02;  
Matches 0; Conservative 18; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 UUUUUUUUUUUUUUUUUUU 18  
  
RESULT 1365  
AAZ87162/C  
ID AAZ87162 standard; RNA; 18 BP.  
XX  
AC AAZ87162;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Oligoarabinonucleotide SEQ ID NO:3.  
XX  
KW Beta-D-arabinose; antisense; inhibition; transcription; expression;  
KW reverse transcription; viral replication; RNase H cleavage;  
KW triple helix formation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Ribose moiety replaced by beta-D-arabinose"  
XX  
PN WO9967378-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 17-JUN-1999; 99WO-CA000571.  
XX  
PR 19-JUN-1998; 98CA-02241361.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
XX WPI; 2000-160584/14.  
DR  
XX  
PT Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX  
PS Example 1; Page 29; 91pp; English.  
XX  
CC The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent

CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss  
CC RNA, but not complementary ss DNA, so may be useful for targetting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87160-Z87164 represent  
CC oligoarabinonucleotides containing beta-D-arabinose used in an  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 1366  
AAZ87166  
ID AAZ87166 standard; DNA; 18 BP.  
XX  
AC AAZ87166;  
XX  
DT 08-MAY-2000 (first entry)  
XX  
DE Deoxyarabinonucleotide SEQ ID NO:7.  
XX  
KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;  
KW transcription; expression; reverse transcription; viral replication;  
KW RNase H cleavage; triple helix formation; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-  
FT fluoro-beta-D-arabinose"  
XX  
PN WO9967378-A1.  
XX  
PD 29-DEC-1999.  
XX  
PF 17-JUN-1999; 99WO-CA000571.  
XX  
PR 19-JUN-1998; 98CA-02241361.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;  
XX WPI; 2000-160584/14.  
DR  
XX  
PT Therapeutic composition containing antisense oligonucleotides that  
PT include arabinose sugars, particularly for inhibiting viral replication.  
XX  
PS Example 2; Page 31; 91pp; English.  
XX  
CC The invention relates to a new composition for selective, sequence-  
CC specific inhibition of gene transcription and expression in a host. The  
CC composition comprises oligonucleotides containing arabinose sugars that  
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H  
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple  
CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific





CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87165-287169 represent  
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-  
CC arabinose used in an exemplification of the present invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1369

AAZ87167/c

ID AAZ87167 standard; DNA; 18 BP.

XX

AC AAZ87167;

XX

DT 08-MAY-2000 (first entry)

XX

DE Deoxyarabinonucleotide SEQ ID NO:8.

XX

KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;

KW transcription; expression; reverse transcription; viral replication;

KW RNase H cleavage; triple helix formation; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..18

FT /\*tag= a

FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-

FT fluoro-beta-D-arabinose"

XX

PN WO9967378-A1.

XX

PD 29-DEC-1999.

XX

PF 17-JUN-1999; 99WO-CA000571.

XX

PR 19-JUN-1998; 98CA-02241361.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;

XX

DR WPI; 2000-160584/14.

XX

PT Therapeutic composition containing antisense oligonucleotides that

PT include arabinose sugars, particularly for inhibiting viral replication.

XX

PS Example 2; Page 31; 91pp; English.

XX

CC The invention relates to a new composition for selective, sequence-

CC specific inhibition of gene transcription and expression in a host. The

CC composition comprises oligonucleotides containing arabinose sugars that

CC can hybridise to either a single-stranded (ss) RNA to induce RNase H

CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple

CC helix, thereby inhibiting DNA replication and/or transcription. The  
CC oligoarabinonucleotides are used for antisense inhibition of gene  
CC expression or to prevent DNA replication, or reverse transcription of RNA  
CC by retroviruses. The compositions are therefore particularly used to  
CC inhibit retroviral replication. The oligoarabinonucleotides can also be  
CC used, in combination with RNase H, as reagents for sequence-specific  
CC cleavage or RNA mapping, and additionally for the study and control of  
CC gene expression in cells. The oligoarabinonucleotides have excellent  
CC affinity for RNA, increased resistance to nucleases and show little if  
CC any non-specific binding to cellular or serum proteins. They target ss  
CC RNA, but not complementary ss DNA, so may be useful for targeting  
CC retroviral genomic RNA to inhibit the early stages of viral replication.  
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices  
CC with significantly higher thermal stability than those produced by normal  
CC oligonucleotides. Sequences AAZ87165-287169 represent  
CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'fluoro-beta-D-  
CC arabinose used in an exemplification of the present invention  
XX

SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTT 1

RESULT 1370

AAZ03565

ID AAZ03565 standard; DNA; 18 BP.

XX

AC AAZ03565;

XX

DT 19-JUN-2001 (first entry)

XX

DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.

XX

KW Rat; secreted factor; clone P00188 D12; cardiant; antiinflammatory;

KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;

KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;

KW antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;

KW nootropic; neuroprotective; congestive heart failure; myocarditis;

KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;

KW kidney disease; acute renal failure; renal glucosuria; renal infarction;

KW polycystic kidney disease; hereditary nephritis; inflammatory disease;

KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;

KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;

KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.

XX Rattus norvegicus.

OS

XX WO200123564-A1.

PN

PD 05-APR-2001.

XX

PF 27-SEP-2000; 2000WO-US026544.

XX

PR 27-SEP-1999; 99US-0156280P.

XX

PA (SCIO-) SCIOS INC.

XX

PI Stanton LW, Kapoun AM;

XX

DR WPI; 2001-266159/27.

XX

PT Novel secreted factor encoded by clone P00188D12 which is differentially

PT expressed in certain disease states, useful in diagnosing and treating

PT cardiac, renal or inflammatory diseases.

XX

PS Example 1; Page 42; 71pp; English.

XX



CC The patent discloses novel secreted factor protein encoded by clone  
CC P00188\_D12. The secreted factor is differentially expressed in certain  
CC disease states. Secreted protein, its antibodies, antagonists or  
CC compositions comprising them are useful in the diagnosis and treatment of  
CC cardiac diseases such as congestive heart failure, myocarditis,  
CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,  
CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal  
CC failure, renal glucosuria, renal infarction, nephrogenic diabetes  
CC insipidus, polycystic kidney disease, hereditary nephritis and  
CC inflammatory diseases such as asthma, autoimmune diabetes, tumour  
CC angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,  
CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,  
CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted  
CC protein DNA is useful in antisense-mediated gene inhibition and in gene  
CC therapy. An array comprising one or more oligonucleotides complementary  
CC to reference RNA or DNA encoding the secreted factor is useful for  
CC detecting cardiac, kidney and inflammatory disease. The present DNA  
CC sequence is an oligonucleotide which is used in the preparation of a  
CC normalised cDNA library containing secreted factor DNAs. The normalised  
CC cDNA libraries are used in the identification of differentially expressed  
CC rat secreted factor P00188\_D12 gene  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1371  
AAD03565/c  
ID AAD03565 standard; DNA; 18 BP.

XX AAD03565;

DT 19-JUN-2001 (first entry)

XX Oligonucleotide #6 used for the preparation of normalised cDNA libraries.

XX Rat; secreted factor; clone P00188 D12; cardiant; antiinflammatory;  
KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;  
KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;  
KW antibacterial; osteopathic; cerebroprotective; vasotropic; antiulcer;  
KW nootropic; neuroprotective; congestive heart failure; myocarditis;  
KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;  
KW kidney disease; acute renal failure; renal glucosuria; renal infarction;  
KW polycystic kidney disease; hereditary nephritis; inflammatory disease;  
KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;  
KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;  
KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.

XX Rattus norvegicus.

XX WO200123564-A1.

PD 05-APR-2001.

PF 27-SEP-2000; 2000WO-US026544.

PR 27-SEP-1999; 99US-0156280P.

XX (SCIO-) SCIOS INC.

XX Stanton LW, Kapoun AM;

XX WPI; 2001-266159/27.

XX Novel secreted factor encoded by clone P00188D12 which is differentially  
PT expressed in certain disease states, useful in diagnosing and treating

PT cardiac, renal or inflammatory diseases.  
XX Example 1; Page 42; 71pp; English.  
PS  
XX The patent discloses novel secreted factor protein encoded by clone  
CC P00188\_D12. The secreted factor is differentially expressed in certain  
CC disease states. Secreted protein, its antibodies, antagonists or  
CC compositions comprising them are useful in the diagnosis and treatment of  
CC cardiac diseases such as congestive heart failure, myocarditis,  
CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,  
CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal  
CC failure, renal glucosuria, renal infarction, nephrogenic diabetes  
CC insipidus, polycystic kidney disease, hereditary nephritis and  
CC inflammatory diseases such as asthma, autoimmune diabetes, tumour  
CC angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,  
CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,  
CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted  
CC protein DNA is useful in antisense-mediated gene inhibition and in gene  
CC therapy. An array comprising one or more oligonucleotides complementary  
CC to reference RNA or DNA encoding the secreted factor is useful for  
CC detecting cardiac, kidney and inflammatory disease. The present DNA  
CC sequence is an oligonucleotide which is used in the preparation of a  
CC normalised cDNA library containing secreted factor DNAs. The normalised  
CC cDNA libraries are used in the identification of differentially expressed  
CC rat secreted factor P00188\_D12 gene  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 18 AAAAAA AAAAAA AAAAAA 1

RESULT 1372  
AAD17014

ID AAD17014 standard; DNA; 18 BP.

XX AAD17014;

DT 29-NOV-2001 (first entry)

DE Oligonucleotide A18-2PEG linker.

XX Scaffold protein; antibody mimic; fibronectin type III domain;  
KW randomised loop; randomised beta-sheet; diagnostic purpose;  
KW protein designing; ss.

XX Unidentified.

OS Key Location/Qualifiers  
FH misc\_feature 18  
FT /tag= a  
FT /note= "Linked to (PEG)2CCPuromycin"

XX WO200164942-A1.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006414.

XX 29-FEB-2000; 2000US-00515260.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2001-557782/62.

XX Fibronectin scaffold protein array for obtaining a protein/compound which

PT binds to a compound/protein, comprises a fibronectin type III domain  
PT having a randomized loop, a randomized beta-sheet or their combination.  
XX  
PS Disclosure; Page 25; 67pp; English.  
XX  
CC The present invention relates to an array of proteins (antibody mimics)  
CC comprising a fibronectin type III domain having a randomized loop, a  
CC randomised beta-sheet, or their combination, and has the capacity to bind  
CC to a compound that is not bound by a corresponding naturally- occurring  
CC fibronectin, immobilised onto a solid support. The antibody mimics is  
CC useful for detecting a compound preferably a protein, in a biological  
CC sample. It is also useful to detect one or more different analytes  
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It  
CC is also useful for the purpose of designing proteins capable of binding  
CC to virtually any compound of interest. The present sequence is an  
CC oligonucleotide A18-2PEG linker used in an exemplification of the  
CC invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18  
RESULT 1373  
AAD17014/c  
ID AAD17014 standard; DNA; 18 BP.  
XX  
AC AAD17014;  
XX  
DT 29-NOV-2001 (first entry)  
XX  
DE Oligonucleotide A18-2PEG linker.  
XX  
KW Scaffold protein; antibody mimic; fibronectin type III domain;  
KW randomised loop; randomised beta-sheet; diagnostic purpose;  
KW protein designing; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 18  
FT /\*tag= a  
FT /note= "Linked to (PEG)2CCPuromycin"  
XX  
PN WO200164942-A1.  
XX  
PD 07-SEP-2001.  
XX  
PF 28-FEB-2001; 2001WO-US006414.  
XX  
PR 29-FEB-2000; 2000US-00515260.  
XX  
PA (PHYL-) PHYLLOS INC.  
XX  
PI Lipovsek D, Wagner RW, Kuimelis RG;  
XX  
DR WPI; 2001-557782/62.  
XX  
PT Fibronectin scaffold protein array for obtaining a protein/compound which  
PT binds to a compound/protein, comprises a fibronectin type III domain  
PT having a randomized loop, a randomized beta-sheet or their combination.  
XX  
PS Disclosure; Page 25; 67pp; English.  
XX  
CC The present invention relates to an array of proteins (antibody mimics)  
CC comprising a fibronectin type III domain having a randomized loop, a  
CC randomised beta-sheet, or their combination, and has the capacity to bind

CC to a compound that is not bound by a corresponding naturally- occurring  
CC fibronectin, immobilised onto a solid support. The antibody mimics is  
CC useful for detecting a compound preferably a protein, in a biological  
CC sample. It is also useful to detect one or more different analytes  
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It  
CC is also useful for the purpose of designing proteins capable of binding  
CC to virtually any compound of interest. The present sequence is an  
CC oligonucleotide A18-2PEG linker used in an exemplification of the  
CC invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 18 TTTT TTTT TTTT TTTT TTTT TTTT 1  
RESULT 1374  
AAF75598/c  
ID AAF75598 standard; DNA; 18 BP.  
XX  
AC AAF75598;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Binary encoded sequence tag method anchored primer #3.  
XX  
KW Binary encoded sequence tag; BEST; nucleic acid analysis;  
KW gene expression; adaptor; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200112855-A2.  
XX  
PD 22-FEB-2001.  
XX  
PF 11-AUG-2000; 2000WO-US022164.  
XX  
PR 13-AUG-1999; 99US-0148870P.  
PR 06-APR-2000; 2000US-00544713.  
XX  
PA (UYVA ) UNIV YALE.  
XX  
PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;  
XX  
DR WPI; 2001-202878/20.  
XX  
PT Producing binary sequence tags, useful for analyzing nucleic acid  
PT sequence tags, gene expression or gene-expression patterns, involves  
PT generating nucleic acid fragments, which are mixed with offset adaptors  
PT and adaptor-indexers.  
XX  
PS Disclosure; Page 101; 101pp; English.  
XX  
CC The present invention describes a method of producing binary sequence  
CC tags from nucleic acid fragments in a sample, involving incubating the  
CC sample with cleaving reagents, mixing offset adaptors with the sample,  
CC incubating with more cleaving reagents and mixing the sample with adaptor  
CC -indexers where the adaptors are coupled to binary sequence tags. The  
CC method is useful in sequence analysis, including analysis and comparison  
CC of gene expression, nucleic acid samples and genomes  
XX  
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGA AAAAAAAAAAAAAAAAAA 2801

Db	18	TGAAAAAAAAAAAAAA 1	
		RESULT 1375	
		AAF99708	
ID	AAF99708	standard; DNA; 18 BP.	
XX			
AC	AAF99708;		
XX			
DT	12-JUN-2001	(first entry)	
XX			
DE		Immunostimulatory nucleic acid #824.	
XX			
KW		Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;	
KW		immunostimulatory; tumour; viral infection; bacterial infection;	
KW		fungal infection; parasitic infection; cancer; asthma;	
KW		infectious disease; allergy; immune deficiency; phosphorothioate; ss.	
XX			
OS		Synthetic.	
XX			
PN	WO200122972-A2.		
XX			
PD	05-APR-2001.		
XX			
PF	25-SEP-2000;	2000WO-US026383.	
XX			
PR	25-SEP-1999;	99US-0156113P.	
PR	27-SEP-1999;	99US-0156135P.	
PR	23-AUG-2000;	2000US-0227436P.	
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
PA	(COLE-) COLEY PHARM GMBH.		
XX			
PI	Krieg AM, Schetter C, Vollmer J;		
XX			
DR	WPI; 2001-273485/28.		
XX			
PT	Vaccinating against tumors, infectious diseases, allergies and asthma		
PT	using immunostimulatory Py-rich and TG nucleic acids.		
XX			
PS	Claim 101; Page 56; 338pp; English.		
XX			
CC	The present invention relates to a method for stimulating an immune		
CC	response. The method comprises administering an immunostimulatory nucleic		
CC	acid to a non-rodent subject in sufficient quantity to stimulate an		
CC	immune response. The present sequence is one such immunostimulatory		
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich		
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects		
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae		
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,		
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or		
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is		
CC	also useful for preventing cancer, asthma, infectious disease, allergy or		
CC	immune deficiency. The present sequence can also be used to redirect a		
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the		
CC	present sequence may have a phosphorothioate backbone		
XX			
SQ	Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;		
		Query Match 0.6%; Score 18; DB 1; Length 18;	
		Best Local Similarity 100.0%; Pred. No. 7.3e+02;	
		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2166	TTTTTTTTTTTTTTTTTT 2183	
Db	1	TTTTTTTTTTTTTTTTTT 18	
		RESULT 1376	
		AAF99708/c	
ID	AAF99708	standard; DNA; 18 BP.	
XX			

AC	AAF99708;		
XX			
DT	12-JUN-2001	(first entry)	
XX			
DE		Immunostimulatory nucleic acid #824.	
XX			
KW		Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;	
KW		immunostimulatory; tumour; viral infection; bacterial infection;	
KW		fungal infection; parasitic infection; cancer; asthma;	
KW		infectious disease; allergy; immune deficiency; phosphorothioate; ss.	
XX			
OS		Synthetic.	
XX			
PN	WO200122972-A2.		
XX			
PD	05-APR-2001.		
XX			
PF	25-SEP-2000;	2000WO-US026383.	
XX			
PR	25-SEP-1999;	99US-0156113P.	
PR	27-SEP-1999;	99US-0156135P.	
PR	23-AUG-2000;	2000US-0227436P.	
XX			
PA	(IOWA ) UNIV IOWA RES FOUND.		
PA	(COLE-) COLEY PHARM GMBH.		
XX			
PI	Krieg AM, Schetter C, Vollmer J;		
XX			
DR	WPI; 2001-273485/28.		
XX			
PT	Vaccinating against tumors, infectious diseases, allergies and asthma		
PT	using immunostimulatory Py-rich and TG nucleic acids.		
XX			
PS	Claim 101; Page 56; 338pp; English.		
XX			
CC	The present invention relates to a method for stimulating an immune		
CC	response. The method comprises administering an immunostimulatory nucleic		
CC	acid to a non-rodent subject in sufficient quantity to stimulate an		
CC	immune response. The present sequence is one such immunostimulatory		
CC	nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich		
CC	(py-rich) or thymidine (T) rich. The method is used to vaccinate subjects		
CC	against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae		
CC	and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,		
CC	haemophilus, campylobacter, clostridium, Escherichia coli and/or		
CC	staphylococcus), fungal antigens and/or parasitic antigens. The method is		
CC	also useful for preventing cancer, asthma, infectious disease, allergy or		
CC	immune deficiency. The present sequence can also be used to redirect a		
CC	Th2 to a Th1 immune response and to activate immune cells. Note: the		
CC	present sequence may have a phosphorothioate backbone		
XX			
SQ	Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;		
		Query Match 0.6%; Score 18; DB 1; Length 18;	
		Best Local Similarity 100.0%; Pred. No. 7.3e+02;	
		Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2166	TTTTTTTTTTTTTTTTTT 2183	
Db	1	TTTTTTTTTTTTTTTTTT 18	
		RESULT 1377	
		AAF99734	
ID	AAF99734	standard; DNA; 18 BP.	
XX			
AC	AAF99734;		
XX			
DT	12-JUN-2001	(first entry)	
XX			
DE		Immunostimulatory nucleic acid #850.	
XX			
KW		Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;	
KW		immunostimulatory; tumour; viral infection; bacterial infection;	

KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX Synthetic.  
XX WO200122972-A2.  
XX 05-APR-2001.  
XX 25-SEP-2000; 2000WO-US026383.  
XX 25-SEP-1999; 99US-0156113P.  
PR 27-SEP-1999; 99US-0156135P.  
PR 23-AUG-2000; 2000US-0227436P.  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX Krieg AM, Schetter C, Vollmer J;  
PI WPI; 2001-273485/28.  
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XX Claim 101; Page 56; 338pp; English.  
XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
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CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18  
RESULT 1378  
AAF99734/c  
ID AAF99734 standard; DNA; 18 BP.  
XX AAF99734;  
AC AAF99734;  
XX 12-JUN-2001 (first entry)  
DT Immunostimulatory nucleic acid #850.  
XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
KW immunostimulatory; tumour; viral infection; bacterial infection;  
KW fungal infection; parasitic infection; cancer; asthma;  
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
XX Synthetic.  
OS WO200122972-A2.  
XX 05-APR-2001.

XX 25-SEP-2000; 2000WO-US026383.  
XX 25-SEP-1999; 99US-0156113P.  
PR 27-SEP-1999; 99US-0156135P.  
PR 23-AUG-2000; 2000US-0227436P.  
XX (IOWA ) UNIV IOWA RES FOUND.  
PA (COLE-) COLEY PHARM GMBH.  
XX Krieg AM, Schetter C, Vollmer J;  
PI WPI; 2001-273485/28.  
XX Vaccinating against tumors, infectious diseases, allergies and asthma  
PT using immunostimulatory Py-rich and TG nucleic acids.  
XX Claim 101; Page 56; 338pp; English.  
XX The present invention relates to a method for stimulating an immune  
CC response. The method comprises administering an immunostimulatory nucleic  
CC acid to a non-rodent subject in sufficient quantity to stimulate an  
CC immune response. The present sequence is one such immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
CC also useful for preventing cancer, asthma, infectious disease, allergy or  
CC immune deficiency. The present sequence can also be used to redirect a  
CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
CC present sequence may have a phosphorothioate backbone  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2803  
Db 18 AAAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1379  
AAF82472  
ID AAF82472 standard; DNA; 18 BP.  
XX AAF82472;  
AC AAF82472;  
XX 29-JUN-2001 (first entry)  
DT Phagemid vector pCR2.1 polylinker oligonucleotide #6.  
XX Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;  
DE nephrotropic; antiinflammatory; gene therapy; cardiac disease;  
XX renal disease; inflammatory disease; polylinker; ss.  
XX Synthetic.  
OS WO200123419-A2.  
XX 05-APR-2001.  
PD 27-SEP-2000; 2000WO-US026582.  
XX 27-SEP-1999; 99US-0156277P.  
XX (SCIO-) SCIOS INC.  
PA Stanton LW, Kapoun AM;  
PI XX



DR WPI; 2001-328177/34.

XX Novel secreted factor encoded by clone P00210D09 useful for diagnosing,

PT treating and/or preventing various cardiac, renal and inflammatory

PT diseases.

XX Example 1; Page 41; 69pp; English.

XX The present sequence corresponds to polylinker DNA of the phagemid vector

CC pCR2.1. It was used in the construction of a normalised rat cDNA library,

CC which was used in an example demonstrating differential expression of a

CC rat gene referred to as clone P00210D09. The invention relates to a

CC polypeptide comprising a sequence of at least 80% identity to residues 22

CC -122 of the present sequence, or a sequence encoded by a nucleic acid

CC hybridising under stringent conditions to the complement of the coding

CC region comprising 1031 nucleotides, and having at least one biological

CC activity of the polypeptide encoded by clone P00210D09. The polypeptides

CC and polynucleotides of the invention are useful for the treatment of

CC cardiac, renal and inflammatory diseases. The polynucleotides are useful

CC in antisense mediated gene inhibition and in gene therapy. The

CC polypeptides are useful in assays for identifying lead compounds that may

CC be used as therapeutic agents in the treatment of cardiac, kidney or

CC inflammatory diseases

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

SQ

Query Match 0.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183

DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1380

AAF82472/c

ID AAF82472 standard; DNA; 18 BP.

XX

AC AAF82472;

XX

DT 29-JUN-2001 (first entry)

XX

DE Phagemid vector pCR2.1 polylinker oligonucleotide #6.

XX

XX Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiac;

KW nephrotropic; anti-inflammatory; gene therapy; cardiac disease;

KW renal disease; inflammatory disease; polylinker; ss.

XX

OS Synthetic.

XX

PN WO200123419-A2.

XX

PD 05-APR-2001.

XX

PF 27-SEP-2000; 2000WO-US026582.

XX

PR 27-SEP-1999; 99US-0156277P.

XX

PA (SCIO-) SCIOS INC.

XX

PI Stanton LW, Kapoun AM;

XX

DR WPI; 2001-328177/34.

XX

PT Novel secreted factor encoded by clone P00210D09 useful for diagnosing,

PT treating and/or preventing various cardiac, renal and inflammatory

PT diseases.

XX Example 1; Page 41; 69pp; English.

PS

XX The present sequence corresponds to polylinker DNA of the phagemid vector

CC pCR2.1. It was used in the construction of a normalised rat cDNA library,

CC which was used in an example demonstrating differential expression of a

CC rat gene referred to as clone P00210D09. The invention relates to a

CC polypeptide comprising a sequence of at least 80% identity to residues 22

CC -122 of the present sequence, or a sequence encoded by a nucleic acid

CC hybridising under stringent conditions to the complement of the coding

CC region comprising 1031 nucleotides, and having at least one biological

CC activity of the polypeptide encoded by clone P00210D09. The polypeptides

CC and polynucleotides of the invention are useful for the treatment of

CC cardiac, renal and inflammatory diseases. The polynucleotides are useful

CC in antisense mediated gene inhibition and in gene therapy. The

CC polypeptides are useful in assays for identifying lead compounds that may

CC be used as therapeutic agents in the treatment of cardiac, kidney or

CC inflammatory diseases

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

SQ

Query Match 0.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2803

DB 18 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 1381

AAS94743

ID AAS94743 standard; DNA; 18 BP.

XX

AC AAS94743;

XX

DT 12-MAR-2002 (first entry)

XX

DE Rat secreted factor DNA oligonucleotide probe #6.

XX

XX Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;

KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;

KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;

KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;

KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;

KW renal infarction; hereditary nephritis; polycystic kidney disease;

KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;

KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;

KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;

KW Alzheimer's disease; gene therapy.

XX

OS Synthetic.

XX

PN WO200174901-A2.

XX

PD 11-OCT-2001.

XX

PF 23-MAR-2001; 2001WO-US009555.

XX

PR 31-MAR-2000; 2000US-0193548P.

PR 14-MAR-2001; 2001US-00809545.

XX

PA (SCIO-) SCIOS INC.

XX

PI Stanton LW, White RT;

XX

DR WPI; 2002-010779/01.

XX

PT Novel secreted factor polypeptide useful for treating cardiac diseases

PT such as arteriosclerosis, myocardial infarction, inflammatory diseases

PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.

XX Example 1; Page 51; 189pp; English.

PS

XX The invention relates to rat secreted factor polypeptides and the

CC polynucleotides encoding them. The sequences are useful for treating

CC cardiac, renal or inflammatory diseases. These include cardiac diseases

CC such as congestive heart failure, myocarditis, dilated congestive

CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac  
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and  
CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic  
CC syndrome, renal infarction, hereditary nephritis, polycystic kidney  
CC disease, chronic renal failure, renal vein thrombosis and medullary  
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid  
CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus  
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's  
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode  
CC the secreted factor polypeptides of the invention, and oligonucleotide  
CC probes and PCR primers  
XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1382  
AAS94743/c  
ID AAS94743 standard; DNA; 18 BP.

XX AAS94743;

DT 12-MAR-2002 (first entry)

DE Rat secreted factor DNA oligonucleotide probe #6.

XX Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;  
KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;  
KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;  
KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;  
KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;  
KW renal infarction; hereditary nephritis; polycystic kidney disease;  
KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;  
KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;  
KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;  
KW Alzheimer's disease; gene therapy.

XX Synthetic.

XX WO200174901-A2.

XX 11-OCT-2001.

XX 23-MAR-2001; 2001WO-US009555.

XX 31-MAR-2000; 2000US-0193548P.

PR 14-MAR-2001; 2001US-00809545.

XX (SCIO-) SCIOS INC.

XX Stanton LW, White RT;

XX WPI; 2002-010779/01.

XX Novel secreted factor polypeptide useful for treating cardiac diseases  
PT such as arteriosclerosis, myocardial infarction, inflammatory diseases  
PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.

PS Example 1; Page 51; 189pp; English.

XX The invention relates to rat secreted factor polypeptides and the  
CC polynucleotides encoding them. The sequences are useful for treating  
CC cardiac, renal or inflammatory diseases. These include cardiac diseases  
CC such as congestive heart failure, myocarditis, dilated congestive  
CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac  
CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and

CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic  
CC syndrome, renal infarction, hereditary nephritis, polycystic kidney  
CC disease, chronic renal failure, renal vein thrombosis and medullary  
CC sponge kidney and inflammatory diseases such as asthma, rheumatoid  
CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus  
CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's  
CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode  
CC the secreted factor polypeptides of the invention, and oligonucleotide  
CC probes and PCR primers  
XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAA AAAA AAAA AAAA AAAA 2803  
Db 18 AAAA AAAA AAAA AAAA AAAA 1

RESULT 1383  
ABS78455  
ID ABS78455 standard; DNA; 18 BP.

XX ABS78455;

DT 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #939.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.

XX Synthetic.

XX WO200253141-A2.

XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.

XX 14-DEC-2000; 2000US-0255534P.

XX (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

XX WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 36; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other; 0; Indels 0; Gaps 0;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1384  
ABS78455/c  
ID ABS78455 standard; DNA; 18 BP.  
XX  
AC ABS78455;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #939.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
XX  
PI Bratzler RL;  
XX  
DR WPI; 2002-566690/60.  
XX  
PT Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.  
PS Claim 2; Page 36; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1385  
ABS78429  
ID ABS78429 standard; DNA; 18 BP.  
XX  
AC ABS78429;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #913.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophilic joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
XX  
PI Bratzler RL;  
XX  
DR WPI; 2002-566690/60.  
XX  
PT Inhibiting angiogenesis in a subject, involves administering at least one  
XX antiangiogenic nucleic acid molecule to the subject.  
PS Claim 2; Page 35; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT 18



RESULT 1386  
ABS78429/C  
ID ABS78429 standard; DNA; 18 BP.  
XX  
AC ABS78429;  
XX  
DT 13-DEC-2002 (first entry)  
XX  
DE Angiogenesis inhibitory oligonucleotide #913.  
XX  
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KW plaque neovascularisation; telangiectasia; haemophiliac joint;  
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KW scleroderma; hypertrophic scar.  
XX  
OS Synthetic.  
XX  
PN WO200253141-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 14-DEC-2001; 2001WO-US048458.  
XX  
PR 14-DEC-2000; 2000US-0255534P.  
XX  
PA (COLE-) COLEY PHARM GROUP INC.  
XX  
PI Bratzler RL;  
XX  
DR WPI; 2002-566690/60.  
XX  
PT Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.  
XX  
PS Claim 2; Page 35; 276pp; English.  
XX  
CC The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
DB 18 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 1387  
ABL39401  
ID ABL39401 standard; DNA; 18 BP.  
XX  
AC ABL39401;  
XX  
DT 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 837.  
DE  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate backbone"  
XX  
PN WO200197843-A2.  
XX  
PD 27-DEC-2001.  
XX  
PF 22-JUN-2001; 2001WO-US020154.  
XX  
PR 22-JUN-2000; 2000US-0213346P.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Weiner G, Hartmann G;  
XX  
DR WPI; 2002-154611/20.  
XX  
PT Treating or preventing cancer, such as basal cell carcinoma, comprises  
PT administering immunostimulatory nucleic acids that induce expression of  
PT cell surface antigens and antibodies to a subject having or at risk of  
PT developing cancer.  
XX  
PS Disclosure; Page 308; 312pp; English.  
XX  
CC The present invention relates to methods for treating or preventing  
CC cancer, involving administering to a subject having or at risk of  
CC developing cancer immunostimulatory nucleic acids that induce expression  
CC of cell surface antigens and antibodies. The methods are useful for  
CC treating or preventing cancer such as basal cell carcinoma, bladder  
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,  
CC breast cancer, cervical cancer, colon and rectum cancer, connective  
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The  
CC present sequence is an immunostimulatory oligonucleotide described in the  
CC exemplification of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183  
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18  
  
RESULT 1388  
ABL39401/C  
ID ABL39401 standard; DNA; 18 BP.  
XX  
AC ABL39401;  
XX  
DT 16-APR-2002 (first entry)  
XX  
DE Immunostimulatory nucleic acid SEQ ID NO: 837.  
XX  
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
KW angiogenesis; metastasis; cytostatic; ss.



XX OS Synthetic.  
XX OS  
XX PH Key Location/Qualifiers  
XX FT modified\_base 1..18  
XX FT /tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "phosphorothioate backbone"

XX WO200197843-A2.  
XX PN  
XX PD 27-DEC-2001.  
XX XX  
XX PF 22-JUN-2001; 2001WO-US020154.  
XX XX  
XX PR 22-JUN-2000; 2000US-0213346P.  
XX XX  
XX PA (IOWA ) UNIV IOWA RES FOUND.

XX PI Weiner G, Hartmann G;  
XX XX  
XX DR WPI; 2002-154611/20.

XX Treating or preventing cancer, such as basal cell carcinoma, comprises  
XX administering immunostimulatory nucleic acids that induce expression of  
XX cell surface antigens and antibodies to a subject having or at risk of  
XX developing cancer.

XX Disclosure; Page 308; 312pp; English.  
XX  
XX The present invention relates to methods for treating or preventing  
XX cancer, involving administering to a subject having or at risk of  
XX developing cancer immunostimulatory nucleic acids that induce expression  
XX of cell surface antigens and antibodies. The methods are useful for  
XX treating or preventing cancer such as basal cell carcinoma, bladder  
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,  
XX breast cancer, cervical cancer, colon and rectum cancer, connective  
XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx  
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The  
XX present sequence is an immunostimulatory oligonucleotide described in the  
XX exemplification of the invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1389  
AAD41497  
ID AAD41497 standard; DNA; 18 BP.  
XX  
XX AAD41497;  
XX  
XX 30-OCT-2002 (first entry)  
XX  
XX Oligonucleotide used for amplifying sea hare cyplasin L DNA.  
XX Apoptosis; ion channel modulator; hyperproliferative disease; tumour;  
KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;  
KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;  
KW heart disease; stroke; vascular disease; nootropic; neuroprotective;  
KW cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.  
XX  
XX Unidentified.

XX WO200231144-A2.  
XX PN  
XX OS  
XX PD 18-APR-2002.  
XX XX  
XX PF 12-OCT-2001; 2001WO-EP011837.  
XX XX  
XX PR 13-OCT-2000; 2000EP-00122466.  
XX XX  
XX PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
XX PI Butzke D, Machuy N, Rudel T, Meyer TF;  
XX XX  
XX DR WPI; 2002-537205/57.  
XX XX

XX Novel polypeptide having cytotoxic activity obtainable from Aplysia,  
XX useful for destroying tumors, for identifying novel targets for the  
XX development of anti-tumor agents, and as specific ion channel modulators.  
XX  
XX Example 5; Page 37; 87pp; English.

XX The present invention relates to novel polypeptides having cytotoxic  
XX activity obtainable from sea hare Aplysia. Sequences of the invention are  
XX useful for the manufacture of cytotoxic agents against apoptosis-  
XX resistant cells, where the agents are useful for diagnosis, prevention,  
XX treatment of disorders associated with dysfunctions of GAP-SH3 binding  
XX protein, factors for generating or detoxifying reactive oxygen species  
XX (ROS) and factors for blocking and/or by-passing of caspases. They are  
XX useful for tumour therapy. Cytotoxic proteins of the invention are useful  
XX for destroying tumours and/or selectively killing cells in tissues, for  
XX identifying novel targets for the development of pharmaceutical agents,  
XX preferably anti-tumour agents and as specific ion channel modulators,  
XX e.g., blockers or openers for therapy, diagnostic or research. They are  
XX useful for the diagnosis and therapy of hyperproliferative diseases,  
XX preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.  
XX They are also useful for development of drugs for the treatment of  
XX degenerative diseases such as Alzheimer's disease, Parkinson's disease,  
XX arteriosclerosis, heart diseases, stroke and vascular diseases. The  
XX present sequence is an oligonucleotide which is used for amplifying sea  
XX hare cyplasin L DNA. This sequence is used in the exemplification of the  
XX invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1390  
AAD41497/c  
ID AAD41497 standard; DNA; 18 BP.  
XX  
XX AAD41497;  
XX  
XX 30-OCT-2002 (first entry)  
XX  
XX Oligonucleotide used for amplifying sea hare cyplasin L DNA.  
XX Apoptosis; ion channel modulator; hyperproliferative disease; tumour;  
KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;  
KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;  
KW heart disease; stroke; vascular disease; nootropic; neuroprotective;  
KW cerebroprotective; cardiant; cytotoxic protein; cyplasin L; ss.  
XX  
XX Unidentified.

XX WO200231144-A2.

PD 18-APR-2002.  
XX  
PF 12-OCT-2001; 2001WO-EP011837.  
XX  
PR 13-OCT-2000; 2000EP-00122466.  
XX  
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
PA  
XX Butzke D, Machuy N, Rudel T, Meyer TF;  
PI  
XX WPI; 2002-537205/57.  
DR  
XX Novel polypeptide having cytotoxic activity obtainable from Aplysia,  
PT useful for destroying tumors, for identifying novel targets for the  
PT development of anti-tumor agents, and as specific ion channel modulators.  
XX  
PS Example 5; Page 37; 87pp; English.  
XX  
CC The present invention relates to novel polypeptides having cytotoxic  
CC activity obtainable from sea hare Aplysia. Sequences of the invention are  
CC useful for the manufacture of cytotoxic agents against apoptosis-  
CC resistant cells, where the agents are useful for diagnosis, prevention,  
CC treatment of disorders associated with dysfunctions of GAP-SH3 binding  
CC protein, factors for generating or detoxifying reactive oxygen species  
CC (ROS) and factors for blocking and/or by-passing of caspases. They are  
CC useful for tumour therapy. Cytotoxic proteins of the invention are useful  
CC for destroying tumours and/or selectively killing cells in tissues, for  
CC identifying novel targets for the development of pharmaceutical agents,  
CC preferably anti-tumour agents and as specific ion channel modulators,  
CC e.g., blockers or openers for therapy, diagnostic or research. They are  
CC useful for the diagnosis and therapy of hyperproliferative diseases,  
CC preferably tumours, e.g., leukaemia, carcinoma, sarcoma and melanoma.  
CC They are also useful for development of drugs for the treatment of  
CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,  
CC arteriosclerosis, heart diseases, stroke and vascular diseases. The  
CC present sequence is an oligonucleotide which is used for amplifying sea  
CC hare cytoplasmic DNA. This sequence is used in the exemplification of the  
CC invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1391  
ABS53437  
ID ABS53437 standard; DNA; 18 BP.  
XX  
AC ABS53437;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE Poly d(T) primer.  
XX  
KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer;  
KW poly d(T).  
XX  
OS Synthetic.  
XX  
PN WO200265093-A2.  
XX  
PD 22-AUG-2002.  
XX  
PF 14-FEB-2002; 2002WO-US005713.  
XX  
PR 14-FEB-2001; 2001US-0268645P.  
PR 14-FEB-2001; 2001US-0268664P.

PR 18-JUL-2001; 2001US-0306216P.  
PR 07-NOV-2001; 2001US-0344557P.  
PR 07-NOV-2001; 2001US-0348242P.  
PR 09-NOV-2001; 2001US-0350176P.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (REME-) RES FOUND MENTAL HYGIENE INC.  
XX  
PI Ginsberg SD, Che S;  
XX  
DR WPI; 2002-567050/60.  
XX  
PT Increasing efficiency of second strand cDNA synthesis using terminal  
PT continuation model before performing further RNA amplification by RNA  
PT transcription.  
XX  
PS Example 7; Page 80; 128pp; English.  
XX  
CC This invention relates to a novel method for increasing the efficiency of  
CC second strand cDNA synthesis through a mechanism of terminal  
CC continuation. In the method an RNA molecule is obtained and a first  
CC primer is added that comprises a region that hybridises to a  
CC complementary region of the molecule before a second primer is added  
CC comprising at least one riboguanine at the 3' end of the primer. A first  
CC complementary nucleic acid molecule is synthesised, the RNA molecule and  
CC second primer are removed and a second complementary nucleic acid  
CC molecule is synthesised to form a second hybrid with an extension product  
CC of the third primer bound to the first complementary molecule. The method  
CC of the invention is useful for increasing the efficiency of second strand  
CC cDNA synthesis and may be used for linear amplification of genetic  
CC signals from histologically stained tissue. The present sequence  
CC represents a poly d(T) PCR primer used in the method of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTTTT 18  
  
RESULT 1392  
ABS53437/c  
ID ABS53437 standard; DNA; 18 BP.  
XX  
AC ABS53437;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE Poly d(T) primer.  
XX  
KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer;  
KW poly d(T).  
XX  
OS Synthetic.  
XX  
PN WO200265093-A2.  
XX  
PD 22-AUG-2002.  
XX  
PF 14-FEB-2002; 2002WO-US005713.  
XX  
PR 14-FEB-2001; 2001US-0268645P.  
PR 14-FEB-2001; 2001US-0268664P.  
PR 18-JUL-2001; 2001US-0306216P.  
PR 07-NOV-2001; 2001US-0344557P.  
PR 07-NOV-2001; 2001US-0348242P.  
PR 09-NOV-2001; 2001US-0350176P.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.

PA (REME-) RES FOUND MENTAL HYGIENE INC.  
XX  
PI Ginsberg SD, Che S;  
XX  
XX WPI; 2002-567050/60.  
DR  
XX Increasing efficiency of second strand cDNA synthesis using terminal  
PT continuation model before performing further RNA amplification by RNA  
PT transcription.  
PT  
XX Example 7; Page 80; 128pp; English.  
PS  
XX This invention relates to a novel method for increasing the efficiency of  
CC second strand cDNA synthesis through a mechanism of terminal  
CC continuation. In the method an RNA molecule is obtained and a first  
CC primer is added that comprises a region that hybridises to a  
CC complementary region of the molecule before a second primer is added  
CC comprising at least one riboguanine at the 3' end of the primer. A first  
CC complementary nucleic acid molecule is synthesised, the RNA molecule and  
CC second primer are removed and a second complementary nucleic acid  
CC molecule is synthesised to form a second hybrid with an extension product  
CC of the third primer bound to the first complementary molecule. The method  
CC of the invention is useful for increasing the efficiency of second strand  
CC cDNA synthesis and may be used for linear amplification of genetic  
CC signals from histologically stained tissue. The present sequence  
CC represents a poly d(T) PCR primer used in the method of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1393  
ABA93239  
ID ABA93239 standard; DNA; 18 BP.  
XX  
AC ABA93239;  
XX  
DT 18-APR-2002 (first entry)  
XX  
DE Adaptor oligonucleotide SEQ ID NO:2.  
XX  
KW Detection; comparative detection; adaptor; ss.  
XX  
OS Synthetic.  
XX  
PN JP2001333800-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 30-MAY-2000; 2000JP-00160324.  
XX  
PR 30-MAY-2000; 2000JP-00160324.  
XX  
PA (UNIT-) UNITECH CO LTD.  
XX  
XX WPI; 2002-135950/18.  
XX  
PT Comparative detection of the amounts of RNA and DNA.  
XX  
PS Disclosure; Page 9; 9pp; Japanese.  
XX  
CC The present invention describes a method for the comparative detection of  
CC the amount of an RNA. The method comprises: (a) cDNAs obtained by  
CC transcribing respectively from at least two tissue RNAs are respectively  
CC fragmented by using a same restriction enzyme; (b) each different adaptor  
CC and a common adaptor are added to each of the cDNA fragments derived from  
CC the same or different tissues by the step (a); (c) the resultant adaptor-  
CC added cDNAs are mixed together; (d) an adaptor primer having the common  
CC sequence to said different adaptor and a gene-specific adaptor are used  
CC to amplify said adaptor-added cDNAs containing no region derived from  
CC polyadenylic acid of the mRNA before the addition of the adaptor among  
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
CC from the measured result; (g) each different adaptor and a common adaptor  
CC are added to each of the genomic DNA fragments derived from a same or

CC the same or different tissues by the step (a); (c) the resultant adaptor-  
CC added cDNAs are mixed together; (d) an adaptor primer having the common  
CC sequence to said different adaptor and a gene-specific adaptor are used  
CC to amplify said adaptor-added cDNAs containing no region derived from  
CC polyadenylic acid of the mRNA before the addition of the adaptor among  
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
CC from the measured result; (g) each different adaptor and a common adaptor  
CC are added to each of the genomic DNA fragments derived from a same or  
CC different individuals; (h) the resultant adaptor-added genomic DNAs are  
CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
CC an adaptor primer having the common sequence to the different adaptor and  
CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts  
CC of the genomic DNAs are measured between the individuals. The method is  
CC used for the detection of the amounts of RNA and DNA. The present  
CC sequence represents an oligonucleotide which is used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTT 18  
  
RESULT 1394  
ABA93239/C  
ID ABA93239 standard; DNA; 18 BP.  
XX  
AC ABA93239;  
XX  
DT 18-APR-2002 (first entry)  
XX  
DE Adaptor oligonucleotide SEQ ID NO:2.  
XX  
KW Detection; comparative detection; adaptor; ss.  
XX  
OS Synthetic.  
XX  
PN JP2001333800-A.  
XX  
PD 04-DEC-2001.  
XX  
PF 30-MAY-2000; 2000JP-00160324.  
XX  
PR 30-MAY-2000; 2000JP-00160324.  
XX  
PA (UNIT-) UNITECH CO LTD.  
XX  
XX WPI; 2002-135950/18.  
XX  
PT Comparative detection of the amounts of RNA and DNA.  
XX  
PS Disclosure; Page 9; 9pp; Japanese.  
XX  
CC The present invention describes a method for the comparative detection of  
CC the amount of an RNA. The method comprises: (a) cDNAs obtained by  
CC transcribing respectively from at least two tissue RNAs are respectively  
CC fragmented by using a same restriction enzyme; (b) each different adaptor  
CC and a common adaptor are added to each of the cDNA fragments derived from  
CC the same or different tissues by the step (a); (c) the resultant adaptor-  
CC added cDNAs are mixed together; (d) an adaptor primer having the common  
CC sequence to said different adaptor and a gene-specific adaptor are used  
CC to amplify said adaptor-added cDNAs containing no region derived from  
CC polyadenylic acid of the mRNA before the addition of the adaptor among  
CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the  
CC cDNA amounts are measured between the tissues; (f) the RNA is detected  
CC from the measured result; (g) each different adaptor and a common adaptor  
CC are added to each of the genomic DNA fragments derived from a same or

CC different individuals; (h) the resultant adaptor-added genomic DNAs are  
CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using  
CC an adaptor primer having the common sequence to the different adaptor and  
CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts  
CC of the genomic DNAs are measured between the individuals. The method is  
CC used for the detection of the amounts of RNA and DNA. The present  
CC sequence represents an oligonucleotide which is used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1395  
AAD56466  
ID AAD56466 standard; RNA; 18 BP.  
XX  
AC AAD56466;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Target RNA #1 used in the exemplification of the invention.  
XX  
KW Acyclic linker; gene expression; gene therapy; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX

PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 5; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is a target RNA, used in the exemplification of the invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 1 AAAAAAAAAAAAAAAAAA 18  
RESULT 1396  
AAD56466/C  
ID AAD56466 standard; RNA; 18 BP.  
XX  
AC AAD56466;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Target RNA #1 used in the exemplification of the invention.  
XX  
KW Acyclic linker; gene expression; gene therapy; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX

PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 5; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is a target RNA, used in the exemplification of the invention  
XX  
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTT 1

RESULT 1397  
AAD56440  
ID AAD56440 standard; DNA; 18 BP.  
XX  
AC AAD56440;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Antisense oligo #1, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.



OS Unidentified.  
XX  
XX WO2003037909-A1.  
PN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 29-OCT-2002; 2002WO-CA001628.  
PF  
XX  
XX 29-OCT-2001; 2001US-0330719P.  
PR  
XX  
XX (UYMC-) UNIV MCGILL.  
PA  
XX  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI  
XX WPI; 2003-421516/39.  
DR  
XX  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
XX Example 2; Fig 9; 104pp; English.  
PS  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT 18  
RESULT 1398  
AAD56440/c  
ID AAD56440 standard; DNA; 18 BP.  
XX  
XX AAD56440;  
AC  
XX 07-AUG-2003 (first entry)  
DT  
XX Antisense oligo #1, to elicit RNase H degradation of target RNA.  
DE  
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
XX Unidentified.  
OS  
XX WO2003037909-A1.  
PN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 29-OCT-2002; 2002WO-CA001628.  
PF  
XX  
XX 29-OCT-2001; 2001US-0330719P.  
PR  
XX  
XX (UYMC-) UNIV MCGILL.  
PA  
XX

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX WPI; 2003-421516/39.  
DR  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
XX Example 2; Fig 9; 104pp; English.  
PS  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1399  
AAD56446  
ID AAD56446 standard; DNA; 18 BP.  
XX  
XX AAD56446;  
AC  
XX 07-AUG-2003 (first entry)  
DT  
XX 2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.  
DE  
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..18  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
XX  
XX WO2003037909-A1.  
PN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 29-OCT-2002; 2002WO-CA001628.  
PF  
XX  
XX 29-OCT-2001; 2001US-0330719P.  
PR  
XX  
XX (UYMC-) UNIV MCGILL.  
PA  
XX  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI  
XX WPI; 2003-421516/39.  
DR  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX

XX Example 2; Fig 7; 104pp; English.

PS The invention relates to an acyclic linker-containing oligonucleotide

XX comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.

CC They are useful for selectively preventing gene expression in a sequence-

CC specific manner, for hybridising to complementary RNA such as cellular

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments

CC to prevent or treat a disease characterised by the expression of a

CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)

CC H degradation of target RNA. This sequence is used in the exemplification

CC of the invention

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1400

AD56446/c

ID AAD56446 standard; DNA; 18 BP.

XX

AC AAD56446;

XX

DT 07-AUG-2003 (first entry)

XX

DE 2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.

XX

KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

KW antisense; ss.

XX

OS Unidentified.

XX

XX

FH Key Location/Qualifiers

FT modified\_base 1..18

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

XX

PN WO2003037909-A1.

XX

PD 08-MAY-2003.

XX

PF 29-OCT-2002; 2002WO-CA001628.

XX

PR 29-OCT-2001; 2001US-0330719P.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX

DR WPI; 2003-421516/39.

XX

PT Novel acyclic linker-containing oligonucleotide useful for preventing or

PT decreasing translation, reverse transcription and/or replication of a

PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX

PS Example 2; Fig 7; 104pp; English.

XX

CC The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.

CC They are useful for selectively preventing gene expression in a sequence-

CC specific manner, for hybridising to complementary RNA such as cellular

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments

CC to prevent or treat a disease characterised by the expression of a

CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)

CC H degradation of target RNA. This sequence is used in the exemplification

CC of the invention

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1401

ACH03247

ID ACH03247 standard; DNA; 18 BP.

XX

AC ACH03247;

XX

DT 25-SEP-2003 (first entry)

XX

DE Immunostimulatory nucleic acid #882.

XX

KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;

KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX

OS Synthetic.

XX

PN US2003050268-A1.

XX

PD 13-MAR-2003.

XX

PF 29-MAR-2002; 2002US-00112653.

XX

PR 29-MAR-2001; 2001US-0279642P.

XX

PA (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX

PI Krieg AM, Berg DJ;

XX

DR WPI; 2003-521815/49.

XX

PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,

PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.

XX

PS Disclosure; Page 33; 229pp; English.

XX

CC The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of

CC developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as

CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or

CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 7.3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
PR 01-FEB-2002; 2002US-0352873P.
XX (UYMC-) UNIV MCGILL.
PA Damha MJ, Parniak MA;
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
PT
XX Example 2; Page 35; 73pp; English.
XX
XX The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense oligonucleotide used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. NO. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1405
AAD57878
ID AAD57878 standard; DNA; 18 BP.
XX
AC AAD57878;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .3
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 7. .9
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 13. .15
FT /*tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
```

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XX 31-JAN-2003; 2003WO-CA000129.
XX
XX 01-FEB-2002; 2002US-0352873P.
XX
XX (UYMC-) UNIV MCGILL.
XX
XX Damha MJ, Parniak MA;
XX WPI; 2003-689523/65.
XX
XX New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
PT
XX Example 2; Page 35; 73pp; English.
XX
XX The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. NO. 7.3e+02;
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
DB 1 UUUUUUUUUUUUUUUU 18

RESULT 1406
AAD57878/c
ID AAD57878 standard; DNA; 18 BP.
XX
AC AAD57878;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1. .3
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 7. .9
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT 13. .15
FT /*tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
XX
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PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-CA000129.  
XX  
PR 01-FEB-2002; 2002US-0352873P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA;  
XX  
XX WPI; 2003-689523/65.  
DR  
XX  
XX New oligonucleotide, useful for preventing or treating a disease related  
PT to a target RNA in a system, e.g., AIDS or hepatitis B.  
PT  
XX  
PS Example 2; Page 35; 73pp; English.  
XX  
CC The present invention relates to a new oligonucleoside which comprises  
CC alternating first and second segments. The first segment comprises at  
CC least one sugar modified nucleoside. The second segment comprises at  
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
CC each of the first and second segments, so that it comprises at least 4  
CC alternating segments. The oligonucleotide is useful for preparing a  
CC composition for inducing RNase H-mediated cleavage of a target RNA in a  
CC system, preventing or decreasing translation, transcription or  
CC replication of a target RNA in a system, detecting the presence of a  
CC target RNA in a system, validating a gene target corresponding to a  
CC target RNA in a system or preventing or treating a disease related to a  
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
CC or hepatitis B. The invention is useful in gene therapy. The present  
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of  
CC the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 1409  
AAD57877  
ID AAD57877 standard; DNA; 18 BP.  
XX  
AC AAD57877;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.  
XX  
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;  
KW ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 1  
FT /\*tag= a  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 3  
FT misc\_RNA  
FT /\*tag= b  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 5  
FT misc\_RNA  
FT /\*tag= c  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"

FT misc\_RNA 7  
FT /\*tag= d  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 9  
FT misc\_RNA  
FT /\*tag= e  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 11  
FT misc\_RNA  
FT /\*tag= f  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 13  
FT misc\_RNA  
FT /\*tag= g  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 15  
FT misc\_RNA  
FT /\*tag= h  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT 17  
FT misc\_RNA  
FT /\*tag= i  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
XX WO2003064441-A2.  
PN  
XX 07-AUG-2003.  
PD  
XX 31-JAN-2003; 2003WO-CA000129.  
PF  
XX 01-FEB-2002; 2002US-0352873P.  
PR  
XX (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA;  
XX  
DR WPI; 2003-689523/65.  
XX  
PT New oligonucleotide, useful for preventing or treating a disease related  
PT to a target RNA in a system, e.g., AIDS or hepatitis B.  
XX  
PS Example 2; Page 35; 73pp; English.  
XX  
CC The present invention relates to a new oligonucleoside which comprises  
CC alternating first and second segments. The first segment comprises at  
CC least one sugar modified nucleoside. The second segment comprises at  
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
CC each of the first and second segments, so that it comprises at least 4  
CC alternating segments. The oligonucleotide is useful for preparing a  
CC composition for inducing RNase H-mediated cleavage of a target RNA in a  
CC system, preventing or decreasing translation, transcription or  
CC replication of a target RNA in a system, detecting the presence of a  
CC target RNA in a system, validating a gene target corresponding to a  
CC target RNA in a system or preventing or treating a disease related to a  
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
CC or hepatitis B. The invention is useful in gene therapy. The present  
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of  
CC the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 50.0%; Pred. No. 7.3e+02;  
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 1 UTUTUTUTUTUTUTUTUT 18  
  
RESULT 1410  
AAD57877/c

ID AAD57877 standard; DNA; 18 BP.  
XX  
AC AAD57877;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.  
XX  
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;  
KW ss.  
XX  
OS Unidentified.  
XX  
PH Key  
FT misc\_RNA  
FT Location/Qualifiers  
FT 1  
FT /\*tag= a  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 3  
FT /\*tag= b  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 5  
FT /\*tag= c  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 7  
FT /\*tag= d  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 9  
FT /\*tag= e  
FT /label= RNA  
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FT 11  
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FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 13  
FT /\*tag= g  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 15  
FT /\*tag= h  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 17  
FT /\*tag= i  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
XX WO2003064441-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-CA000129.  
XX  
PR 01-FEB-2002; 2002US-0352873P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA;  
XX  
XX WPI; 2003-689523/65.  
XX  
DR New oligonucleotide, useful for preventing or treating a disease related  
XX to a target RNA in a system, e.g., AIDS or hepatitis B.  
XX  
PT Example 4; Page 38; 73pp; English.  
XX  
CC The present invention relates to a new oligonucleoside which comprises  
CC alternating first and second segments. The first segment comprises at  
CC least one sugar modified nucleoside. The second segment comprises at  
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
CC each of the first and second segments, so that it comprises at least 4  
CC alternating segments. The oligonucleoside is useful for preparing a  
CC composition for inducing RNase H-mediated cleavage of a target RNA in a  
CC system, preventing or decreasing translation, transcription or  
CC replication of a target RNA in a system, detecting the presence of a  
CC target RNA in a system, validating a gene target corresponding to a  
CC target RNA in a system or preventing or treating a disease related to a  
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
CC or hepatitis B. The invention is useful in gene therapy. The present  
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of  
CC the invention  
XX  
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred.No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1411  
AAD57890  
ID AAD57890 standard; RNA; 18 BP.  
XX  
AC AAD57890;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Target RNA #1 used in RNase H assay.  
XX  
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
KW hepatitis B; gene therapy; virucide; anti-HIV; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003064441-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-CA000129.  
XX  
PR 01-FEB-2002; 2002US-0352873P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA;  
XX  
XX WPI; 2003-689523/65.  
XX  
DR New oligonucleotide, useful for preventing or treating a disease related  
XX to a target RNA in a system, e.g., AIDS or hepatitis B.  
XX  
PT Example 4; Page 38; 73pp; English.  
XX  
CC The present invention relates to a new oligonucleoside which comprises  
CC alternating first and second segments. The first segment comprises at  
CC least one sugar modified nucleoside. The second segment comprises at  
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of  
CC each of the first and second segments, so that it comprises at least 4  
CC alternating segments. The oligonucleoside is useful for preparing a  
CC composition for inducing RNase H-mediated cleavage of a target RNA in a  
CC system, preventing or decreasing translation, transcription or  
CC replication of a target RNA in a system, detecting the presence of a  
CC target RNA in a system, validating a gene target corresponding to a  
CC target RNA in a system or preventing or treating a disease related to a  
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)  
CC or hepatitis B. The invention is useful in gene therapy. The present  
CC sequence is a target RNA used in RNase H assay. This sequence is used in

ID AAD57877 standard; DNA; 18 BP.  
XX  
AC AAD57877;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.  
XX  
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;  
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;  
KW ss.  
XX  
OS Unidentified.  
XX  
PH Key  
FT misc\_RNA  
FT Location/Qualifiers  
FT 1  
FT /\*tag= a  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 3  
FT /\*tag= b  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 5  
FT /\*tag= c  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 7  
FT /\*tag= d  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
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FT 9  
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FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
FT 11  
FT /\*tag= f  
FT /label= RNA  
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FT  
FT 13  
FT /\*tag= g  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
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FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
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FT 17  
FT /\*tag= i  
FT /label= RNA  
FT /note= "2'-O-methyl-D-uridine"  
FT  
XX WO2003064441-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 31-JAN-2003; 2003WO-CA000129.  
XX  
PR 01-FEB-2002; 2002US-0352873P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Parniak MA;  
XX  
XX WPI; 2003-689523/65.  
XX  
DR New oligonucleotide, useful for preventing or treating a disease related  
XX to a target RNA in a system, e.g., AIDS or hepatitis B.  
XX  
PT Example 2; Page 35; 73pp; English.  
XX  
CC The present invention relates to a new oligonucleoside which comprises  
CC alternating first and second segments. The first segment comprises at

```
CC the exemplification of the invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1412
AAD57890/c
ID AAD57890 standard; RNA; 18 BP.
XX
AC AAD57890;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target RNA #1 used in RNase H assay.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS Unidentified.
XX
PN WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA;
XX
DR WPI; 2003-689523/65.
XX
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 4; Page 38; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is a target RNA used in RNase H assay. This sequence is used in
CC the exemplification of the invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 18 TTTTTTTTTTTTTTTTTT 1

the exemplification of the invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 18 TTTTTTTTTTTTTTTTTT 1
```

```
RESULT 1413
ADB37210
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1414
ADB37210/c
ID ADB37210 standard; DNA; 18 BP.
XX
AC ADB37210;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
```



XX 02-FEB-2001; 2001US-00776479.  
XX 03-FEB-2000; 2000US-0179991P.  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Disclosure; Page 17; 221pp; English.  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1415  
ADB37236  
ID ADB37236 standard; DNA; 18 BP.  
XX ADB37236;  
XX 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #850.  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
XX US2003087848-A1.  
XX 08-MAY-2003.  
XX 02-FEB-2001; 2001US-00776479.  
XX 03-FEB-2000; 2000US-0179991P.  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Disclosure; Page 18; 221pp; English.  
XX The invention relates to a method of treating or preventing allergy or

CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTTTT 18  
RESULT 1416  
ADB37236/C  
ID ADB37236 standard; DNA; 18 BP.  
XX ADB37236;  
AC ADB37236;  
XX 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #850.  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
XX US2003087848-A1.  
XX 08-MAY-2003.  
XX 02-FEB-2001; 2001US-00776479.  
XX 03-FEB-2000; 2000US-0179991P.  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Disclosure; Page 18; 221pp; English.  
XX The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1417  
ADE77617

```
ID ADE77617 standard; DNA; 18 BP.
XX
AC ADE77617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
KW cystic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033012.
XX
PR 15-OCT-2001; 2001US-0329427P.
PR 15-OCT-2001; 2001US-0329428P.
PR 15-OCT-2001; 2001US-0329619P.
PR 15-OCT-2001; 2001US-0329619P.
PR 14-MAR-2002; 2002US-0364416P.
XX
PA (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI Li AX, Hashmi G, Seoul M;
XX
DR WPI; 2003-393553/37.
XX
PT Concurrent interrogation of a number of polymorphic sites, useful for
PT genetic testing, carrier screening, genetic profiling, and identity
PT testing, comprises conducting a multiplexed elongation assay using
PT probes.
XX
PS Example 9; Page 46; 143pp; English.
XX
CC This invention relates to a novel method for the concurrent interrogation
CC of a number of polymorphic sites in the presence of, and without
CC interference from, non-designated polymorphic sites. Specifically, it
CC comprises conducting a multiplexed elongation assay by applying one or
CC more temperature cycles to achieve linear amplification of the target or
CC a combination of annealing and elongation steps under temperature-
CC controlled conditions. Furthermore, this detection method uses probe
CC extension or elongation and relies on enzymatic recognition, a superior
CC technique that no longer depends on differential hybridisation. The
CC present invention describes probes and methods useful for identifying or
CC detecting polymorphisms at one or more designated sites, such that they
CC can identify mutations within the cystic fibrosis conductance
CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC genes. In addition, concurrent interrogation of a multiplicity of
CC polymorphic sites is useful for genetic testing, carrier screening,
CC genotyping or genetic profiling, and identity testing. This
CC oligonucleotide is the negative control probe used for the elongation
CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1418
```

```
ADE77617/c
ID ADE77617 standard; DNA; 18 BP.
XX
AC ADE77617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
KW cystic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US033012.
XX
PR 15-OCT-2001; 2001US-0329427P.
PR 15-OCT-2001; 2001US-0329428P.
PR 15-OCT-2001; 2001US-0329619P.
PR 15-OCT-2001; 2001US-0329619P.
PR 14-MAR-2002; 2002US-0364416P.
XX
PA (BIOA-) BIOARRAY SOLUTIONS LTD.
XX
PI Li AX, Hashmi G, Seoul M;
XX
DR WPI; 2003-393553/37.
XX
PT Concurrent interrogation of a number of polymorphic sites, useful for
PT genetic testing, carrier screening, genetic profiling, and identity
PT testing, comprises conducting a multiplexed elongation assay using
PT probes.
XX
PS Example 9; Page 46; 143pp; English.
XX
CC This invention relates to a novel method for the concurrent interrogation
CC of a number of polymorphic sites in the presence of, and without
CC interference from, non-designated polymorphic sites. Specifically, it
CC comprises conducting a multiplexed elongation assay by applying one or
CC more temperature cycles to achieve linear amplification of the target or
CC a combination of annealing and elongation steps under temperature-
CC controlled conditions. Furthermore, this detection method uses probe
CC extension or elongation and relies on enzymatic recognition, a superior
CC technique that no longer depends on differential hybridisation. The
CC present invention describes probes and methods useful for identifying or
CC detecting polymorphisms at one or more designated sites, such that they
CC can identify mutations within the cystic fibrosis conductance
CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
CC genes. In addition, concurrent interrogation of a multiplicity of
CC polymorphic sites is useful for genetic testing, carrier screening,
CC genotyping or genetic profiling, and identity testing. This
CC oligonucleotide is the negative control probe used for the elongation
CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
CC invention.
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 18 TTTTTTTTTTTTTTTTTT 1
```



```

KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAAAAA 2802
Db 18 GAAAAAAAAAAAAAAAAAAAAA 1
|||||
|||||

RESULT 1424
AAQ75557/c
ID AAQ75557 standard; DNA; 19 BP.
XX
XX AC AAQ75557;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 5; 11pp; Japanese.
XX

```



CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1425  
ABL51521  
ID ABL51521 standard; DNA; 19 BP.

AC ABL51521;

DT 01-JUL-2002 (first entry)

XX Tailing reaction related exemplary primer dA18U SEQ ID NO:2.

XX Tailing reaction; tailed primer; primer; probe; identification;  
KW detection; linear amplification scheme; chain extending enzyme;  
KW telomerase; ss.

OS Synthetic.

XX Key misc\_RNA Location/Qualifiers  
FH 19  
FT /\*tag= a

XX US2002031776-A1.

XX 14-MAR-2002.

XX 26-JUL-2001; 2001US-00917138.

XX 28-MAY-1999; 99US-0136545P.

XX 25-MAY-2000; 2000US-00580358.

XX (TULL/) TULLIS R H.  
PA (STRE/) STREIFEL J A.

XX Tullis RH, Streifel JA;

XX WPI; 2002-361176/39.

XX Identifying and detecting nucleic acids, particularly DNA hybridization  
PT probes, involves employing chain extending enzymes (e.g. telomerase) to  
PT elongate probes to render them readily detectable.

PS Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid  
CC probe, which comprises using chain extending enzymes to elongate probes.  
CC The method comprises: (a) treating the sample with a chain terminating  
CC reagent to prevent polynucleotide chain growth from the nucleic acid in  
CC the sample; (b) contacting the sample with the probe containing a  
CC terminus capable of elongation by a chain extending enzyme, where the  
CC probe hybridises to the nucleic acid in the sample; (c) contacting the  
CC sample with a chain extending enzyme and its substrates, which elongates  
CC the probe; and (d) detecting the elongated hybridised probe. Also  
CC described is a method comprising: (a) treating nucleic acid molecules or  
CC modified nucleic acids in a sample with a reagent or reagents that render

CC the nucleic acid chains unextendable by a non-template-dependent enzyme;  
CC (b) hybridising the treated molecules with a nucleic acid probe that  
CC includes an extendable terminus, under conditions where hybrids form; and  
CC (c) treating any hybrids formed with a non-template dependent chain  
CC elongating enzyme and its substrates, where any hybridised probe is  
CC extended. The method is useful for identifying and detecting nucleic  
CC acids, particularly DNA hybridisation probes. The present sequence  
CC represents a tailing reaction exemplary primer, which is used in an  
CC example from the present invention  
XX  
SQ Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred.No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1426  
ABL51521/c  
ID ABL51521 standard; DNA; 19 BP.

AC ABL51521;

DT 01-JUL-2002 (first entry)

XX Tailing reaction related exemplary primer dA18U SEQ ID NO:2.

XX Tailing reaction; tailed primer; primer; probe; identification;  
KW detection; linear amplification scheme; chain extending enzyme;  
KW telomerase; ss.

OS Synthetic.

XX Key misc\_RNA Location/Qualifiers  
FH 19  
FT /\*tag= a

XX US2002031776-A1.

XX 14-MAR-2002.

XX 26-JUL-2001; 2001US-00917138.

XX 28-MAY-1999; 99US-0136545P.

XX 25-MAY-2000; 2000US-00580358.

XX (TULL/) TULLIS R H.  
PA (STRE/) STREIFEL J A.

XX Tullis RH, Streifel JA;

XX WPI; 2002-361176/39.

XX Identifying and detecting nucleic acids, particularly DNA hybridization  
PT probes, involves employing chain extending enzymes (e.g. telomerase) to  
PT elongate probes to render them readily detectable.

PS Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid  
CC probe, which comprises using chain extending enzymes to elongate probes.  
CC The method comprises: (a) treating the sample with a chain terminating  
CC reagent to prevent polynucleotide chain growth from the nucleic acid in  
CC the sample; (b) contacting the sample with the probe containing a  
CC terminus capable of elongation by a chain extending enzyme, where the  
CC probe hybridises to the nucleic acid in the sample; (c) contacting the  
CC sample with a chain extending enzyme and its substrates, which elongates  
CC the probe; and (d) detecting the elongated hybridised probe. Also  
CC described is a method comprising: (a) treating nucleic acid molecules or  
CC described is a method comprising: (a) treating nucleic acid molecules or

CC modified nucleic acids in a sample with a reagent or reagents that render  
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;  
CC (b) hybridising the treated molecules with a nucleic acid probe that  
CC includes an extendable terminus, under conditions where hybrids form; and  
CC (c) treating any hybrids formed with a non-template dependent chain  
CC elongating enzyme and its substrates, where any hybridised probe is  
CC extended. The method is useful for identifying and detecting nucleic  
CC acids, particularly DNA hybridisation probes. The present sequence  
CC represents a tailing reaction exemplary primer, which is used in an  
CC example from the present invention  
XX  
SQ Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 1427  
ABZ75398  
ID ABZ75398 standard; DNA; 19 BP.  
XX  
AC ABZ75398;  
XX  
DT 07-MAY-2003 (first entry)  
XX  
DE Synthetic nuclease-resistant oligomeric compound #54.  
DE  
KW Nuclease resistant; ds; pharmaceutical; topical administration;  
KW transdermal patch; enzymatic degradation resistant.  
XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT modified\_base 19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phenoxazine"

XX  
PN WO2003004602-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 01-JUL-2002; 2002WO-US020934.  
XX  
PR 03-JUL-2001; 2001US-0302682P.  
PR 28-NOV-2001; 2001US-00996292.  
PR 10-DEC-2001; 2001US-00013295.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Maier MA, Prakash TP, Rajeev KG;  
XX  
DR WPI; 2003-256318/25.  
XX  
PT Nuclease-resistant oligomeric compound useful as pharmaceuticals for  
PT topical administration such as transdermal patches.

PS Disclosure; Page 234; 234pp; English.  
XX  
CC The invention relates to novel nuclease-resistant oligomeric compounds.  
CC The compounds of the invention are useful as pharmaceuticals for topical  
CC administration such as transdermal patches. The oligomeric compound is  
CC resistant to enzymatic degradation. The sequences shown in ABZ75345-  
CC ABZ75399 represent the nuclease-resistant compounds of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT 18  
  
RESULT 1428  
ABZ75398/c  
ID ABZ75398 standard; DNA; 19 BP.  
XX  
AC ABZ75398;  
XX  
DT 07-MAY-2003 (first entry)  
XX  
DE Synthetic nuclease-resistant oligomeric compound #54.  
XX  
KW Nuclease resistant; ds; pharmaceutical; topical administration;  
KW transdermal patch; enzymatic degradation resistant.  
XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT modified\_base 19  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phenoxazine"

XX  
PN WO2003004602-A2.  
XX  
PD 16-JAN-2003.  
XX  
PF 01-JUL-2002; 2002WO-US020934.  
XX  
PR 03-JUL-2001; 2001US-0302682P.  
PR 28-NOV-2001; 2001US-00996292.  
PR 10-DEC-2001; 2001US-00013295.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Manoharan M, Maier MA, Prakash TP, Rajeev KG;  
XX  
DR WPI; 2003-256318/25.  
XX  
PT Nuclease-resistant oligomeric compound useful as pharmaceuticals for  
PT topical administration such as transdermal patches.  
XX  
PS Disclosure; Page 234; 234pp; English.  
XX  
CC The invention relates to novel nuclease-resistant oligomeric compounds.  
CC The compounds of the invention are useful as pharmaceuticals for topical  
CC administration such as transdermal patches. The oligomeric compound is  
CC resistant to enzymatic degradation. The sequences shown in ABZ75345-  
CC ABZ75399 represent the nuclease-resistant compounds of the invention  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 18 AAAAAA AAAAAA AAAAAA 1

RESULT 1429  
ABZ75399  
ID ABZ75399 standard; DNA; 19 BP.  
XX  
AC ABZ75399;  
XX



XX New stem cell factor polypeptide(s) - for stimulating the growth of  
PT primitive progenitor cells, esp. for treating disorders involving blood  
PT cells.  
XX  
XX Example 3; Fig 12C; 127pp; English.  
PS  
XX AAT04915-T04922 are oligonucleotide primers and probes used for the  
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-  
CC naturally occurring SCF and C-terminally truncated polypeptides, having  
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,  
CC stimulate growth of primitive progenitors such as haematopoietic  
CC progenitor cells, neural stem cells and primordial germ stem cells. The  
CC peptides can be used in a composition for treating leucopenia, anaemia or  
CC thrombocytopenia, for enhancing engraftment of bone marrow during  
CC transplantation or for bone marrow recovery after chemotherapy or  
CC radiation-induced bone marrow aplasia or myelosuppression. They can also  
CC be used for treating neoplasia, nerve damage, infertility, intestinal  
CC damage or myeloproliferative disorders. Antibodies may be raised against  
CC the peptides for use in detection or neutralisation of SCF in serum. SCF  
CC may be useful for the treatment of AIDS and severe combined  
CC immunodeficiency (SCID) states alone or in combination with other factors  
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
DB 18 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1432  
AAT04918  
ID AAT04918 standard; cDNA; 20 BP.  
XX  
AC AAT04918;  
XX  
DT 25-MAR-2003 (revised)  
DT 15-MAY-1996 (first entry)  
XX  
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.  
XX  
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;  
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;  
KW transplant; neoplasia; myelosuppression; bone marrow; ss.  
XX  
OS Synthetic.  
XX  
PN EP676470-A1.  
XX  
PD 11-OCT-1995.  
XX  
PF 04-OCT-1990; 95EP-00105391.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
XX  
XX WPI; 1995-346090/45.  
DR  
XX New stem cell factor polypeptide(s) - for stimulating the growth of  
PT primitive progenitor cells, esp. for treating disorders involving blood  
PT cells.

XX Example 3; Fig 12C; 127pp; English.  
PS  
XX AAT04915-T04922 are oligonucleotide primers and probes used for the  
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-  
CC naturally occurring SCF and C-terminally truncated polypeptides, having  
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,  
CC stimulate growth of primitive progenitors such as haematopoietic  
CC progenitor cells, neural stem cells and primordial germ stem cells. The  
CC peptides can be used in a composition for treating leucopenia, anaemia or  
CC thrombocytopenia, for enhancing engraftment of bone marrow during  
CC transplantation or for bone marrow recovery after chemotherapy or  
CC radiation-induced bone marrow aplasia or myelosuppression. They can also  
CC be used for treating neoplasia, nerve damage, infertility, intestinal  
CC damage or myeloproliferative disorders. Antibodies may be raised against  
CC the peptides for use in detection or neutralisation of SCF in serum. SCF  
CC may be useful for the treatment of AIDS and severe combined  
CC immunodeficiency (SCID) states alone or in combination with other factors  
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
DB 1 TTTTTTTTTTTTTTTTTT 18  
RESULT 1433  
AAA13753/C  
ID AAA13753 standard; DNA; 20 BP.  
XX  
AC AAA13753;  
XX  
DT 27-JUL-2000 (first entry)  
XX  
DE Stem cell factor universal oligonucleotide 220-7.  
XX  
KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;  
KW primitive progenitor cell; haematopoietic disorder; syngeneic;  
KW allogeneic; autologous bone marrow transplant; gene therapy;  
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;  
KW cancer; ss.  
XX  
OS Synthetic.  
XX  
PN EP992579-A1.  
XX  
PD 12-APR-2000.  
XX  
PF 04-OCT-1990; 99EP-00122861.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
PR 04-OCT-1990; 90US-00310899.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;  
XX  
XX WPI; 2000-259135/23.  
DR  
XX Production of hematopoietic cells suitable for administration to a  
PT subject using progenitor cells and expanding the cells using stem cell  
PT factor.  
XX  
PS Example 3; Fig 12C; 123pp; English.



XX CC A method has been developed of making haematopoietic cells suitable for  
CC administration to a subject. The method comprises: (a) obtaining  
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells  
CC by adding to the cells a haematopoietically effective dose of a  
CC polypeptide product having at least part of the primary structural  
CC confirmation and one or more of the biological properties of naturally  
CC occurring stem cell factor (SCF). The method is useful for stimulating  
CC primitive progenitor cells including early haematopoietic progenitor  
CC cells which are capable of maturing to erythroid, megakaryocyte,  
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute  
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.  
CC SCF is useful for treating haematopoietic disorders. The method is useful  
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic  
CC or autologous bone marrow transplant. SCF is useful for enhancing the  
CC efficiency of gene therapy based on transfecting haematopoietic stem  
CC cells. SCF is also useful for combating the myelosuppressive effects of  
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery  
CC after acute blood loss and as a boost to the immune system for fighting  
CC neoplasia (cancer). The present sequence represents a universal  
CC oligonucleotide which is used in an example from the present invention  
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 2786 ANAAAAA 2803  
Db 18 ANAAAAA 1

RESULT 1434  
AAH13754  
ID AAH13754 standard; DNA; 20 BP.

XX AC AAH13754;

XX DT 27-JUL-2000 (first entry)

XX DE Stem cell factor universal oligonucleotide 220-11.

XX KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;  
KW primitive progenitor cell; haematopoietic disorder; syngeneic;  
KW allogeneic; autologous bone marrow transplant; gene therapy;  
KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;  
KW cancer; ss.

XX OS Synthetic.

XX PN EP992579-A1.

XX PD 12-APR-2000.

XX PF 04-OCT-1990; 99EP-00122861.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 28-SEP-1990; 90WO-US005548.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 04-OCT-1990; 90EP-00310899.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX DR WPI; 2000-259135/23.

XX PT Production of hematopoietic cells suitable for administration to a  
PT subject using progenitor cells and expanding the cells using stem cell  
PT factor.

XX PS Example 3; Fig 12C; 123pp; English.

XX CC A method has been developed of making haematopoietic cells suitable for  
CC administration to a subject. The method comprises: (a) obtaining  
CC haematopoietic progenitor cells from a donor; and (b) expanding the cells  
CC by adding to the cells a haematopoietically effective dose of a  
CC polypeptide product having at least part of the primary structural  
CC confirmation and one or more of the biological properties of naturally  
CC occurring stem cell factor (SCF). The method is useful for stimulating  
CC primitive progenitor cells including early haematopoietic progenitor  
CC cells which are capable of maturing to erythroid, megakaryocyte,  
CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute  
CC increases in haematopoietic cells of both myeloid and lymphoid lineages.  
CC SCF is useful for treating haematopoietic disorders. The method is useful  
CC for expanding early haematopoietic progenitors in syngeneic, allogeneic  
CC or autologous bone marrow transplant. SCF is useful for enhancing the  
CC efficiency of gene therapy based on transfecting haematopoietic stem  
CC cells. SCF is also useful for combating the myelosuppressive effects of  
CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery  
CC after acute blood loss and as a boost to the immune system for fighting  
CC neoplasia (cancer). The present sequence represents a universal  
CC oligonucleotide which is used in an example from the present invention  
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 2166 TTTT 2183  
Db 1 TTTT 18

RESULT 1435  
AAH41332/c  
ID AAH41332 standard; DNA; 20 BP.

XX AC AAH41332;

XX DT 21-AUG-2001 (first entry)

XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.  
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;  
KW gene therapy; PCR primer; mutagenesis; probe; ss.

XX OS Synthetic.

XX PN US6207454-B1.

XX PD 27-MAR-2001.

XX PF 31-DEC-1998; 98US-00224681.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 25-NOV-1992; 92US-00982255.

XX PR 21-DEC-1993; 93US-00172329.

XX PR 24-MAY-1995; 95US-00449653.

XX PR 12-JAN-1998; 98US-00005893.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX DR WPI; 2001-366062/38.

XX PT Enhancing efficiency of transfer of polynucleotide into a target  
PT mammalian cell in vitro, involves exposing cell that expresses a stem

PT cell factor receptor to stem cell factor, and introducing polynucleotide  
PT into cell in vitro.  
XX  
PS Example 3; Fig 12C; 210pp; English.  
XX  
CC The present invention describes a method for enhancing (E) the efficiency  
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in  
CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)  
CC receptor to a biologically active SCF, its analogue or fragment, which  
CC induces cell proliferation, and introducing (I) to (II) in vitro.  
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.  
CC The method is useful for enhancing the efficiency of the transfer of a  
CC polynucleotide into a target mammalian cell in vitro. The method is  
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to  
CC AAB98390 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1436  
AAH41333  
ID AAH41333 standard; DNA; 20 BP.  
XX  
AC AAH41333;  
XX  
DT 21-AUG-2001 (first entry)  
XX  
DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.  
XX  
KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;  
KW gene therapy; PCR primer; mutagenesis; probe; ss.  
XX  
OS Synthetic.  
XX  
PN US6207454-B1.  
XX  
PD 27-MAR-2001.  
XX  
PF 31-DEC-1998; 98US-00224681.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 25-NOV-1992; 92US-00982255.  
PR 21-DEC-1993; 93US-00172329.  
PR 24-MAY-1995; 95US-00449653.  
PR 12-JAN-1998; 98US-00005893.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX  
DR WPI; 2001-366062/38.  
XX  
PT Enhancing efficiency of transfer of polynucleotide into a target  
PT mammalian cell in vitro, involves exposing cell that expresses a stem  
PT cell factor receptor to stem cell factor, and introducing polynucleotide  
PT into cell in vitro.  
XX  
PS Example 3; Fig 12C; 210pp; English.  
XX  
CC The present invention describes a method for enhancing (E) the efficiency  
CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in

CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)  
CC receptor to a biologically active SCF, its analogue or fragment, which  
CC induces cell proliferation, and introducing (I) to (II) in vitro.  
CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.  
CC The method is useful for enhancing the efficiency of the transfer of a  
CC polynucleotide into a target mammalian cell in vitro. The method is  
CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to  
CC AAB98390 represent sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTTTT 18  
RESULT 1437  
AAS04112/C  
ID AAS04112 standard; DNA; 20 BP.  
XX  
AC AAS04112;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.  
XX  
KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6207417-B1.  
XX  
PD 27-MAR-2001.  
XX  
PF 07-JUN-1995; 95US-00482918.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 21-DEC-1993; 93US-00172329.  
XX  
PA (ZSEB/) ZSEBO K M.  
PA (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX  
DR WPI; 2001-298941/31.  
XX  
PT Novel nucleic acids encoding stem cell factor useful for treating  
PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's  
PT disease, Kala azar, anemia and septicemia.  
XX  
PS Example 3; Fig 12C; 209pp; English.  
XX  
CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal  
CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
CC polynucleotides encoding them. SCF stimulate primitive progenitor cells  
CC including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.

CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
CC disorders such as piebaldism and vitiligo  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1438  
AAS04113  
ID AAS04113 standard; DNA; 20 BP.

XX AAS04113;

XX 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.

XX Homo sapiens.

XX US6207417-B1.

XX 27-MAR-2001.

XX 07-JUN-1995; 95US-00482918.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 21-DEC-1993; 93US-00172329.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-298941/31.

XX Novel nucleic acids encoding stem cell factor useful for treating

XX disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's

XX disease, Kala azar, anemia and septicemia.

XX Example 3; Fig 12C; 209pp; English.

XX The present sequence for universal PCR primer 220-11 is 1 of 8 universal  
XX oligonucleotides (AAS04110-AAS04117) used in the isolation of the human  
XX SCF (stem cell factor) cDNA sequence. The present invention relates to  
XX novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the  
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells  
XX including early haematopoietic progenitor cells. The invention also  
XX describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides  
XX (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.

CC The polynucleotide encoding SCF is useful for producing SCF and useful in

CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
CC disorders such as piebaldism and vitiligo  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1439  
AAF89092/c  
ID AAF89092 standard; DNA; 20 BP.

XX AAF89092;

XX 13-JUL-2001 (first entry)

DE Mammalian stem cell factor PCR primer SEQ ID NO: 33.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
KW severe combined immunodeficiency; PCR primer; ss.

XX Mammalia.

XX US6207802-B1.

XX 27-MAR-2001.

XX 09-NOV-1994; 94US-00336728.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide

XX stimulating growth of early hematopoietic progenitor cells, useful for

XX treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,

XX sarcoidosis.

XX Example 3; Fig 12C; 209pp; English.

XX The present invention provides the protein and coding sequences of  
XX mammalian stem cell factors (SCFs). These are capable of stimulating the  
XX growth of early haematopoietic progenitor cells, neural stem cells and  
XX primordial germ stem cells. The sequences are useful in the treatment of  
XX leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
XX nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
XX and intestinal damage, infertility, AIDS and severe combined  
XX immunodeficiency (SCID). The present sequence is primer used to amplify  
XX an SCF in the exemplification of the invention

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1440

AAF89093  
ID AAF89093 standard; DNA; 20 BP.

AC AAF89093;

DT 13-JUL-2001 (first entry)

DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
KW severe combined immunodeficiency; PCR primer; ss.

XX Mammalia.

XX US6207802-B1.

XX 27-MAR-2001.

XX 09-NOV-1994; 94US-00336728.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 01-OCT-1990; 90US-00589701.

XX 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide  
PT stimulating growth of early hematopoietic progenitor cells, useful for  
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,  
PT sarcoidosis.

XX Example 3; Fig 12C; 209pp; English.

XX The present invention provides the protein and coding sequences of  
CC mammalian stem cell factors (SCFs). These are capable of stimulating the  
CC growth of early haematopoietic progenitor cells, neural stem cells and  
CC primordial germ stem cells. The sequences are useful in the treatment of  
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
CC and intestinal damage, infertility, AIDS and severe combined  
CC immunodeficiency (SCID). The present sequence is primer used to amplify  
CC an SCF in the exemplification of the invention

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1441

AAS05714  
ID AAS05714 standard; DNA; 20 BP.  
XX  
AC AAS05714;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Aminopurine substituted region of an RP-TFO.  
XX  
XX reverse phase triplex forming oligonucleotide; RP-TFO;  
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;  
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FT modified\_base 1 /tag= a  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 3  
FT /tag= b  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 5  
FT /tag= c  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT Modified\_base 7  
FT /tag= d  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 9  
FT /tag= f  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 11  
FT /tag= g  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 13  
FT /tag= g  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 15  
FT /tag= h  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 16  
FT /tag= i  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 17  
FT /tag= j  
FT /label= OTHER  
FT /note= "Other= Hypoxanthine or Inosine"  
FT modified\_base 18  
FT /tag= k  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"  
FT modified\_base 20  
FT /tag= l  
FT /label= OTHER  
FT /note= "A is aminopurine substituted"

WO200132929-A1.

10-MAY-2001.

03-NOV-2000; 2000WO-US030534.

03-NOV-1999; 99US-0163356P.

03-NOV-1999; 99US-0163416P.



```
PR 21-DEC-1999; 99US-0171348P.
XX 07-JUL-2000; 2000US-0216579P.
XX
PA (CYGE-) CYGENE INC.
PA (OSTE/) OSTE C C.
XX
PI Oste CC, Ramberg ER;
XX
XX WPI; 2001-343488/36.
DR
XX
XX Analyzing target nucleic acid sequences, useful for population genetics,
PT drug development and diagnosing cancer, comprises hybridizing triple
PT forming oligonucleotide and probe to target sequence.
XX
XX Example 2; Page 66; 141pp; English.
XX
XX The sequence is a second reverse phase triplex forming oligonucleotide,
CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC method of the invention. The invention relates to analysing target
CC nucleic acid sequences comprising restricting isolated DNA, hybridising
CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',
CC exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC structure, hybridising the captured structure with a single nucleotide
CC polymorphisms (SNP) identification probe and determining the SNP score.
CC The methods can be used for analysing target nucleic acid sequences,
CC especially genomic DNA sequences, to determine if they contain SNPs or
CC short tandem repeats (STRs). The methods can be used to detect SNPs for
CC use in population genetics, drug development, forensics, cancer, genetic
CC disease research, genomic analysis, diagnostics and therapeutics in
CC humans, plants and animals
XX
XX Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 1 AAAAAAAAAAAAAAAAAA 19
RESULT 1442
AAS05715/C
ID AAS05715 standard; DNA; 20 BP.
XX
XX AAS05715;
XX
DT 07-SEP-2001 (first entry)
XX
DE 8-aminopurine substituted region of an RP-TFO.
XX
XX reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 17
FT /*tag= a
FT /label= OTHER
FT /note= "Other= Hypoxanthine or Inosine"
XX
XX WO200132929-A1.
XX
XX 10-MAY-2001.
PD
XX
XX 03-NOV-2000; 2000WO-US030534.
PF
XX
XX 03-NOV-1999; 99US-0163356P.
PR
XX 03-NOV-1999; 99US-0163416P.
PR
XX 21-DEC-1999; 99US-0171348P.
PR
```

```
PR 07-JUL-2000; 2000US-0216579P.
XX (CYGE-) CYGENE INC.
PA (OSTE/) OSTE C C.
XX
PI Oste CC, Ramberg ER;
XX
XX WPI; 2001-343488/36.
DR
XX
XX Analyzing target nucleic acid sequences, useful for population genetics,
PT drug development and diagnosing cancer, comprises hybridizing triple
PT forming oligonucleotide and probe to target sequence.
XX
XX Example 2; Page 66; 141pp; English.
XX
XX The sequence is a second reverse phase triplex forming oligonucleotide,
CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
CC method of the invention. The invention relates to analysing target
CC nucleic acid sequences comprising restricting isolated DNA, hybridising
CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',
CC exonuclease to form a protected nucleic acid sequence (PNAS) tail
CC structure, hybridising the captured structure with a single nucleotide
CC polymorphisms (SNP) identification probe and determining the SNP score.
CC The methods can be used for analysing target nucleic acid sequences,
CC especially genomic DNA sequences, to determine if they contain SNPs or
CC short tandem repeats (STRs). The methods can be used to detect SNPs for
CC use in population genetics, drug development, forensics, cancer, genetic
CC disease research, genomic analysis, diagnostics and therapeutics in
CC humans, plants and animals
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;
SQ
Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2804
DB 20 AAAAAAAAAAAAAAAAAA 2
RESULT 1443
AAH23891
ID AAH23891 standard; DNA; 20 BP.
XX
XX AAH23891;
XX
DT 07-AUG-2001 (first entry)
XX
DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
KW PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6204363-B1.
XX
XX 20-MAR-2001.
XX
XX 25-NOV-1992; 92US-00982255.
XX
XX 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 10-APR-1991; 91US-00684535.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI
```



PS Example 3; Fig 12C; 167pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal

CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human

CC SCF (stem cell factor) cDNA sequence. The present invention relates to

CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)

CC and the polynucleotides encoding them. SCF stimulate primitive progenitor

CC cells including early haematopoietic progenitor cells. The invention also

CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides

CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.

CC The polynucleotide encoding SCF is useful for producing SCF and useful in

CC gene therapy. It is useful for treating disorders involving blood cells

CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple

CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,

CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,

CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12

CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation

CC disorders such as piebaldism and vitiligo

XX

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1446

AAS04214

ID AAS04214 standard; DNA; 20 BP.

XX

AC AAS04214;

XX

DT 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.

XX

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;

KW PCR primer; ss.

XX

OS Homo sapiens.

XX

XX US6218148-B1.

PN

XX

PD 17-APR-2001.

XX

PF 21-DEC-1993; 93US-00172329.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

XX

XX (AMGE-) AMGEN INC.

PA

XX

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI

XX

XX WPI; 2001-281051/29.

DR

XX

XX Isolated DNA sequence, encoding polypeptide product useful for

PT stimulating growth of early hematopoietic progenitor cells.

PT

XX

XX Example 3; Fig 12C; 167pp; English.

PS

XX

XX The present sequence for universal PCR primer 220-11 is 1 of 8 universal

CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human

CC SCF (stem cell factor) cDNA sequence. The present invention relates to

CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)

CC and the polynucleotides encoding them. SCF stimulate primitive progenitor

CC cells including early haematopoietic progenitor cells. The invention also

CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides

CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.

CC The polynucleotide encoding SCF is useful for producing SCF and useful in

CC gene therapy. It is useful for treating disorders involving blood cells

CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple

CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,

CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,

CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12

CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation

CC disorders such as piebaldism and vitiligo

XX

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1447

AAS10449

ID AAS10449 standard; DNA; 20 BP.

XX

AC AAS10449;

XX

DT 24-OCT-2001 (first entry)

DE Human stem cell factor (SCF) cDNA universal PCR primer 220-11.

XX

XX Human; stem cell factor; SCF; haematopoietic progenitor cell;

KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;

KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

XX

OS Homo sapiens.

XX

XX US6248319-B1.

PN

XX

PD 19-JUN-2001.

XX

PF 24-MAY-1995; 95US-00449653.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

XX

XX (ZSEB/) ZSEBO K M.

PA

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI

XX

XX WPI; 2001-407312/43.

DR

XX

XX Increasing the number of early hematopoietic progenitor cells in the

PT peripheral blood useful for the treatment of blood disorders including

PT Hodgkin's disease comprises the administration of human stem cell factor.

XX

XX Example 3; Fig 12C; 210pp; English.

PS

XX

XX The present sequence for universal PCR primer 220-11 is 1 of 19 PCR

CC primers (AAS10435-AAS10453) used to amplify various portions of the human

CC SCF cDNA sequence. The sequence is described in an invention relating to

CC novel stem cell factors, the polynucleotides encoding them and methods  
CC for producing the stem cell factors. The methods involve increasing the  
CC number of early haematopoietic progenitor cells in human peripheral blood  
CC by administering a haematopoietically effective human stem cell factor  
CC polypeptide. The methods are useful for the treatment of blood disorders,  
CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic  
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,  
CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation  
CC disorders i.e. piebaldism and viral induced disorders, including AIDS  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1448  
AAS10448/C  
ID AAS10448 standard; DNA; 20 BP.

XX AAS10448;

XX 24-OCT-2001 (first entry)

DE Human stem cell factor (SCF) cDNA universal PCR primer 220-7.

XX Human; stem cell factor; SCF; haematopoietic progenitor cell;  
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.

XX Homo sapiens.

PN US6248319-B1.

PD 19-JUN-2001.

XX 24-MAY-1995; 95US-00449653.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI WPI; 2001-407312/43.

DR Increasing the number of early hematopoietic progenitor cells in the  
XX peripheral blood useful for the treatment of blood disorders including  
XX Hodgkin's disease comprises the administration of human stem cell factor.  
PS Example 3; Fig 12C; 210pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 19 PCR  
CC primers (AAS10435-AAS10453) used to amplify various portions of the human  
CC SCF cDNA sequence. The sequence is described in an invention relating to  
CC novel stem cell factors, the polynucleotides encoding them and methods  
CC for producing the stem cell factors. The methods involve increasing the  
CC number of early haematopoietic progenitor cells in human peripheral blood

CC by administering a haematopoietically effective human stem cell factor  
CC polypeptide. The methods are useful for the treatment of blood disorders,  
CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic  
CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,  
CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,  
CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation  
CC disorders i.e. piebaldism and viral induced disorders, including AIDS  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 18 AAAAAA AAAAAA AAAAAA 1

RESULT 1449  
AAD35465/C  
ID AAD35465 standard; DNA; 20 BP.

XX AAD35465;

XX 25-JUL-2002 (first entry)

DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.

XX Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;  
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;  
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;  
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcooidosis;  
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;  
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;  
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;  
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;  
KW acquired immune deficiency syndrome; malaria; military tuberculosis;  
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;  
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;  
KW primer; ss.

XX Rattus sp.

OS US2002018763-A1.

XX 14-FEB-2002.

XX 12-JAN-1998; 98US-00005243.

XX 24-MAY-1995; 95US-00449653.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI WPI; 2002-350789/38.

DR Novel non-naturally-occurring stem cell factor polypeptide, useful for  
XX treating leucopenia, thrombocytopenia, anemia and for enhancing  
XX engraftment of bone marrow during transplantation in a mammal.  
PS Example 3; Fig 12C; 217pp; English.

XX The present invention relates to novel non-naturally-occurring stem cell  
CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
CC duplicative of that of naturally-occurring SCF to allow possession of  
CC haematopoietic biological activity of naturally occurring SCF. Sequences  
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,  
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,





PR 04-OCT-1990; 90EP-00310899.  
PR 04-OCT-1990; 95EP-00105391.  
PA (AMGE-) AMGEN INC.  
XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
PI WPI; 2002-684093/74.  
DR Production of a human stem cell factor (SCF) polypeptide for treating  
XX disorders involving blood cells, such as leukemia, comprises culturing  
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
PT encoding the human SCF.  
XX Example 3; Fig 12C; 120pp; English.  
PS The present invention relates to novel stem cell factors (SCFs),  
XX polynucleotide sequences encoding the SCFs, and methods of producing  
CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
CC mammals, particularly humans. The method of the invention is useful for  
CC the production of human SCF. The stem cell factors are useful to treat  
CC disorders involving blood cells e.g. metastatic carcinoma, acute  
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
CC disease, malaria, and vitiligo. The present sequence representing a  
CC universal oligonucleotide for SCF DNA is used in the examples of the  
XX present invention  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1452  
ABS73850  
ID ABS73850 standard; DNA; 20 BP.  
XX  
AC ABS73850;  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE SCF universal oligonucleotide 220-11.  
XX  
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;  
KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
KW disseminated fungus disease; haematopoietic; tuberculostatic;  
KW antianaemic; antifungal; antimalarial; dermatological; ss.  
XX  
OS Synthetic.  
XX  
FN EP1241258-A2.  
XX  
PD 18-SEP-2002.  
XX  
PF 04-OCT-1990; 2002EP-00008587.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
PR 04-OCT-1990; 90EP-00310899.  
PR 04-OCT-1990; 95EP-00105391.  
XX  
PA (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
XX WPI; 2002-684093/74.  
DR Production of a human stem cell factor (SCF) polypeptide for treating  
XX disorders involving blood cells, such as leukemia, comprises culturing  
PT mammalian cells comprising non-human SCF promoter DNA linked to DNA  
PT encoding the human SCF.  
XX Example 3; Fig 12C; 120pp; English.  
PS The present invention relates to novel stem cell factors (SCFs),  
XX polynucleotide sequences encoding the SCFs, and methods of producing  
CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
CC mammals, particularly humans. The method of the invention is useful for  
CC the production of human SCF. The stem cell factors are useful to treat  
CC disorders involving blood cells e.g. metastatic carcinoma, acute  
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
CC disease, malaria, and vitiligo. The present sequence representing a  
CC universal oligonucleotide for SCF DNA is used in the examples of the  
XX present invention  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTTTT 18  
RESULT 1453  
ABZ89678  
ID ABZ89678 standard; DNA; 20 BP.  
XX  
AC ABZ89678;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX lung inflammation; respiratory disease; ds.  
OS Homo sapiens.  
XX  
FN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4920; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1454

ABZ89677

ID ABZ89677 standard; DNA; 20 BP.

XX AC ABZ89677;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX DR

XX PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4919; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1455

ABZ89240

ID ABZ89240 standard; DNA; 20 BP.

XX AC ABZ89240;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX DR

XX PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.



XX PS Disclosure; SEQ ID NO 4482; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 18 A; 1 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 3 AAAAAAAAAAAAAAAAAA 20

RESULT 1456

ADE52462

ID ADE52462 standard; DNA; 20 BP.

XX AC ADE52462;

XX DT 29-JAN-2004 (first entry)

XX DE Stem cell factor (SCF) related DNA #33.

XX KW Stem cell factor; SCF; haematopoietic activity; infertility;

XX KW intestinal damage; myeloproliferative disorder; leucopenia;

XX KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

XX KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

XX KW miliary tuberculosis; haematopoietic progenitor cell; ss.

XX OS Synthetic.

XX PN US2002031491-A1.

XX PD 14-MAR-2002.

XX PF 31-DEC-1998; 98US-00224683.

XX PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2003-851459/79.

DR New non-natural stem cell factor, useful for treating e.g. leucopenia or

XX immune deficiency, also related nucleic acid and antibodies.

PT Disclosure; SEQ ID NO 34; 217pp; English.

XX CC The invention relates to stem cell factor (SCF) polypeptides with

CC haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1457

ADE52461/C

ID ADE52461 standard; DNA; 20 BP.

XX AC ADE52461;

XX DT 29-JAN-2004 (first entry)

XX DE Stem cell factor (SCF) related DNA #32.

XX KW Stem cell factor; SCF; haematopoietic activity; infertility;

XX KW intestinal damage; myeloproliferative disorder; leucopenia;

XX KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

XX KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

XX KW miliary tuberculosis; haematopoietic progenitor cell; ss.

XX OS Synthetic.

XX PN US2002031491-A1.

XX PD 14-MAR-2002.

XX PF 31-DEC-1998; 98US-00224683.

XX PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.

PA



PA (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
DR WPI; 2003-851459/79.  
XX New non-natural stem cell factor, useful for treating e.g. leucopenia or  
PT immune deficiency, also related nucleic acid and antibodies.  
XX Disclosure; SEQ ID NO 33; 217pp; English.  
PS The invention relates to stem cell factor (SCF) polypeptides with  
XX haematopoietic activity and the polynucleotides encoding them. The  
CC polypeptides are used for treating infertility, intestinal damage,  
CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,  
CC for improving engraftment of bone marrow transplants, for enhancing bone  
CC marrow recovery after radiotherapy or chemotherapy and in treatment of  
CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic  
CC carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are  
CC also used to expand haematopoietic progenitor cells for transplantation  
CC and to prepare such cells for recombination with a gene. The SCF  
CC polynucleotides can be used for recombinant expression of the  
CC polypeptides and also as probes for mapping of the SCF gene, for  
CC identifying SCF-related diseases and as a marker for neighbouring genes.  
CC Antibodies raised against the polypeptides are useful in diagnosis and to  
CC remove SCF from blood. This sequence represents SCF related DNA of the  
CC invention.  
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 1458  
AAQ75588  
ID AAQ75588 standard; DNA; 20 BP.  
XX AC AAQ75588;  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN 01-NOV-1994.  
PD 16-APR-1993; 93JP-00112515.  
PF 16-APR-1993; 93JP-00112515.  
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 5; 11pp; Japanese.  
KW Analysis of cDNA and gene expression - by amplification of mRNA followed  
KW by digestion with restriction enzymes.  
XX Disclosure; Page 5; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 18  
RESULT 1459  
AAQ75601/C  
ID AAQ75601 standard; DNA; 20 BP.  
XX AC AAQ75601;  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN 01-NOV-1994.  
PD 16-APR-1993; 93JP-00112515.  
PF 16-APR-1993; 93JP-00112515.  
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 5; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
RESULT 1460

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 18  
RESULT 1459  
AAQ75601/C  
ID AAQ75601 standard; DNA; 20 BP.  
XX AC AAQ75601;  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN 01-NOV-1994.  
PD 16-APR-1993; 93JP-00112515.  
PF 16-APR-1993; 93JP-00112515.  
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 5; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
RESULT 1460

AAQ75591/c  
ID AAQ75591 standard; DNA; 20 BP.  
XX  
AC AAQ75591;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db |||||  
18 GAAAAAAAAAAAAAAAAA 1  
XX  
RESULT 1461  
AAQ75605/c  
ID AAQ75605 standard; DNA; 20 BP.  
XX  
AC AAQ75605;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
WPI; 1995-018287/03.  
Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.  
Disclosure; Page 5; 11pp; Japanese.  
A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily  
Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db |||||  
18 GAAAAAAAAAAAAAAAAA 1  
XX  
RESULT 1462  
AAQ75575  
ID AAQ75575 standard; DNA; 20 BP.  
XX  
AC AAQ75575;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
XX



CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1466  
AAQ75583

ID AAQ75583 standard; DNA; 20 BP.

AC AAQ75583;

DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

JP06303997-A.

01-NOV-1994.

16-APR-1993; 93JP-00112515.

16-APR-1993; 93JP-00112515.

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

Disclosure; Page 5; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2170 TTTTITTTTTTTTTTTT 2187  
|||||  
Db 1 TTTTITTTTTTTTTTTT 18

RESULT 1467  
AAQ75606/c

ID AAQ75606 standard; DNA; 20 BP.

AC AAQ75606;

DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

JP06303997-A.

01-NOV-1994.

16-APR-1993; 93JP-00112515.

16-APR-1993; 93JP-00112515.

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

Disclosure; Page 5; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1468  
AAQ75603/c

ID AAQ75603 standard; DNA; 20 BP.

AC AAQ75603;

DT 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

JP06303997-A.

01-NOV-1994.

16-APR-1993; 93JP-00112515.

16-APR-1993; 93JP-00112515.



PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1  
  
RESULT 1469  
AAQ75576  
ID AAQ75576 standard; DNA; 20 BP.  
XX  
AC AAQ75576;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2170 TTTTTT TTTTTTTT 2187  
Db 1 TTTTTT TTTTTTTT 18  
  
RESULT 1471  
AAQ75587  
ID AAQ75587 standard; DNA; 20 BP.  
XX  
AC AAQ75587;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2170 TTTTTT TTTTTTTT 2187  
Db 1 TTTTTT TTTTTTTT 18  
  
RESULT 1471  
AAQ75599/c  
ID AAQ75599 standard; DNA; 20 BP.  
XX  
AC AAQ75599;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX

PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1  
  
RESULT 1469  
AAQ75576  
ID AAQ75576 standard; DNA; 20 BP.  
XX  
AC AAQ75576;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1  
  
RESULT 1469  
AAQ75576  
ID AAQ75576 standard; DNA; 20 BP.  
XX  
AC AAQ75576;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;

OS Synthetic.  
 XX JP06303997-A.  
 PN 01-NOV-1994.  
 XX 16-APR-1993; 93JP-00112515.  
 PF 16-APR-1993; 93JP-00112515.  
 XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
 PA WPI; 1995-018287/03.  
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
 PT by digestion with restriction enzymes.  
 XX Disclosure; Page 5; 11pp; Japanese.  
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
 CC and using the aggregate of mRNAs as the template for each reverse  
 CC transcription primer; (b) digesting each of the prepared aggregates of  
 CC the double-stranded cDNAs with restriction enzyme and; (c)  
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
 CC method can be used to analyse gene expression rapidly and easily  
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2785 GAAAAA AAAAAA AAAAAA 2802  
 Db 18 GAAAAA AAAAAA AAAAAA 1  
 RESULT 1472  
 AAT04917  
 ID AAT04917 standard; cDNA; 20 BP.  
 XX AAT04917;  
 AC AAT04917;  
 XX 25-MAR-2003 (revised)  
 DT 15-MAY-1996 (first entry)  
 XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.  
 DE Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;  
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;  
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.  
 XX Synthetic.  
 OS EP676470-A1.  
 XX 11-OCT-1995.  
 PD 04-OCT-1990; 95EP-00105391.  
 XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 28-SEP-1990; 90WO-US005548.  
 PR 01-OCT-1990; 90US-00589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
 XX WPI; 1995-346090/45.  
 PI New stem cell factor polypeptide(s) - for stimulating the growth of  
 XX primitive progenitor cells, esp. for treating disorders involving blood  
 DR cells.

XX New stem cell factor polypeptide(s) - for stimulating the growth of  
 PT primitive progenitor cells, esp. for treating disorders involving blood  
 PT cells.  
 XX Example 3; Fig 12C; 127pp; English.  
 PS AAT04915-T04922 are oligonucleotide primers and probes used for the  
 XX amplification and sequencing of mammalian stem cell factor (SCF). Non-  
 CC naturally occurring SCF and C-terminally truncated polypeptides, having  
 CC amino acid sequences sufficiently duplicative of naturally occurring SCF,  
 CC stimulate growth of primitive progenitors such as haematopoietic  
 CC progenitor cells, neural stem cells and primordial germ stem cells. The  
 CC peptides can be used in a composition for treating leucopenia, anaemia or  
 CC thrombocytopenia, for enhancing engraftment of bone marrow during  
 CC transplantation or for bone marrow recovery after chemotherapy or  
 CC radiation-induced bone marrow aplasia or myelosuppression. They can also  
 CC be used for treating neoplasia, nerve damage, infertility, intestinal  
 CC damage or myeloproliferative disorders. Antibodies may be raised against  
 CC the peptides for use in detection or neutralisation of SCF in serum. SCF  
 CC may be useful for the treatment of AIDS and severe combined  
 CC immunodeficiency (SCID) states alone or in combination with other factors  
 CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
 Db 1 TTTT TTTT TTTT TTTT TTTT 18  
 RESULT 1473  
 AAT04917/c  
 ID AAT04917 standard; cDNA; 20 BP.  
 XX AAT04917;  
 AC AAT04917;  
 XX 25-MAR-2003 (revised)  
 DT 15-MAY-1996 (first entry)  
 XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.  
 DE Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;  
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;  
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.  
 XX Synthetic.  
 OS EP676470-A1.  
 XX 11-OCT-1995.  
 PD 04-OCT-1990; 95EP-00105391.  
 XX 16-OCT-1989; 89US-00422383.  
 PR 11-JUN-1990; 90US-00537198.  
 PR 24-AUG-1990; 90US-00573616.  
 PR 28-SEP-1990; 90WO-US005548.  
 PR 01-OCT-1990; 90US-00589701.  
 XX (AMGE-) AMGEN INC.  
 PA Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
 XX WPI; 1995-346090/45.  
 PI New stem cell factor polypeptide(s) - for stimulating the growth of  
 XX primitive progenitor cells, esp. for treating disorders involving blood  
 DR cells.

XX PS Example 3; Fig 12C; 127pp; English.

XX CC AAT04915-T04922 are oligonucleotide primers and probes used for the

CC amplification and sequencing of mammalian stem cell factor (SCF). Non-

CC naturally occurring SCF and C-terminally truncated polypeptides, having

CC amino acid sequences sufficiently duplicative of naturally occurring SCF,

CC stimulate growth of primitive progenitors such as haematopoietic

CC progenitor cells, neural stem cells and primordial germ stem cells. The

CC peptides can be used in a composition for treating leucopenia, anaemia or

CC thrombocytopenia, for enhancing engraftment of bone marrow during

CC transplantation or for bone marrow recovery after chemotherapy or

CC radiation-induced bone marrow aplasia or myelosuppression. They can also

CC be used for treating neoplasia, nerve damage, infertility, intestinal

CC damage or myeloproliferative disorders. Antibodies may be raised against

CC the peptides for use in detection or neutralisation of SCF in serum. SCF

CC may be useful for the treatment of AIDS and severe combined

CC immunodeficiency (SCID) states alone or in combination with other factors

CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1474

AAA13752

ID AAA13752 standard; DNA; 20 BP.

XX AC AAA13752;

XX DT 27-JUL-2000 (first entry)

XX DE Stem cell factor universal oligonucleotide 220-3.

XX KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;

KW primitive progenitor cell; haematopoietic disorder; syngeneic;

KW allogeneic; autologous bone marrow transplant; gene therapy;

KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;

KW cancer; ss.

XX OS Synthetic.

XX PN EP992579-A1.

XX PD 12-APR-2000.

XX PF 04-OCT-1990; 99EP-00122861.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 28-SEP-1990; 90WO-US005548.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 04-OCT-1990; 90EP-00310899.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX DR WPI; 2000-259135/23.

XX PT Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell

PT factor.

XX PS Example 3; Fig 12C; 123pp; English.

XX CC A method has been developed of making haematopoietic cells suitable for

CC administration to a subject. The method comprises: (a) obtaining the cells

CC haematopoietic progenitor cells from a donor; and (b) expanding the cells

CC by adding to the cells a haematopoietically effective dose of a

CC polypeptide product having at least part of the primary structural

CC confirmation and one or more of the biological properties of naturally

CC occurring stem cell factor (SCF). The method is useful for stimulating

CC primitive progenitor cells including early haematopoietic progenitor

CC cells which are capable of maturing to erythroid, megakaryocyte,

CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute

CC increases in haematopoietic cells of both myeloid and lymphoid lineages.

CC SCF is useful for treating haematopoietic disorders. The method is useful

CC for expanding early haematopoietic progenitors in syngeneic, allogeneic

CC or autologous bone marrow transplant. SCF is useful for enhancing the

CC efficiency of gene therapy based on transfecting haematopoietic stem

CC cells. SCF is also useful for combating the myelosuppressive effects of

CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery

CC after acute blood loss and as a boost to the immune system for fighting

CC neoplasia (cancer). The present sequence represents a universal

CC oligonucleotide which is used in an example from the present invention

XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1475

AAA13752/c

ID AAA13752 standard; DNA; 20 BP.

XX AC AAA13752;

XX DT 27-JUL-2000 (first entry)

XX DE Stem cell factor universal oligonucleotide 220-3.

XX KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;

KW primitive progenitor cell; haematopoietic disorder; syngeneic;

KW allogeneic; autologous bone marrow transplant; gene therapy;

KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;

KW cancer; ss.

XX OS Synthetic.

XX PN EP992579-A1.

XX PD 12-APR-2000.

XX PF 04-OCT-1990; 99EP-00122861.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 28-SEP-1990; 90WO-US005548.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 04-OCT-1990; 90EP-00310899.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;

XX DR WPI; 2000-259135/23.

XX PT Production of hematopoietic cells suitable for administration to a

PT subject using progenitor cells and expanding the cells using stem cell

PT factor.

XX Example 3; Fig 12C; 123pp; English.

PS A method has been developed of making haematopoietic cells suitable for

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CC haematopoietic progenitor cells from a donor; and (b) expanding the cells

CC by adding to the cells a haematopoietically effective dose of a

CC polypeptide product having at least part of the primary structural

CC confirming stem cell factor (SCF). The method is useful for stimulating

CC occurrence of progenitor cells including early haematopoietic progenitor

CC cells which are capable of maturing to erythroid, megakaryocyte,

CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute

CC increases in haematopoietic cells of both myeloid and lymphoid lineages.

CC SCF is useful for treating haematopoietic disorders. The method is useful

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CC or autologous bone marrow transplant. SCF is useful for enhancing the

CC efficiency of gene therapy based on transfecting haematopoietic stem

CC cells. SCF is also useful for combating the myelosuppressive effects of

CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery

CC after acute blood loss and as a boost to the immune system for fighting

CC neoplasia (cancer). The present sequence represents a universal

CC oligonucleotide which is used in an example from the present invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1476

AAH41331

ID AAH41331 standard; DNA; 20 BP.

XX

AC AAH41331;

XX

DT 21-AUG-2001 (first entry)

XX

DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.

XX

KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;

KW gene therapy; PCR primer; mutagenesis; probe; ss.

XX

OS Synthetic.

XX

PN US6207454-B1.

XX

PD 27-MAR-2001.

XX

PF 31-DEC-1998; 98US-00224681.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX

PA (AMGE-) AMGEN INC.

XX

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX

DR WPI; 2001-366062/38.

XX

PT Enhancing efficiency of transfer of polynucleotide into a target

PT mammalian cell in vitro, involves exposing cell that expresses a stem

PT cell factor receptor to stem cell factor, and introducing polynucleotide

PT into cell in vitro.

XX

PS Example 3; Fig 12C; 210pp; English.

XX

CC The present invention describes a method for enhancing (E) the efficiency

CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in

CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)

CC receptor to a biologically active SCF, its analogue or fragment, which

CC induces cell proliferation, and introducing (I) to (II) in vitro.

CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.

CC The method is useful for enhancing the efficiency of the transfer of a

CC polynucleotide into a target mammalian cell in vitro. The method is

CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to

CC AAB98390 represent sequences used in the exemplification of the present

CC invention

XX

SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1477

AAH41331/c

ID AAH41331 standard; DNA; 20 BP.

XX

AC AAH41331;

XX

DT 21-AUG-2001 (first entry)

XX

DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.

XX

KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;

KW gene therapy; PCR primer; mutagenesis; probe; ss.

XX

OS Synthetic.

XX

PN US6207454-B1.

XX

PD 27-MAR-2001.

XX

PF 31-DEC-1998; 98US-00224681.

XX

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24-MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX

PA (AMGE-) AMGEN INC.

XX

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX

DR WPI; 2001-366062/38.

XX

PT Enhancing efficiency of transfer of polynucleotide into a target

PT mammalian cell in vitro, involves exposing cell that expresses a stem

PT cell factor receptor to stem cell factor, and introducing polynucleotide

PT into cell in vitro.

XX

PS Example 3; Fig 12C; 210pp; English.

XX

CC The present invention describes a method for enhancing (E) the efficiency

CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in





CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, Fulminating septicemia, malaria, vitamin B12  
CC disorders such as piebaldism and vitiligo  
CC  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1480  
AAF89091  
ID AAF89091 standard; DNA; 20 BP.  
XX  
AC AAF89091;  
XX  
DT 13-JUL-2001 (first entry)  
XX  
DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.

XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
KW severe combined immunodeficiency; PCR primer; ss.

XX Mammalia.

PN US6207802-B1.

XX 27-MAR-2001.

PF 09-NOV-1994; 94US-00336728.

XX 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide  
PT stimulating growth of early hematopoietic progenitor cells, useful for  
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,  
PT sarcoidosis.

XX Example 3; Fig 12C; 209pp; English.

XX The present invention provides the protein and coding sequences of  
CC mammalian stem cell factors (SCFs). These are capable of stimulating the  
CC growth of early haematopoietic progenitor cells, neural stem cells and  
CC primordial germ stem cells. The sequences are useful in the treatment of  
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
CC and intestinal damage, infertility, AIDS and severe combined  
CC immunodeficiency (SCID). The present sequence is primer used to amplify  
CC an SCF in the exemplification of the invention

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 1 TTTTTTTTTTTTTTTT 18

RESULT 1481  
AAF89091/c  
ID AAF89091 standard; DNA; 20 BP.  
XX  
AC AAF89091;  
XX  
DT 13-JUL-2001 (first entry)  
XX

DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.  
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;  
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;  
KW neurological damage; intestinal damage; infertility; AIDS; SCID;  
KW severe combined immunodeficiency; PCR primer; ss.

XX Mammalia.

PN US6207802-B1.

XX 27-MAR-2001.

PF 09-NOV-1994; 94US-00336728.

XX 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-353108/37.

XX Novel isolated non-human mammalian stem cell factor polypeptide  
PT stimulating growth of early hematopoietic progenitor cells, useful for  
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,  
PT sarcoidosis.

XX Example 3; Fig 12C; 209pp; English.

XX The present invention provides the protein and coding sequences of  
CC mammalian stem cell factors (SCFs). These are capable of stimulating the  
CC growth of early haematopoietic progenitor cells, neural stem cells and  
CC primordial germ stem cells. The sequences are useful in the treatment of  
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal  
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological  
CC and intestinal damage, infertility, AIDS and severe combined  
CC immunodeficiency (SCID). The present sequence is primer used to amplify  
CC an SCF in the exemplification of the invention

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1482



XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.  
DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;  
KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX Homo sapiens.  
OS US6218148-B1.  
XX 17-APR-2001.  
PN 21-DEC-1993; 93US-00172329.  
PD 16-OCT-1989; 89US-00422383.  
XX 11-JUN-1990; 90US-00537198.  
XX 24-AUG-1990; 90US-00573616.  
PF 01-OCT-1990; 90US-00589701.  
XX 25-NOV-1992; 92US-00982255.  
PA (AMGE-) AMGEN INC.  
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
PI WPI; 2001-281051/29.  
XX Isolated DNA sequence, encoding polypeptide product useful for  
PT stimulating growth of early hematopoietic progenitor cells.  
XX Example 3; Fig 12C; 167pp; English.  
PS The present sequence for universal PCR primer 220-3 is 1 of 8 universal  
XX oligonucleotides (AAS04211-AAS04218) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)  
CC and the polynucleotides encoding them. SCF stimulate primitive progenitor  
CC cells including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides  
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
CC disorders such as piebaldism and vitiligo  
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183  
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18  
RESULT 1485  
AAS04212/c  
ID AAS04212 standard; DNA; 20 BP.  
XX AAS04212;  
AC 29-AUG-2001 (first entry)  
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-3.  
DE Human; stem cell factor; SCF; early haematopoietic progenitor cell;  
KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;  
KW PCR primer; ss.  
XX Homo sapiens.  
OS US6218148-B1.  
XX 17-APR-2001.  
PD 21-DEC-1993; 93US-00172329.  
XX 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 01-OCT-1990; 90US-00589701.  
PR 25-NOV-1992; 92US-00982255.  
XX (AMGE-) AMGEN INC.  
PA Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX WPI; 2001-281051/29.  
DR Isolated DNA sequence, encoding polypeptide product useful for  
XX stimulating growth of early hematopoietic progenitor cells.  
XX Example 3; Fig 12C; 167pp; English.  
PS The present sequence for universal PCR primer 220-3 is 1 of 8 universal  
XX oligonucleotides (AAS04211-AAS04218) used in the isolation of the human  
CC SCF (stem cell factor) cDNA sequence. The present invention relates to  
CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)  
CC and the polynucleotides encoding them. SCF stimulate primitive progenitor  
CC cells including early haematopoietic progenitor cells. The invention also  
CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides  
CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.  
CC The polynucleotide encoding SCF is useful for producing SCF and useful in  
CC gene therapy. It is useful for treating disorders involving blood cells  
CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple  
CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,  
CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,  
CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12  
CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation  
CC disorders such as piebaldism and vitiligo  
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2803  
DB 18 AAAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1486  
AAS10447  
ID AAS10447 standard; DNA; 20 BP.  
XX AAS10447;  
AC 24-OCT-2001 (first entry)  
XX Human stem cell factor (SCF) cDNA universal PCR primer 220-3.  
DE Human; stem cell factor; SCF; haematopoietic progenitor cell;  
KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;  
KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.  
XX Homo sapiens.  
OS US6248319-B1.  
XX



```
XX PD 19-JUN-2001.
XX PF 24-MAY-1995; 95US-00449653.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PA (ZSEB/) ZSEBO K M.
XX PA (BOSS/) BOSSELMAN R A.
XX PA (SUGG/) SUGGS S V.
XX PA (MART/) MARTIN F H.
XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-407312/43.
XX PT Increasing the number of early hematopoietic progenitor cells in the
XX PT peripheral blood useful for the treatment of blood disorders including
XX PT Hodgkin's disease comprises the administration of human stem cell factor.
XX PS Example 3; Fig 12C; 210pp; English.
XX CC The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
XX CC primers (AAS10435-AAS10453) used to amplify various portions of the human
XX CC SCF cDNA sequence. The sequence is described in an invention relating to
XX CC novel stem cell factors, the polynucleotides encoding them and methods
XX CC for producing the stem cell factors. The methods involve increasing the
XX CC number of early hematopoietic progenitor cells in human peripheral blood
XX CC by administering a haematopoietically effective human stem cell factor
XX CC polypeptide. The methods are useful for the treatment of blood disorders,
XX CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
XX CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
XX CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
XX CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
XX CC disorders i.e. piebaldism and viral induced disorders, including AIDS
XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 1487
AAS10447/c
ID AAS10447 standard; DNA; 20 BP.
XX AC AAS10447;
XX XX 24-OCT-2001 (first entry)
XX DT Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
XX DE Human; stem cell factor; SCF; haematopoietic progenitor cell;
XX KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
XX KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
XX XX Homo sapiens.
XX OS US6248319-B1.
XX PN 19-JUN-2001.
XX PD 19-JUN-2001.

24-MAY-1995; 95US-00449653.
16-OCT-1989; 89US-00422383.
11-JUN-1990; 90US-00537198.
24-AUG-1990; 90US-00573616.
01-OCT-1990; 90US-00589701.
10-APR-1991; 91US-00684535.
25-NOV-1992; 92US-00982255.
21-DEC-1993; 93US-00172329.
(ZSEB/) ZSEBO K M.
(BOSS/) BOSSELMAN R A.
(SUGG/) SUGGS S V.
(MART/) MARTIN F H.
Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
WPI; 2001-407312/43.
Increasing the number of early hematopoietic progenitor cells in the
peripheral blood useful for the treatment of blood disorders including
Hodgkin's disease comprises the administration of human stem cell factor.
Example 3; Fig 12C; 210pp; English.
The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
primers (AAS10435-AAS10453) used to amplify various portions of the human
SCF cDNA sequence. The sequence is described in an invention relating to
novel stem cell factors, the polynucleotides encoding them and methods
for producing the stem cell factors. The methods involve increasing the
number of early hematopoietic progenitor cells in human peripheral blood
by administering a haematopoietically effective human stem cell factor
polypeptide. The methods are useful for the treatment of blood disorders,
including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
malaria, vitamin B12 and folic acid deficiency, hypopigmentation
disorders i.e. piebaldism and viral induced disorders, including AIDS
Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2803
Db 18 AAAAAA AAAAAA AAAAAA AAAAAA 1

RESULT 1488
AAD35464
ID AAD35464 standard; DNA; 20 BP.
XX AC AAD35464;
XX XX 25-JUL-2002 (first entry)
XX DT Rat SCF 5' cDNA amplifying PCR primer, 220-3.
XX DE Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
XX KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
XX KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;
XX KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcooidosis;
XX KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
XX KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
XX KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
XX KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
XX KW acquired immune deficiency syndrome; malaria; military tuberculosis;
XX KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
XX KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
XX KW primer; ss.
XX XX
```

OS Rattus sp.  
XX US2002018763-A1.  
PN 14-FEB-2002.  
PD  
XX 12-JAN-1998; 98US-00005243.  
PF 24-MAY-1995; 95US-00449653.  
PR (ZSEB/) ZSEBO K M.  
XX (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX WPI; 2002-350789/38.  
DR  
XX Novel non-naturally-occurring stem cell factor polypeptide, useful for  
PT treating leucopenia, thrombocytopenia, anemia and for enhancing  
PT engraftment of bone marrow during transplantation in a mammal.  
XX  
PS Example 3; Fig 12C; 217pp; English.  
XX  
CC The present invention relates to novel non-naturally-occurring stem cell  
CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
CC duplicative of that of naturally-occurring SCF to allow possession of  
CC haematopoietic biological activity of naturally occurring SCF. Sequences  
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,  
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
CC engraftment of bone marrow during transplantation in mammals and chemical  
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
CC are also useful for treating acquired immune deficiency in a human, nerve  
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
CC damage in a mammal. SCF sequences are useful for preparing biologically  
CC active polymer polypeptide adduct, for enhancing transfection of early  
CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,  
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
CC splenic pancytopenia, disseminated fungus disease, malaria, military  
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12  
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
CC and vitiligo. The present sequence is a PCR primer which is used for  
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
CC exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 18  
  
RESULT 1489  
AAD35464/c  
ID AAD35464 standard; DNA; 20 BP.  
XX  
AC AAD35464;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Rat SCF 5' cDNA amplifying PCR primer, 220-3.  
XX  
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;

KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;  
KW infertility; neoplasia; myelofibrosis; myelosclerosis; osteopetrosis;  
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;  
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;  
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;  
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;  
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;  
KW acquired immune deficiency syndrome; malaria; military tuberculosis;  
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;  
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;  
XX primer; ss.  
OS Rattus sp.  
XX  
PN US2002018763-A1.  
XX 14-FEB-2002.  
PD  
XX 12-JAN-1998; 98US-00005243.  
PF 24-MAY-1995; 95US-00449653.  
PR (ZSEB/) ZSEBO K M.  
XX (BOSS/) BOSSELMAN R A.  
PA (SUGG/) SUGGS S V.  
PA (MART/) MARTIN F H.  
XX  
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;  
XX WPI; 2002-350789/38.  
DR  
XX Novel non-naturally-occurring stem cell factor polypeptide, useful for  
PT treating leucopenia, thrombocytopenia, anemia and for enhancing  
PT engraftment of bone marrow during transplantation in a mammal.  
XX  
PS Example 3; Fig 12C; 217pp; English.  
XX  
CC The present invention relates to novel non-naturally-occurring stem cell  
CC factor (SCF) polypeptides having an amino acid sequence sufficiently  
CC duplicative of that of naturally-occurring SCF to allow possession of  
CC haematopoietic biological activity of naturally occurring SCF. Sequences  
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,  
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,  
CC engraftment of bone marrow during transplantation in mammals and chemical  
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They  
CC are also useful for treating acquired immune deficiency in a human, nerve  
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal  
CC damage in a mammal. SCF sequences are useful for preparing biologically  
CC active polymer polypeptide adduct, for enhancing transfection of early  
CC haematopoietic progenitor cells with a gene, and transfer of a gene into  
CC a mammal. They are useful for treating myelofibrosis, myelosclerosis,  
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,  
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,  
KW Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo  
KW syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary  
KW splenic pancytopenia, disseminated fungus disease, malaria, military  
KW tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12  
KW and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation  
KW disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)  
KW and vitiligo. The present sequence is a PCR primer which is used for  
KW amplifying the 5' end of rat SCF cDNA. This sequence is used in the  
KW exemplification of the invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1  
  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 1490  
ABS73848  
ID ABS73848 standard; DNA; 20 BP.  
XX  
AC  
XX  
AC  
XX  
05-DEC-2002 (first entry)  
XX  
DE  
XX  
SCF universal oligonucleotide 220-3.  
XX  
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;  
KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
KW disseminated fungus disease; haematopoietic; tuberculous; ss.  
KW antianaemic; antifungal; antimalarial; dermatological; ss.  
XX  
OS Synthetic.  
XX  
PN EP1241258-A2.  
XX  
PD  
XX  
PF  
XX  
PD  
XX  
18-SEP-2002.  
XX  
PF  
XX  
04-OCT-1990; 2002EP-00008587.  
XX  
PR  
XX  
16-OCT-1989; 89US-00422383.  
PR  
11-JUN-1990; 90US-00537198.  
PR  
24-AUG-1990; 90US-00573616.  
PR  
28-SEP-1990; 90WO-US005548.  
PR  
01-OCT-1990; 90US-00589701.  
PR  
04-OCT-1990; 90EP-00310899.  
PR  
04-OCT-1990; 95EP-00105391.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
XX  
DR WPI; 2002-684093/74.  
XX  
XX  
Production of a human stem cell factor (SCF) polypeptide for treating  
disorders involving blood cells, such as leukemia, comprises culturing  
mammalian cells comprising non-human SCF promoter DNA linked to DNA  
encoding the human SCF.  
XX  
PS Example 3; Fig 12C; 120pp; English.  
XX  
CC The present invention relates to novel stem cell factors (SCFs),  
CC polynucleotide sequences encoding the SCFs, and methods of producing  
CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
CC mammals, particularly humans. The method of the invention is useful for  
CC the production of human SCF. The stem cell factors are useful to treat  
CC disorders involving blood cells e.g. metastatic carcinoma, acute  
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
CC disease, malaria, and vitiligo. The present sequence representing a  
CC universal oligonucleotide for SCF DNA is used in the examples of the  
CC present invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18  
RESULT 1491  
ABS73848/c  
ID ABS73848 standard; DNA; 20 BP.

XX  
AC ABS73848;  
XX  
DT 05-DEC-2002 (first entry)  
XX  
DE SCF universal oligonucleotide 220-3.  
XX  
KW Stem cell factor; SCF; blood-forming system; blood cell disorder;  
KW haematopoietic system; metastatic carcinoma; acute leukaemia;  
KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;  
KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;  
KW disseminated fungus disease; haematopoietic; tuberculous; ss.  
KW antianaemic; antifungal; antimalarial; dermatological; ss.  
XX  
OS Synthetic.  
XX  
PN EP1241258-A2.  
XX  
PD 18-SEP-2002.  
XX  
PF 04-OCT-1990; 2002EP-00008587.  
XX  
PR 16-OCT-1989; 89US-00422383.  
PR 11-JUN-1990; 90US-00537198.  
PR 24-AUG-1990; 90US-00573616.  
PR 28-SEP-1990; 90WO-US005548.  
PR 01-OCT-1990; 90US-00589701.  
PR 04-OCT-1990; 90EP-00310899.  
PR 04-OCT-1990; 95EP-00105391.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Zsebo KM, Suggs SV, Bosselman RA, Martin FH;  
XX  
DR WPI; 2002-684093/74.  
XX  
XX  
Production of a human stem cell factor (SCF) polypeptide for treating  
disorders involving blood cells, such as leukemia, comprises culturing  
mammalian cells comprising non-human SCF promoter DNA linked to DNA  
encoding the human SCF.  
XX  
PS Example 3; Fig 12C; 120pp; English.  
XX  
CC The present invention relates to novel stem cell factors (SCFs),  
CC polynucleotide sequences encoding the SCFs, and methods of producing  
CC them. SCFs are involved in the blood-forming (haematopoietic) system in  
CC mammals, particularly humans. The method of the invention is useful for  
CC the production of human SCF. The stem cell factors are useful to treat  
CC disorders involving blood cells e.g. metastatic carcinoma, acute  
CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory  
CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus  
CC disease, malaria, and vitiligo. The present sequence representing a  
CC universal oligonucleotide for SCF DNA is used in the examples of the  
CC present invention  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 18 AAAAAA AAAAAA AAAAAA 1  
RESULT 1492  
ABZ89896  
ID ABZ89896 standard; DNA; 20 BP.  
XX  
AC ABZ89896;  
XX  
DT 17-OCT-2003 (first entry)



XX DE Human oligonucleotide sequence.  
XX DE  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX OS  
XX OS Homo sapiens.  
XX PN WO200285308-A2.  
XX PN  
XX PD 31-OCT-2002.  
XX PD  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PF  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PR  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PA  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX PI  
XX DR WPI; 2003-229219/22.  
XX DR  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX PT  
XX PS Disclosure; SEQ ID NO 5138; 872pp; English.  
XX PS  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX CC  
XX SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
DB 3 GAAAAAAAAAAAAAAAAA 20  
RESULT 1493  
ABZ89703/C  
ID ABZ89703 standard; DNA; 20 BP.  
XX AC ABZ89703;  
XX AC  
XX DT 17-OCT-2003 (first entry)  
DT

XX DE Human oligonucleotide sequence.  
XX DE  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX OS  
XX OS Homo sapiens.  
XX PN WO200285308-A2.  
XX PN  
XX PD 31-OCT-2002.  
XX PD  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PF  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PR  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PA  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX PI  
XX DR WPI; 2003-229219/22.  
XX DR  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX PT  
XX PS Disclosure; SEQ ID NO 4945; 872pp; English.  
XX PS  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX CC  
XX SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 18; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2171 TTTTTTTTTTTTTTTTAA 2188  
DB 20 TTTTTTTTTTTTTTTTAA 3  
RESULT 1494  
ABZ89719/C  
ID ABZ89719 standard; DNA; 20 BP.  
XX AC ABZ89719;  
XX AC  
XX DT 17-OCT-2003 (first entry)  
DT



XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

DR Pharmaceutical composition for treating ailments associated with impaired

XX PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4961; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802

Db 20 GAAAAAAAAAAAAAAAAA 3

RESULT 1495

ADE52460

ID ADE52460 standard; DNA; 20 BP.

XX AC ADE52460;

XX XX 29-JAN-2004 (first entry)

DT

XX DE Stem cell factor (SCF) related DNA #31.

XX KW Stem cell factor; SCF; haematopoietic activity; infertility;

KW intestinal damage; myeloproliferative disorder; leucopenia;

KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;

KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;

KW milary tuberculosis; haematopoietic progenitor cell; ss.

XX OS Synthetic.

XX PN US2002031491-A1.

XX PD 14-MAR-2002.

XX PF 31-DEC-1998; 98US-00224683.

XX PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 10-APR-1991; 91US-00684535.

PR 25-NOV-1992; 92US-00982255.

PR 21-DEC-1993; 93US-00172329.

PR 24 MAY-1995; 95US-00449653.

PR 12-JAN-1998; 98US-00005893.

XX (ZSEB/) ZSEBO K M.

PA (BOSS/) BOSSELMAN R A.

PA (SUGG/) SUGGS S V.

PA (MART/) MARTIN F H.

XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

PI WPI; 2003-851459/79.

XX New non-natural stem cell factor, useful for treating e.g. leucopenia or

PT immune deficiency, also related nucleic acid and antibodies.

XX Disclosure; SEQ ID NO 32; 217pp; English.

PS The invention relates to stem cell factor (SCF) polypeptides with

XX haematopoietic activity and the polynucleotides encoding them. The

CC polypeptides are used for treating infertility, intestinal damage,

CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia,

CC for improving engraftment of bone marrow transplants, for enhancing bone

CC marrow recovery after radiotherapy or chemotherapy and in treatment of

CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic

CC carcinoma, leukaemia and milary tuberculosis. The SCF polypeptides are

CC also used to expand haematopoietic progenitor cells for transplantation

CC and to prepare such cells for transfection with a gene. The SCF

CC polynucleotides can be used for recombinant expression of the

CC polypeptides and also as probes for mapping of the SCF gene, for

CC identifying SCF-related diseases and as a marker for neighbouring genes.

CC Antibodies raised against the polypeptides are useful in diagnosis and to

CC remove SCF from blood. This sequence represents SCF related DNA of the

CC invention.

XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183

Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1496

ADE52460/c

ID ADE52460 standard; DNA; 20 BP.

XX









ID AAQ75735 standard; DNA; 21 BP.  
XX  
AC AAQ75735;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1505  
AAQ75738/c  
ID AAQ75738 standard; DNA; 21 BP.  
XX  
AC AAQ75738;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
WPI; 1995-018287/03.  
Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.  
Disclosure; Page 8; 11pp; Japanese.  
A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily  
Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1506  
AAQ75748/c  
ID AAQ75748 standard; DNA; 21 BP.  
XX  
AC AAQ75748;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
DR  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1506  
AAQ75748/c  
ID AAQ75748 standard; DNA; 21 BP.  
XX  
AC AAQ75748;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
DR  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1506  
AAQ75738/c  
ID AAQ75738 standard; DNA; 21 BP.  
XX  
AC AAQ75738;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
| | | | | | | | | | | | | | | | | |  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1507  
AAQ75795/c  
ID AAQ75795 standard; DNA; 21 BP.  
XX  
AC AAQ75795;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-00112515.  
XX  
XX PR 16-APR-1993; 93JP-00112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2170 TTTTTTTTTTTTTTTTA 2187  
| | | | | | | | | | | | | | | | | |  
Db 1 TTTTTTTTTTTTTTTTA 18

RESULT 1509  
AAQ75736/c  
ID AAQ75736 standard; DNA; 21 BP.  
XX  
AC AAQ75736;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-00112515.  
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XX PR 16-APR-1993; 93JP-00112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
| | | | | | | | | | | | | | | | | |  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1508  
AAQ75671  
ID AAQ75671 standard; DNA; 21 BP.  
XX  
AC AAQ75671;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1

RESULT 1510  
AAQ75798/c  
ID AAQ75798 standard; DNA; 21 BP.  
XX  
AC AAQ75798;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1

RESULT 1511  
AAQ75674  
ID AAQ75674 standard; DNA; 21 BP.

XX  
AC AAQ75674;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2170 TTTTTT TTTTTT TTTT 2187  
Db 1 TTTTTT TTTTTT TTTT 18

RESULT 1512  
AAQ75687  
ID AAQ75687 standard; DNA; 21 BP.  
XX  
AC AAQ75687;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.









QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1521  
AAQ75791/C  
ID AAQ75791 standard; DNA; 21 BP.  
XX  
AC AAQ75791;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1522  
AAQ75743/C  
ID AAQ75743 standard; DNA; 21 BP.  
XX  
AC AAQ75743;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX

PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1523  
AAQ75769/C  
ID AAQ75769 standard; DNA; 21 BP.  
XX  
AC AAQ75769;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC

CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1524  
AAQ75796/c  
ID AAQ75796 standard; DNA; 21 BP.  
XX  
AC AAQ75796;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1525  
AAQ75797/c  
ID AAQ75797 standard; DNA; 21 BP.  
XX  
AC AAQ75797;  
XX

XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
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PA  
XX WPI; 1995-018287/03.  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 1526  
AAQ75689  
ID AAQ75689 standard; DNA; 21 BP.  
XX  
AC AAQ75689;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR









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Db      |||||
18 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1535
AAQ75784/c
ID  AAQ75784 standard; DNA; 21 BP.
XX
AC  AAQ75784;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 9; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2802
Db      |||||
18 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1536
AAQ75785/c
ID  AAQ75785 standard; DNA; 21 BP.
XX
AC  AAQ75785;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03..
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 7; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2802
Db      |||||
18 GAAAAAAAAAAAAAAAAAAAA 1

RESULT 1537
AAQ75704
ID  AAQ75704 standard; DNA; 21 BP.
XX
AC  AAQ75704;
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03..
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 7; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAA 2802
Db      |||||
18 GAAAAAAAAAAAAAAAAAAAA 1
```





PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 1lpp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2802  
DB 18 GAAAAAAGAAAAA 1  
  
RESULT 1541  
AAQ75707  
ID AAQ75707 standard; DNA; 21 BP.  
AC AAQ75707;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
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DR WPI; 1995-018287/03.  
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PS Disclosure; Page 7; 1lpp; Japanese.  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2170 TTTTTTTTTTTTTTTA 2187  
DB 18 GAAAAAAGAAAAA 1

Db 1 TTTTTTTTTTTTTTTA 18  
  
RESULT 1542  
AAQ75750/c  
ID AAQ75750 standard; DNA; 21 BP.  
XX  
AC AAQ75750;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
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PF 16-APR-1993; 93JP-00112515.  
XX  
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XX  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
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CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2802  
DB 18 GAAAAAAGAAAAA 1  
  
RESULT 1543  
AAQ75710  
ID AAQ75710 standard; DNA; 21 BP.  
XX  
AC AAQ75710;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.



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XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAA 2802  
Db 18 GAAAAAAAAAAAAA 1  
RESULT 1547  
AAQ75709  
ID AAQ75709 standard; DNA; 21 BP.  
XX  
AC AAQ75709;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.

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XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 18  
RESULT 1548  
AAQ75711  
ID AAQ75711 standard; DNA; 21 BP.  
XX  
AC AAQ75711;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
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PF 16-APR-1993; 93JP-00112515.  
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PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
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XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTT 2187  
Db 1 TTTTTTTTTTTTTTTT 18



RESULT 1549  
AAQ75744/C  
ID AAQ75744 standard; DNA; 21 BP.  
XX  
AC AAQ75744;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1  
RESULT 1550  
AAQ75783/C  
ID AAQ75783 standard; DNA; 21 BP.  
XX  
AC AAQ75783;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX

PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 18 GAAAAA AAAAAAAAAA 1  
RESULT 1551  
AAQ75792/C  
ID AAQ75792 standard; DNA; 21 BP.  
XX  
AC AAQ75792;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

```
XX SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.6%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802
Db 18 GAAAAAAAAAAAAAAAAA 1

RESULT 1552
AAQ64706
ID AAQ64706 standard; cDNA to mRNA; 22 BP.
XX
AC AAQ64706;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1995 (first entry)
XX
DE 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX
KW antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4
FT /*tag= a
FT /label= 2',5'-linked tetraadenylate
FT /note= "nucleotides linked through phosphodiester bonds
FT at hydroxyl groups of 2' and 5' carbons"
FT misc_feature 5..22
FT /*tag= b
FT /note= "antisense region"
XX
PN WO9409129-A2.
XX
PD 28-APR-1994.
XX
PF 20-OCT-1993; 93WO-US010103.
XX
PR 21-OCT-1992; 92US-00965666.
PR 17-SEP-1993; 93US-00123449.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI Torrence P, Silverman R, Maitra R, Lesiak K;
XX WPI; 1994-151315/18.
DR
XX
PT Specific cleavage of RNA, useful partic. for treating viral infection,
PT cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT of 2-5A dependent RNase.
XX
PS Example 1; Page 68; 86pp; English.
XX
CC This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
CC molecule. The antisense region targets the chimeric molecule to a
CC particular region of RNA to be specifically cleaved and the 2',5'-linked
CC tetraadenylate tail activates the 2-5A RNase. Typical applications are
CC treatment of viral infections (esp. for cleavage of an RNA virus genome),
CC cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
CC angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5
```

```
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2183
Db 5 TTTTTTTTTTTTTTTTTT 22

RESULT 1553
AAQ64706/c
ID AAQ64706 standard; cDNA to mRNA; 22 BP.
XX
AC AAQ64706;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1995 (first entry)
XX
DE 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
XX
KW antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4
FT /*tag= a
FT /label= 2',5'-linked tetraadenylate
FT /note= "nucleotides linked through phosphodiester bonds
FT at hydroxyl groups of 2' and 5' carbons"
FT misc_feature 5..22
FT /*tag= b
FT /note= "antisense region"
XX
PN WO9409129-A2.
XX
PD 28-APR-1994.
XX
PF 20-OCT-1993; 93WO-US010103.
XX
PR 21-OCT-1992; 92US-00965666.
PR 17-SEP-1993; 93US-00123449.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI Torrence P, Silverman R, Maitra R, Lesiak K;
XX WPI; 1994-151315/18.
DR
XX
PT Specific cleavage of RNA, useful partic. for treating viral infection,
PT cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT of 2-5A dependent RNase.
XX
PS Example 1; Page 68; 86pp; English.
XX
CC This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
CC molecule. The antisense region targets the chimeric molecule to a
CC particular region of RNA to be specifically cleaved and the 2',5'-linked
CC tetraadenylate tail activates the 2-5A RNase. Typical applications are
CC treatment of viral infections (esp. for cleavage of an RNA virus genome),
CC cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
CC angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 22 AAAAAAAAAAAAAAAAAA 5
```



XX 24-NOV-1994.  
PD 13-MAY-1994; 94WO-US005407.  
XX 13-MAY-1993; 93US-00061694.  
PF (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Fields HA, Khudyakov YE;  
XX WPI; 1995-006819/01.  
DR Solid phase immunoassay using oligo:nucleotide as label - also new  
XX conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for  
PT diagnosing hepatitis C or E virus infection.  
PT Example; Page 13; 34pp; English.  
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
CC They are used in a method for detecting an antigen in a subject. The  
CC method involves binding the antigen to a solid support and then reacting  
CC it with an immunoreactive ligand (L) bound to an oligo; removing any  
CC unreacted L, and then detecting the presence of the oligo. A similar  
CC method can be used to detect Abs, in which case the ligand is an oligo-  
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab  
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which  
CC can be covalently attached by the 5'-terminus to the N- or C-terminal of  
CC a synthetic peptide. For ICR using oligo AAQ75024, oligos 1-4 (see  
CC AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 23 TTTT TTTT TTTT TTTT TTTT 6  
RESULT 1557  
AAQ75029  
ID AAQ75029 standard; RNA; 23 BP.  
XX AC AAQ75029;  
XX 25-MAR-2003 (revised)  
DT 03-AUG-1995 (first entry)  
XX LCR oligo 3.  
XX Synthetic oligo; solid phase immunoassay; ss.  
OS Synthetic.  
XX WO9426932-A1.  
PN 24-NOV-1994.  
XX 13-MAY-1994; 94WO-US005407.  
PF 13-MAY-1993; 93US-00061694.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Fields HA, Khudyakov YE;  
XX WPI; 1995-006819/01.  
XX Solid phase immunoassay using oligo:nucleotide as label - also new

PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for  
PT diagnosing hepatitis C or E virus infection.  
XX Example; Page 13; 34pp; English.  
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
CC They are used in a method for detecting an antigen in a subject. The  
CC method involves binding the antigen to a solid support and then reacting  
CC it with an immunoreactive ligand (L) bound to an oligo; removing any  
CC unreacted L, and then detecting the presence of the oligo. A similar  
CC method can be used to detect Abs, in which case the ligand is an oligo-  
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab  
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which  
CC can be covalently attached by the 5'-terminus to the N- or C-terminal of  
CC a synthetic peptide. For ICR using oligo AAQ75024, oligos 1-4 (see  
CC AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;  
SQ Query Match 0.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 0.0%; Pred. No. 1.3e+03;  
Matches 0; Conservative 18; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183  
Db 1 UUUUUUUUUUUUUUUUUUUU 18  
RESULT 1558  
AAQ75029/C  
ID AAQ75029 standard; RNA; 23 BP.  
XX AC AAQ75029;  
XX 25-MAR-2003 (revised)  
DT 03-AUG-1995 (first entry)  
XX LCR oligo 3.  
XX Synthetic oligo; solid phase immunoassay; ss.  
OS Synthetic.  
XX WO9426932-A1.  
PN 24-NOV-1994.  
XX 13-MAY-1994; 94WO-US005407.  
PF 13-MAY-1993; 93US-00061694.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Fields HA, Khudyakov YE;  
XX WPI; 1995-006819/01.  
XX Solid phase immunoassay using oligo:nucleotide as label - also new  
PT conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for  
PT diagnosing hepatitis C or E virus infection.  
XX Example; Page 13; 34pp; English.  
XX AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.  
CC They are used in a method for detecting an antigen in a subject. The  
CC method involves binding the antigen to a solid support and then reacting  
CC it with an immunoreactive ligand (L) bound to an oligo; removing any  
CC unreacted L, and then detecting the presence of the oligo. A similar  
CC method can be used to detect Abs, in which case the ligand is an oligo-  
CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab  
CC to be detected at very low levels. An exemplary oligo is AAQ75024 which  
CC can be covalently attached by the 5'-terminus to the N- or C-terminal of



CC a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see  
CC AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 1559  
AAF85497  
ID AAF85497 standard; DNA; 23 BP.  
XX  
AC AAF85497;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE PCR primer for DNA encoding Kalata B1 polypeptide fragments.  
XX  
KW Kalata B2; transgenic plant; cotton; calcium channel binding; pain;  
KW stroke; C5a binding; antiinflammatory; PCR primer; ss.  
XX  
OS Oldenlandia affinis.  
XX  
PN WO200134829-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 03-NOV-2000; 2000WO-AU001352.  
XX  
PR 05-NOV-1999; 99AU-00003884.  
PR 25-NOV-1999; 99AU-00004235.  
XX  
XX (UYQU ) UNIV QUEENSLAND.  
PA (UYLA-) UNIV LATROBE.  
XX  
XX  
PI Craik DJ, Anderson MA, Jennings CV;  
XX  
XX WPI; 2001-343607/36.  
XX  
XX  
PT Novel nucleic acid molecule encoding amino acid sequence capable of  
PT forming cyclic structure, for generating transgenic plants capable of  
PT producing cyclic knotted protein and resistant to pathogens such as  
PT insects.  
XX  
PS Example 10; Fig 1B; 112pp; English.  
XX  
CC PCR primers AAF85495-97 were used to amplify a DNA fragment encoding  
CC Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological  
CC activities. The Kalata B1 polynucleotide represents a nucleic acid  
CC molecule of the invention. The specification describes nucleic acid  
CC molecules which encode an amino acid sequence which is capable of being  
CC cyclised within a cell or a membrane of a cell to form a cyclic backbone.  
CC The amino acid sequence comprises sufficient disulfide bonds to confer a  
CC stabilized folded structure on the three-dimensional structure of the  
CC backbone. The nucleic acid molecules of the invention are useful for  
CC producing transgenic genetically modified food or non-food crop plants,  
CC in particular cotton. The peptides or proteins can be manipulated to  
CC introduce modulating activity, for modulating activity of calcium channel  
CC binding is useful in treatment of pain or stroke and C5a binding activity  
CC useful as an antiinflammatory agent. The nucleic acid molecules are  
CC useful in the generation of molecules having animal or plant therapeutic  
CC properties as well as in a range of diagnostic, industrial and  
CC agricultural including horticultural applications and for protecting  
CC plants such as crop plants from pest and/or pathogen infestation  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTTTT 2182  
Db 6 CTTTTTTTTTTTTTTTTT 23  
  
RESULT 1560  
AAD33503  
ID AAD33503 standard; DNA; 23 BP.  
XX  
AC AAD33503;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS13-23-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
XX Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations of probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1561  
AAD33503/c  
ID AAD33503 standard; DNA; 23 BP.  
XX  
AC AAD33503;  
XX  
DT 01-JUL-2002 (first entry)  
XX





OS Synthetic.  
XX WO200155365-A1.  
PN  
XX 02-AUG-2001.  
PD  
XX 24-JAN-2001; 2001WO-JP000443.  
PF  
XX 27-JAN-2000; 2000JP-00019301.  
PR  
XX (TOJO ) TOYO KOHAN CO LTD.  
PA  
XX Tanga M, Okamura H, Takagi K, Takahashi K;  
PI WPI; 2001-488794/53.  
XX  
DR Support for immobilizing nucleotides.  
XX  
PT  
XX  
XX Example 1; Page 8; 18pp; Japanese.  
PS  
CC The specification describes a support for immobilizing nucleotides which  
CC contributes to the efficient clarification of DNA without damaging the  
CC terminal parts of the DNA. The support is a chemically treated modified  
CC substrate on which oligonucleotides with restriction enzyme cleavage  
CC sites are immobilised. The support is useful for immobilizing nucleic  
CC acids such as DNA. The present sequence represents a synthetic  
CC oligonucleotide used in the course of the invention  
XX  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 23 AAAAAAAAAAAAAAAAAA 6  
RESULT 1567  
ABQ79878  
ID ABQ79878 standard; DNA; 24 BP.  
XX  
AC ABQ79878;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Nucleotide sequence of a PCR primer #8.  
KW Polymerase chain reaction; thermal cycle; immobilisation;  
XX genetic engineering; PCR; primer; ss.  
OS Synthetic.  
XX  
PN JP2002191369-A.  
XX  
PD 09-JUL-2002.  
XX  
PF 27-DEC-2000; 2000JP-00399573.  
XX  
PR 27-DEC-2000; 2000JP-00399573.  
XX  
PA (TOJO ) TOYO KOHAN CO LTD.  
PA (TAKA/) TAKAHASHI K.  
XX  
DR WPI; 2002-630904/68.  
XX  
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
DE a substrate on which a DNA is immobilized used in medical, biochemical,  
XX molecular biological and gene engineering fields.  
KW Polymerase chain reaction; thermal cycle; immobilisation;  
XX genetic engineering; PCR; primer; ss.  
OS Synthetic.  
XX  
PN JP2002191369-A.  
XX  
PD 09-JUL-2002.  
XX  
PF 27-DEC-2000; 2000JP-00399573.  
XX  
PR 27-DEC-2000; 2000JP-00399573.  
XX  
PA (TOJO ) TOYO KOHAN CO LTD.  
PA (TAKA/) TAKAHASHI K.  
XX  
DR WPI; 2002-630904/68.  
XX  
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
PT a substrate on which a DNA is immobilized used in medical, biochemical,  
XX molecular biological and gene engineering fields.  
XX  
PS Example; Page 10; 13pp; Japanese.  
XX

CC The invention relates to performing a thermal cycle of PCR by using a  
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
CC method is useful in the medical, biochemical, molecular biological and  
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
XX used in the method of the invention  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2183  
Db 6 TTTTTTTTTTTTTTTT 23  
RESULT 1568  
ABQ79878/c  
ID ABQ79878 standard; DNA; 24 BP.  
XX  
AC ABQ79878;  
XX  
DT 23-DEC-2002 (first entry)  
XX  
DE Nucleotide sequence of a PCR primer #8.  
XX  
KW Polymerase chain reaction; thermal cycle; immobilisation;  
KW genetic engineering; PCR; primer; ss.  
XX Synthetic.  
OS  
XX JP2002191369-A.  
PN  
PD 09-JUL-2002.  
XX  
PF 27-DEC-2000; 2000JP-00399573.  
XX  
PR 27-DEC-2000; 2000JP-00399573.  
XX  
PA (TOJO ) TOYO KOHAN CO LTD.  
PA (TAKA/) TAKAHASHI K.  
XX  
DR WPI; 2002-630904/68.  
XX  
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
PT a substrate on which a DNA is immobilized used in medical, biochemical,  
XX molecular biological and gene engineering fields.  
PS Example; Page 10; 13pp; Japanese.  
XX  
CC The invention relates to performing a thermal cycle of PCR by using a  
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
CC method is useful in the medical, biochemical, molecular biological and  
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
XX used in the method of the invention  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 23 AAAAAAAAAAAAAAAAAA 6  
RESULT 1569  
AAD33505  
ID AAD33505 standard; DNA; 24 BP.  
XX  
AC AAD33505;



Thu Jun 10 13:10:09 2004

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XX DT 01-JUL-2002 (first entry)
XX DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX KW Molecular array; probe; ss.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PR 11-SEP-2000; 2000US-00659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX CC Calibration of molecular array data by employing calibration probes that
XX PT generate signals proportional to total concentrations of labeled target
XX PT molecules, and molecular arrays incorporating sets of calibration probes.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX CC molecular array. The method involves employing calibrations of labelled
XX CC generate signals proportional to the total concentrations of labelled
XX CC target molecules to which the molecular array probes are directed over an
XX CC entire range of sample solutions and molecular arrays incorporating sets
XX CC of calibration probes. Method is useful for calibrating different types
XX CC of signals scanned from a molecular array, or calibrating signals scanned
XX CC from different molecular arrays. The present sequence is poly (A)
XX CC normalisation probe used in calibration of molecular array data
XX SQ Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 18; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803
DB 1 AAAAAAAAAAAAAAAAAAAAAA 18
RESULT 1570
ID AAD33505 standard; DNA; 24 BP.
XX AC AAD33505;
XX DT 01-JUL-2002 (first entry)
XX DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX KW Molecular array; probe; ss.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PR 11-SEP-2000; 2000US-00659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX CC Calibration of molecular array data by employing calibration probes that
XX PT generate signals proportional to total concentrations of labeled target
XX PT molecules, and molecular arrays incorporating sets of calibration probes.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX CC molecular array. The method involves employing calibrations of labelled
XX CC generate signals proportional to the total concentrations of labelled
XX CC target molecules to which the molecular array probes are directed over an
XX CC entire range of sample solutions and molecular arrays incorporating sets
XX CC of calibration probes. Method is useful for calibrating different types
XX CC of signals scanned from a molecular array, or calibrating signals scanned
XX CC from different molecular arrays. The present sequence is poly (A)
XX CC normalisation probe used in calibration of molecular array data
XX SQ Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 18; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803
DB 1 AAAAAAAAAAAAAAAAAAAAAA 18
RESULT 1570
ID AAD33505/c
XX AC AAD33505 standard; DNA; 24 BP.
XX DT 01-JUL-2002 (first entry)
XX DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX KW Molecular array; probe; ss.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PR 11-SEP-2000; 2000US-00659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
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XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX CC Calibration of molecular array data by employing calibration probes that
XX PT generate signals proportional to total concentrations of labeled target
XX PT molecules, and molecular arrays incorporating sets of calibration probes.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PR 11-SEP-2000; 2000US-00659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282886/33.
XX CC Calibration of molecular array data by employing calibration probes that
XX PT generate signals proportional to total concentrations of labeled target
XX PT molecules, and molecular arrays incorporating sets of calibration probes.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX CC molecular array. The method involves employing calibrations of labelled
XX CC generate signals proportional to the total concentrations of labelled
XX CC target molecules to which the molecular array probes are directed over an
XX CC entire range of sample solutions and molecular arrays incorporating sets
XX CC of calibration probes. Method is useful for calibrating different types
XX CC of signals scanned from a molecular array, or calibrating signals scanned
XX CC from different molecular arrays. The present sequence is poly (A)
XX CC normalisation probe used in calibration of molecular array data
XX SQ Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX Query Match 0.6%; Score 18; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2166 TTTT TTTT TTTT TTTT TTTT 2183
DB 18 TTTT TTTT TTTT TTTT TTTT 1
RESULT 1571
ID ADC75073 standard; DNA; 24 BP.
XX AC ADC75073;
XX DT 01-JAN-2004 (first entry)
XX DE Biosensor related oligonucleotide of the invention SEQ ID NO:1.
XX KW ss; biosensor; hybridisation.
XX OS Synthetic.
XX PN JP2003172737-A.
XX PD 20-JUN-2003.
XX PF 07-DEC-2001; 2001JP-00374764.
XX PR 07-DEC-2001; 2001JP-00374764.
XX PA (TOJO ) TOYO KOHAN CO LTD.
XX DR WPI; 2003-819164/77.
XX PT Solid support body comprising crystal resonator on which a surface
XX PT treatment layer is formed, and a substrate whose surface treatment layer
XX PT is chemically modified, useful as biosensor.
XX PS Disclosure; SEQ ID NO 1; 7pp; Japanese.
XX CC The invention relates to a novel solid support body comprising a crystal
XX CC resonator on which a surface treatment layer is formed. The biosensor is
XX CC useful for analysing biological samples e.g., gene, a protein, and a
XX CC peptide, and for analysing bioactive substances. Preferably, the
XX CC biosensor is useful for analysing base sequences by carrying out
XX CC hybridisation. The present sequence is used in the exemplification of the
XX CC invention.
XX SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
```

Query Match 0.6%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 6 TTTT TTTT TTTT TTTT TTTT TTTT 23

RESULT 1572  
ADC75073/c  
ID ADC75073 standard; DNA; 24 BP.  
XX  
AC ADC75073;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Biosensor related oligonucleotide of the invention SEQ ID NO:1.  
XX  
KW ss; biosensor; hybridisation.  
XX  
OS Synthetic.  
XX  
PN JP2003172737-A.  
XX  
PD 20-JUN-2003.  
XX  
PF 07-DEC-2001; 2001JP-00374764.  
XX  
PR 07-DEC-2001; 2001JP-00374764.  
XX  
PA (TOJO ) TOYO KOHAN CO LTD.  
XX  
DR WPI; 2003-819164/77.  
XX  
PT Solid support body comprising crystal resonator on which a surface  
PT treatment layer is formed, and a substrate whose surface treatment layer  
PT is chemically modified, useful as biosensor.  
XX  
PS Disclosure; SEQ ID NO 1; 7pp; Japanese.  
XX  
CC The invention relates to a novel solid support body comprising a crystal  
CC resonator on which a surface treatment layer is formed. The biosensor is  
CC useful for analysing biological samples e.g., gene, a protein, and a  
CC peptide, and for analysing bioactive substances. Preferably, the  
CC biosensor is useful for analysing base sequences by carrying out  
CC hybridisation. The present sequence is used in the exemplification of the  
CC invention.  
XX  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 23 AAAAAA AAAAAA AAAAAA 6

RESULT 1573  
AAA47833/c  
ID AAA47833 standard; DNA; 25 BP.  
XX  
AC AAA47833;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Adapter sequence for 3' end of lectin cDNA.  
XX  
KW Lectin; mannose; sugar; transgenic plant; crop protection; resistance;  
KW bacteria; virus; fungus; insect; targeting; neutrophil glycoprotein;

KW polymorphonuclear cell; blood typing; primer; ss.  
XX  
OS Hernandia moerenhoutiana.  
XX  
PN WO200044780-A1.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-AU0000039.  
XX  
PR 29-JAN-1999; 99AU-00008395.  
XX  
PA (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.  
XX  
PI Clark TR, Minchinton RM;  
XX  
DR WPI; 2000-532807/48.  
XX  
PT New polypeptide, capable of binding to mannose, isolated from the plant  
PT Hernandia is useful for the generation of transgenic plants which exhibit  
PT enhanced resistance to micro-organisms, fungi, viruses and insects.  
XX  
PS Example 8; Page 35; 63pp; English.  
XX  
CC The Hernandia lectin is capable of binding and/or interacting with  
CC mannose or a sugar chemically related to mannose. The genetic sequence  
CC encoding lectin can be used for the generation of transgenic plants which  
CC exhibit enhanced resistance to micro-organisms, fungi, viruses and  
CC insects. The lectin polypeptide is also useful for targeting neutrophil  
CC glycoproteins for diagnostic and therapeutic applications, including  
CC evaluating the nature of immune cells and can also be used in typing,  
CC e.g. blood group typing of polymorphonuclear cells  
XX  
SQ Sequence 25 BP; 1 A; 3 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2803  
Db 25 AAAAAA AAAAAA AAAAAA 8

RESULT 1574  
ABK87633  
ID ABK87633 standard; DNA; 25 BP.  
XX  
AC ABK87633;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE BamT15G PCR primer.  
XX  
KW Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;  
KW rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;  
KW viral disease; inflammatory colitis; bronchitis; skin disease; primer.  
XX  
OS Unidentified.  
XX  
PN WO200251999-A1.  
XX  
PD 04-JUL-2002.  
XX  
PF 21-DEC-2001; 2001WO-JP011293.  
XX  
PR 21-DEC-2000; 2000JP-00388739.  
XX  
PA (MOCH ) MOCHIDA PHARM CO LTD.  
PA (KAZU-) KAZUSA DNA RES INST.  
XX  
PI Ohara O, Nagase T, Negishi T, Mizushima S, Furusako S;  
XX



AAD333507  
ID AAD333507 standard; DNA; 25 BP.  
XX  
AC AAD333507;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS11-25-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
SQ Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibrations of labeled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18  
RESULT 1578  
AAD333507/c  
ID AAD333507 standard; DNA; 25 BP.  
XX  
AC AAD333507;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS11-25-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX

XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
PT Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibrations of labeled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A) normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTTTT 1  
RESULT 1579  
AAD12516/c  
ID AAD12516 standard; DNA; 26 BP.  
XX  
AC AAD12516;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Thuja sp. pinoresinol/lariciresinol reductase cDNA cloning linker primer.  
XX  
KW Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity; lignan biosynthetic pathway; secoisolariciresinol; western red cedar; PCR primer; ss.  
XX  
OS Thuja plicata.  
XX  
PN WO200149833-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 22-DEC-2000; 2000WO-US035265.  
XX  
PR 30-DEC-1999; 99US-00475316.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Lewis NG, Davin LB, Dinkova-Kostova AT, Fujita M, Gang DR;  
PI Ford JD, Sarkanen S;  
XX  
DR WPI; 2001-465260/50.  
XX  
PT Dirigent and/or pinoresinol/lariciresinol reductase proteins useful for producing optically-pure lignans.  
XX  
PS Example 14; Page 56; 183pp; English.  
XX



CC The present invention relates to an isolated dirigent and/or pinorensinol  
CC /lariciresinol reductase protein from a lignan biosynthetic pathway.  
CC Dirigent and/or pinorensinol/lariciresinol reductase protein and the  
CC nucleic acids that encode it may be expressed either in vivo or in vitro  
CC to produce enzymes involved in the biosynthesis of lignans. The 78-kD  
CC dirigent protein confers stereospecificity in 8,8'-linked lignan  
CC formation and binds to and orients coniferyl alcohol-derived free  
CC radicals, which then under go stereospecific coupling to form (+)-  
CC pinorensinol. Pinorensinol/lariciresinol reductase catalyses the conversion  
CC of pinorensinol to lariciresinol and then to secoisolariciresinol. The  
CC present sequence is 3' linker PCR primer, XhoI-poly(DT) used in the  
CC cloning of Thuja plicata pinorensinol/ lariciresinol reductase cDNA  
XX  
SQ Sequence 26 BP; 1 A; 2 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1580  
AAV35002/c  
ID AAV35002 standard; DNA; 26 BP.  
XX  
AC AAV35002;  
XX  
DT 27-AUG-1998 (first entry)  
XX  
DE Human endothelin-beta 1 receptor PCR primer Vet119.  
XX  
KW Endothelin beta-1 receptor; ETB-1; screening; signal transduction;  
KW agonist; antagonist; vasoconstrictor; vasopressor; cardiogenic shock;  
KW pulmonary hypertension; acute myocardial infarct; uraemia; vasculitis;  
KW Crohn's disease; ulcerative colitis; sepsis; congestive heart failure;  
KW coronary spasm; cyclosporin nephrotoxicity; toxemia; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5773223-A.  
XX  
PD 30-JUN-1998.  
XX  
PF 02-SEP-1993; 93US-00117361.  
XX  
PR 02-SEP-1993; 93US-00117361.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Shyamala V, Olson PT;  
XX  
DR WPI; 1998-386992/33.  
XX  
PT Screening for modulators of the endothelin B1 receptor - by measuring  
PT effect on signal transduction in cells engineered to express the  
PT receptor, potentially useful as agonists and antagonists of endothelin.  
XX  
PS Example 1; Col 18; 23pp; English.  
XX  
CC AAV35002-V35021 are primers used to amplify and isolate a novel human  
CC endothelin-beta1 receptor (ETB-1) which corresponds to a decapeptide  
CC insert. This sequence is used in a method involving the screening of  
CC compounds for their ability to bind to endothelin B1 (ETB1) receptor  
CC polypeptide and to modulate its signal transduction activity by applying  
CC test compound to host cells transformed with DNA encoding ETB-1 and  
CC optionally lysing the cells and then measuring signal transduction  
CC activity. The method is used to identify agonists and antagonists of  
CC endothelin (ET), a known vasoconstrictor/vasopressor agent, associated  
CC with cardiogenic shock, pulmonary hypertension, acute myocardial infarct,

CC uraemia, Crohn's disease, ulcerative colitis, sepsis, congestive heart  
CC failure, coronary spasm, cyclosporin nephrotoxicity, vasculitis and  
CC toxemia in pregnancy, and is also present at elevated levels after  
CC orthotopic liver transplantation and major abdominal surgery  
XX  
SQ Sequence 26 BP; 3 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1581  
AAA88688/c  
ID AAA88688 standard; DNA; 26 BP.  
XX  
AC AAA88688;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
DE Oligo-dT-XhoI primer.  
XX  
KW Sweetgum; angiosperm; cytochrome P450-1; conifer; loblolly pine;  
KW transgenic plant; lignin; paper; pulping; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200058489-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 24-MAR-2000; 2000WO-US008083.  
XX  
PR 26-MAR-1999; 99US-00277248.  
XX  
PA (INTO ) INT PAPER CO.  
XX  
PI Chiang VL, Carraway DT;  
XX  
DR WPI; 2000-647240/62.  
XX  
PT Use of angiosperm coniferyl aldehyde 5-hydroxylase which catalyzes 5-  
PT hydroxylation of coniferyl aldehyde, for modifying lignin biosynthesis in  
PT gymnosperms, involves expressing the enzyme in a gymnosperm plant.  
XX  
PS Example 3; Page 23; 123pp; English.  
XX  
CC The present sequence is that of an oligo-dT primer including a 5' XboI  
CC site. The primer was used with a gene-specific primer to amplify sweetgum  
CC cytochrome P450-1 cDNA (see AAA88688). An aim of the invention is to  
CC identify, sequence and clone specific genes such as P450-1 from an  
CC angiosperm that are involved in production of syringyl lignin, and to  
CC then introduce such genes into the genome of a gymnosperm, such as  
CC loblolly pine, to induce production of syringyl lignin and thereby  
CC provide enhanced pulpability to the wood structure  
XX  
SQ Sequence 26 BP; 2 A; 1 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 26 AAAAAAAAAAAAAAAAAA 9

RESULT 1582  
AAC93128/c

ID: AAC931128 standard; DNA; 26 BP.  
XX  
AC AAC931128;  
XX  
DT 21-MAR-2001 (first entry)  
XX  
DE Stephanian tetrandra S. moore RNA reverse transcriptase primer NotI-dt.  
XX  
KW Stephanian tetrandra S. Moore; IL-6; interleukin-6; hepatotropic;  
KW antiinflammatory; hepatocirrhosis; hepatitis; alcoholism; primer; ss.  
XX  
OS Unidentified.  
XX  
PN US6162437-A.  
XX  
PD 19-DEC-2000.  
XX  
PF 25-NOV-1997; 97US-00978321.  
XX  
PR 05-JUN-1995; 95WO-KR000073.  
XX  
XX 06-DEC-1996; 96US-00750462.  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
XX  
PI Lee J, Kim Y, Kang H, Pyun K, Choi I;  
XX  
DR WPI; 2001-146043/15.  
XX  
PT Treatment of hepatocirrhosis comprises administering an extract of the  
PT root of Stephanian tetrandra in an amount effective to inhibit production  
PT of interleukin-6.  
XX  
PS Example 4; Col 9; 27pp; English.  
XX  
CC The present sequence was used in an example to illustrate a method for  
CC treating hepatocirrhosis. The method comprises administering an extract  
CC of the root of Stephanian tetrandra in an amount effective to inhibit  
CC production of interleukin-6 (IL-6). Hepatocirrhosis is often associated  
CC with chronic hepatitis or chronic alcoholism  
XX  
SQ Sequence 26 BP; 0 A; 4 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 26 AAAAAAAAAAAAAAAAAA 9  
  
RESULT 1583  
AAQ47178  
ID AAQ47178 standard; DNA; 26 BP.  
XX  
AC AAQ47178;  
XX  
DT 25-MAR-2003 (revised)  
DT 25-JAN-1994 (first entry)  
XX  
DE MHC DR A intron binding oligomer Tcon.  
XX  
KW MHC; major histocompatibility complex; class II; control oligomers; DR A;  
KW transplantation; antigen; autoimmune disease; ss.  
XX  
OS Synthetic.  
XX  
PN WO9314769-A1.  
XX  
PD 05-AUG-1993.  
XX  
PF 29-JAN-1993; 93WO-US0000797.  
XX

PR 31-JAN-1992; 92US-00830427.  
PR 14-SEP-1992; 92US-00944868.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;  
XX  
DR WPI; 1993-258367/32.  
XX  
PT Depletion of transplantation antigens in donor cells - using anti-sense  
PT or triplex-forming oligonucleotide(s), used for treating auto-immune  
PT disease and in transplants.  
XX  
PS Example; Page 22; 71pp; English.  
XX  
CC The sequences given in AAQ47176-77 represent triplex forming oligo-  
CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR  
CC A structural gene at positions 851-876. The sequences given in AAQ47178-  
CC 80 represent control oligomers which contain base compositions similar to  
CC that around this DR A region but not containing the correct sequences. DR  
CC A is a transplantation antigen. Binding of this sequence to the DR A gene  
CC inhibits antigen production. This method may be used for treating  
CC individuals with autoimmune disease, characterised by dysfunctional  
CC expression of a transplantation antigen. It may also be used to produce  
CC cells which are more easily transplanted into a recipient. (Updated on 25  
CC -MAR-2003 to correct PN field.)  
XX  
SQ Sequence 26 BP; 0 A; 0 C; 4 G; 22 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 80.8%; Pred. No. 1.7e+03;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2159 TTTCTCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTTGTTTGT TTTT TTTT TTTT TTTT TTTT TTTT 26  
  
RESULT 1584  
AAZ25387  
ID AAZ25387 standard; DNA; 26 BP.  
XX  
AC AAZ25387;  
XX  
DT 16-DEC-1999 (first entry)  
XX  
DE Infectious pancreatic necrosis virus PCR primer #1.  
XX  
KW Infectious pancreatic necrosis virus; IPNV; strain West Buxton;  
KW strain SP; segment A; segment B; nonpathogenic; Birnaviridae family;  
KW infection; live attenuated vaccine; aquaculture industry; Rainbow trout;  
KW Brook trout; Atlantic salmon; PCR primer; ss.  
XX  
OS Synthetic.  
OS Infectious pancreatic necrosis virus.  
XX  
PN WO9950419-A2.  
XX  
PD 07-OCT-1999.  
XX  
PF 31-MAR-1999; 99WO-US004285.  
XX  
PR 31-MAR-1998; 98US-0080178P.  
XX  
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.  
XX  
PI Vakharia VN, Yao K;  
XX  
DR WPI; 1999-591321/50.  
XX  
PT Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,  
PT useful for producing attenuated virus for vaccines useful in the  
PT aquaculture industry.

XX PS Example 1; Page 21; 63pp; English.

XX CC A method has been developed for preparing nonpathogenic, infectious

CC pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA

CC containing the IPNV genome segments A and B where A is modified to

CC prevent expression of an arginine-rich non-structural (NS) protein; 2)

CC transcribing the cDNA to produce RNA; 3) incubating the host cells in a

CC culture medium; and 4) isolating live IPNV from the culture medium. The

CC method is useful to produce live nonpathogenic IPNV, useful to study

CC viral pathogenesis and for the production of live, nonpathogenic IPNV

CC vaccines, since it was demonstrated that the NS protein-deficient virus

CC could replicate but did not invoke a pathological response in hosts.

CC Combination vaccines may also be produced by combining the IPNV with

CC bacterial antigens (especially from gram negative bacteria e.g. Aeromonas

CC salmonicida) and/or antigens from aquatic viruses other than Birnaviruses

CC (the family to which IPNV belongs) e.g. infectious haematopoietic

CC necrosis virus. The method may also be used to generate a nonpathogenic

CC chimeric virus when the cDNA of segment A encodes epitopic determinants

CC from at least two different IPNV strains. IPNV causes a highly contagious

CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic

CC salmon (e.g. highly virulent strains can cause more than 90 % mortality

CC in hatchery stocks less than 4 months old and survivors can remain a

CC lifelong carriers and reservoirs of infection); IPNV is therefore a

CC pathogen of major economic importance to the aquaculture industry. The

CC present sequence represents an IPNV PCR primer used in an example from

CC the present invention

XX SQ Sequence 26 BP; 0 A; 6 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTT TTTT TTTT TTTT TTTT 2181

Db 9 CCTTTT TTTT TTTT TTTT TTTT 26

RESULT 1585

AAA91664/c

ID AAA91664 standard; RNA; 26 BP.

XX AAA91664;

AC AAA91664;

XX 03-JAN-2001 (first entry)

DT HCV(+)RNA oligonucleotide.

DE Hepatitis C virus; HCV; HCV RNA replication inhibitor; ribozyme;

XX antiviral; ss.

KW Hepatitis C virus.

OS US6107028-A.

XX 22-AUG-2000.

PD 15-MAY-1996; 96US-00648272.

XX 14-DEC-1994; 94US-00357508.

PR 07-JUN-1995; 95US-00476257.

PR 11-SEP-1995; 95US-00534220.

XX (UNIW ) UNIV WASHINGTON.

PA Lieber A, Kay MA;

XX WPI; 2000-578530/54.

DR Inhibiting hepatitis C viral RNA replication in an infected cell for

XX treating or preventing viral infection, comprises introducing ribozymes

PT specific for a minus strand of the viral 5' non-coding sequence.

PT

XX PS Example 2; Col 17; 28pp; English.

XX CC The present sequence is an oligonucleotide which was used for in solution

CC hybridisation to quantitate hepatitis C virus (HCV) RNA following

CC ribozyme expression. Ribozymes were identified that can specifically

CC cleave HCV RNA in a HCV 5' non-coding sequence, the capsid sequence, the

CC NS-5 sequence or any other conserved region of the hepatitis C RNA.

CC Ribozymes may be introduced into a cell infected with HCV in order to

CC inhibit HCV RNA replication or expression. Unlike prior art compositions

CC and methods, compositions comprising these ribozymes effectively reduce

CC and eradicate HCV from the infected cells and significantly impair the

CC ability of the virus to replicate, thus preventing further dissemination

CC of the disease. The composition is inherently specific for HCV and has

CC negligible toxicity

XX SQ Sequence 26 BP; 2 A; 5 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;

Best Local Similarity 80.8%; Pred. No. 1.7e+03;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 437 CACCAGCGCGCGCCGCCACAGCGAGCCA 462

Db 26 CACCAACCGTCGCCGCCACAGGAGGTCA 1

RESULT 1586

AAS01617/c

ID AAS01617 standard; DNA; 26 BP.

XX AAS01617;

AC AAS01617;

XX 18-JUL-2001 (first entry)

DT Human MINT31/CACNA1G region 6 bisulfite GM6 reverse PCR primer.

XX Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;

KW cellular proliferative disorder; colorectal cancer; age related disease;

KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;

KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;

KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';

KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;

KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;

KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;

KW chromosome 17; PCR primer; ss.

XX Homo sapiens.

OS WO200119845-A1.

XX 22-MAR-2001.

PD 14-SEP-2000; 2000WO-US025479.

XX 15-SEP-1999; 99US-00398522.

PR (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

PA Issa J;

XX WPI; 2001-244777/25.

DR New nucleic acid molecule for use as a marker for screening cancer,

XX comprises the coding region for a T-type calcium channel and regulatory

PT sequences associated with the channel.

PT Claim 21; Page 35; 125pp; English.

XX The present sequence for bisulfite GM6 reverse PCR primer is used to

CC study the methylation state of region 6 in human MINT31/T-type calcium

CC channel CACNA1G which map to chromosome 17. The methylation state of

CC specific regions within CpG islands associated with the CACNA1G gene

CC

XX PS Example 1; Page 21; 63pp; English.

XX CC A method has been developed for preparing nonpathogenic, infectious

CC pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA

CC containing the IPNV genome segments A and B where A is modified to

CC prevent expression of an arginine-rich non-structural (NS) protein; 2)

CC transcribing the cDNA to produce RNA; 3) incubating the host cells in a

CC culture medium; and 4) isolating live IPNV from the culture medium. The

CC method is useful to produce live nonpathogenic IPNV, useful to study

CC viral pathogenesis and for the production of live, nonpathogenic IPNV

CC vaccines, since it was demonstrated that the NS protein-deficient virus

CC could replicate but did not invoke a pathological response in hosts.

CC Combination vaccines may also be produced by combining the IPNV with

CC bacterial antigens (especially from gram negative bacteria e.g. Aeromonas

CC salmonicida) and/or antigens from aquatic viruses other than Birnaviruses

CC (the family to which IPNV belongs) e.g. infectious haematopoietic

CC necrosis virus. The method may also be used to generate a nonpathogenic

CC chimeric virus when the cDNA of segment A encodes epitopic determinants

CC from at least two different IPNV strains. IPNV causes a highly contagious

CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic

CC salmon (e.g. highly virulent strains can cause more than 90 % mortality

CC in hatchery stocks less than 4 months old and survivors can remain a

CC lifelong carriers and reservoirs of infection); IPNV is therefore a

CC pathogen of major economic importance to the aquaculture industry. The

CC present sequence represents an IPNV PCR primer used in an example from

CC the present invention

XX SQ Sequence 26 BP; 0 A; 6 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTT TTTT TTTT TTTT TTTT 2181

Db 9 CCTTTT TTTT TTTT TTTT TTTT 26

RESULT 1585

AAA91664/c

ID AAA91664 standard; RNA; 26 BP.

XX AAA91664;

AC AAA91664;

XX 03-JAN-2001 (first entry)

DT HCV(+)RNA oligonucleotide.

DE Hepatitis C virus; HCV; HCV RNA replication inhibitor; ribozyme;

XX antiviral; ss.

KW Hepatitis C virus.

OS US6107028-A.

XX 22-AUG-2000.

PD 15-MAY-1996; 96US-00648272.

XX 14-DEC-1994; 94US-00357508.

PR 07-JUN-1995; 95US-00476257.

PR 11-SEP-1995; 95US-00534220.

XX (UNIW ) UNIV WASHINGTON.

PA Lieber A, Kay MA;

XX WPI; 2000-578530/54.

DR Inhibiting hepatitis C viral RNA replication in an infected cell for

XX treating or preventing viral infection, comprises introducing ribozymes

PT specific for a minus strand of the viral 5' non-coding sequence.

PT

CC correlate with several cancerous phenotypes involving various tissue and  
CC cell types. Since aberrant methylation of normally unmethylated CpG  
CC islands is often observed in immortalised and transformed cells, CACNA1G  
CC is implicated in cellular proliferative disorders e.g. leukaemia,  
CC colorectal, lung, breast and other cancers. The nucleic acid coding for  
CC CACNA1G is useful as a marker for screening cancer and age related  
CC diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for  
CC amplification of a CpG-containing nucleic acid, where the primer  
CC hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can  
CC be used for detecting aberrant methylation. The CpG island sequences  
CC (AAS01677-AAS01692) are selected from genes encoding CACNA1G,  
CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2  
CC (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G  
CC HSPA6), RasGAP-related protein (IQGAP2), heat shock 70kD protein 6 (HSP70B';  
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor  
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;  
CC SDC4) or a MINT31 sequence  
XX

SQ Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 1587  
AAS01577/c  
ID AAS01577 standard; DNA; 26 BP.

XX AAS01577;

DT 18-JUL-2001 (first entry)

XX Human T-type calcium channel CACNA1G R6 3'-bisulfite PCR primer.

KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;  
KW cellular proliferative disorder; colorectal cancer; age related disease;  
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;  
KW chromosome 17; PCR primer; ss.

XX Homo sapiens.

XX WO200119845-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025479.

XX 15-SEP-1999; 99US-00398522.

XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Issa J;

XX WPI; 2001-244777/25.

XX New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.

XX Claim 21; Page 34; 125pp; English.

XX The present sequence for 3'-bisulfite PCR primer is used to study the

CC methylation state of region R6 in a novel human T-type calcium channel  
CC CACNA1G which maps to chromosome 17. The methylation state of specific  
CC regions within CpG islands associated with the CACNA1G gene correlate  
CC with several cancerous phenotypes involving various tissue and cell  
CC types. Since aberrant methylation of normally unmethylated CpG islands is  
CC often observed in immortalised and transformed cells, CACNA1G is  
CC implicated in cellular proliferative disorders e.g. leukaemia,  
CC colorectal, lung, breast and other cancers. The nucleic acid coding for  
CC CACNA1G is useful as a marker for screening cancer and age related  
CC diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for  
CC amplification of a CpG-containing nucleic acid, where the primer  
CC hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can  
CC be used for detecting aberrant methylation. The CpG island sequences  
CC (AAS01677-AAS01692) are selected from genes encoding CACNA1G,  
CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2  
CC (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G  
CC protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';  
CC HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-  
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor  
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;  
CC SDC4) or a MINT31 sequence  
XX

SQ Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 1588  
AAS01670  
ID AAS01670 standard; DNA; 26 BP.

AC AAS01670;

XX 18-JUL-2001 (first entry)

XX Human MINT31/CACNA1G region 6 reverse target sequence for bisulfite PCR.

KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;  
KW cellular proliferative disorder; colorectal cancer; age related disease;  
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;  
KW chromosome 17; ds.

XX Homo sapiens.

XX WO200119845-A1.

XX 22-MAR-2001.

XX 14-SEP-2000; 2000WO-US025479.

XX 15-SEP-1999; 99US-00398522.

XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Issa J;

XX WPI; 2001-244777/25.

XX New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.



CC conditions to enzymatically generate sub-population of NAs, where each  
CC gene specific primer has a sequence complementary to a distinct mRNA, and  
CC each labeled NA is generated using a single gene specific primer. The  
CC method is useful for producing a sub-population of labeled NAs which is  
CC useful for analysing the differences in the RNA profiles between several  
CC different physiological sources, where the method comprises producing  
CC subpopulation of labeled NAs for the different physiological sources,  
CC comprising the populations for each physiological source to identify  
CC differences in the population, where the comparison is preferably  
CC performed by hybridising the labeled NAs for each of the distinct  
CC physiological sources to an array of probe NAs stably associated with the  
CC surface of a substrate to produce a hybridisation pattern for each of the  
CC sources, and comparing the patterns for each of the sources, where  
CC differential gene expression assays are utilised in differential  
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal  
CC tissue, or different tissue or subtype types. The present sequence is a  
CC human gene specific PCR primer used in the method of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at <http://wipo.seqdata.uspto.gov/sequence.html?DocID=6352829B1>  
XX  
SQ Sequence 26 BP; 5 A; 8 C; 7 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 80.8%; Pred. No. 1.7e+03;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1093 AGCTGTTTCATTGGCTAGGGACTTTG 1118  
Db 1 AGCTGTTTCATTGGCTAGGGACTTTG 26  
  
RESULT 1590  
AAD33509  
ID AAD33509 standard; DNA; 26 BP.  
XX  
AC AAD33509;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PSI0-26-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations of labeled  
CC generate signals proportional to the total concentrations of labeled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned

PS Claim 20; Page 36; 125pp; English.  
XX  
CC The present sequence for human MINT31/T-type calcium channel CACNA1G  
CC region 6 reverse target sequence is used to study the methylation state  
CC of region 6 in MINT31/CACNA1G which map to chromosome 17. The methylation  
CC state of specific regions within CpG islands associated with the CACNA1G  
CC gene correlate with several cancerous phenotypes involving various tissue  
CC and cell types. Since aberrant methylation of normally unmethylated CpG  
CC islands is often observed in immortalised and transformed cells, CACNA1G  
CC is implicated in cellular proliferative disorders e.g. leukaemia,  
CC colorectal, lung, breast and other cancers. The nucleic acid coding for  
CC CACNA1G is useful as a marker for screening cancer and age related  
CC diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for  
CC amplification of a CpG-containing nucleic acid, where the primer  
CC hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can  
CC be used for detecting aberrant methylation. The CpG island sequences  
CC (AAS01677-AAS01692) are selected from genes encoding CACNA1G,  
CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2  
CC (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G  
CC protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B);  
CC HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-  
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor  
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;  
CC SDC4) or a MINT31 sequence  
XX  
SQ Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 7 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 26  
  
RESULT 1589  
ABK66615  
ID ABK66615 standard; DNA; 26 BP.  
XX  
AC ABK66615;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Human gene specific PCR primer #703.  
XX  
KW Primer; ss; DNA microarray; differential expression analysis; human.  
XX  
OS Homo sapiens.  
XX  
PN US6352829-B1.  
XX  
PD 05-MAR-2002.  
XX  
PF 05-JAN-1999; 99US-00225928.  
XX  
PR 21-MAY-1997; 97US-00859998.  
XX  
PA (CLON-) CLONTECH LAB INC.  
XX  
PI Chenchik A, Jokhadze G, Bibilashvili R;  
XX  
DR WPI; 2002-314699/35.  
XX  
PT Producing sub-population of labeled nucleic acids, useful for analyzing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers.  
XX  
PS Example 3; SEQ ID NO 703; 11pp; English.  
XX  
CC The invention relates to producing a sub-population of labeled nucleic  
CC acids (NAs) comprising contacting a NA sample from a physiological  
CC source, with a pool of 50 distinct gene specific primers under suitable

CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 26 BP; 20 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1591  
AAD33509/c  
ID AAD33509 standard; DNA; 26 BP.  
XX  
AC AAD33509;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS10-26-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-2828B6/33.  
XX  
PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
XX molecules, and molecular arrays incorporating sets of calibration probes.  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 26 BP; 20 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTTTT 1  
  
RESULT 1592  
AAX15434/c  
ID AAX15434 standard; DNA; 27 BP.  
XX

AC AAX15434;  
XX  
DT 07-MAY-1999 (first entry)  
XX  
DE PCR primer used to amplify DNA encoding trehalose phosphorylase.  
XX  
KW Trehalose phosphorylase; trehalose; D-glucose;  
KW alpha-D-glucose-1-phosphate; PCR primer; ss.  
XX  
OS Synthetic.  
OS Grifola frondosa.  
XX  
PN WO9844116-A1.  
XX  
PD 08-OCT-1998.  
XX  
PF 30-MAR-1998; 98WO-JP001423.  
XX  
PR 31-MAR-1997; 97JP-00098173.  
XX  
PA (KURE ) KUREHA CHEM IND CO LTD.  
XX  
PI Horinouchi S, Saitoh K, Takahashi E;  
XX  
DR WPI; 1998-557113/47.  
XX  
PT Trehalose phosphorylase from Grifola frondosa and gene encoding it - for  
XX producing enzyme for industrial scale production of trehalose.  
PS Example 5; Page 25; 52pp; Japanese.  
XX  
CC The present PCR primer was used to amplify DNA encoding a trehalose  
CC phosphorylase enzyme, and is derived from Grifola frondosa. Vectors and  
CC cells containing the nucleic acid sequence can be used in the large scale  
CC production of trehalose phosphorylase for industrial-scale manufacture of  
CC trehalose from D-glucose and alpha-D-glucose-1-phosphate. Trehalose is  
CC used in the foodstuff and drug industries  
XX  
SQ Sequence 27 BP; 1 A; 3 C; 4 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 27 AAAAAAAAAAAAAAAAAA 10  
  
RESULT 1593  
AAT94842/c  
ID AAT94842 standard; DNA; 27 BP.  
XX  
AC AAT94842;  
XX  
DT 27-MAR-1998 (first entry)  
XX  
DE Human ESF I 3' PCR primer.  
XX  
KW Endometrial specific steroid-binding factor I; ESF I; human;  
KW inflammation; asthma; rhinitis; cystic fibrosis; airway disease;  
KW neoplasia; atopy; therapy; diagnosis; primer; PCR; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9734997-A1.  
XX  
PD 25-SEP-1997.  
XX  
PF 21-MAR-1996; 96WO-US003857.  
XX  
PR 21-MAR-1996; 96WO-US003857.

XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ni J, Yu G, Gentz RL;  
XX WPI; 1997-480206/44.  
XX Human endometrial specific steroid-binding factor I, II and III - used to  
PT treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,  
PT neoplasia, atopy etc.  
XX Example 2; Page 52-53; 92pp; English.  
XX This oligonucleotide contains an Asp718 site followed by 18 nucleotides  
CC complementary to a polyA tail. It was used with a 5' primer (see  
CC AAT94839), containing a BamHI site and 20 bases of the human endometrial  
CC specific steroid binding factor I (ESF I) coding sequence (see AAT94830),  
CC to amplify ESF I cDNA deposited as ATCC 97401. The PCR product was  
CC incorporated into baculovirus vector pRG1 and recombinant ESF I was  
CC expressed in Spodoptera frugiperda Sf9 cells. Human ESF I (see AAW35802)  
CC can be used to treat inflammation, asthma, rhinitis, cystic fibrosis,  
CC airway disease, neoplasia, atopy etc  
XX  
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAA 2803  
Db 27 AAAAAAAAAAAAAAAA 10  
RESULT 1594  
AAAS9740/C  
ID AAAS9740 standard; DNA; 27 BP.  
XX  
AC AAAS9740;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE PCR primer for hESF I cDNA sequence amplification.  
XX Endometrial specific steroid-binding factor; human; hESF; inflammation;  
KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;  
KW eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6066724-A.  
XX  
PD 23-MAY-2000.  
XX  
PF 21-MAR-1997; 97US-00821451.  
XX  
PR 21-MAR-1996; 96US-0014724P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Yu G, Gentz R, Ni J;  
XX WPI; 2000-375600/32.  
XX  
XX Novel gene encoding human endometrial specific steroid-binding factor I,  
PT II and III which is useful for treating asthma, rhinitis, cystic  
PT fibrosis, airway disease and neoplasia.  
XX  
PS Example 2; Col 34; 36pp; English.  
XX  
CC This invention relates to nucleic acid molecules encoding portions of the  
CC human endometrial specific steroid-binding factors I, II, and III. Also

CC included in the invention are hESF I, II, and III polypeptide sequences.  
CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,  
CC antiallergic, and cytostatic properties. The polynucleotides are used in  
CC gene therapy to express hESF I, II and III polypeptides in vivo to treat  
CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way  
CC disease, neoplasia and atopy. The polynucleotides are also used to  
CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce  
CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis  
CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid  
CC levels in the human uterus and control the growth of endometrial cells.  
CC The polynucleotides are also useful for detecting complementary  
CC polynucleotides as a diagnostic reagent. The hESF I, II and III  
CC polynucleotides are used to detect complementary polynucleotides such as  
CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III  
CC associated with a dysfunction will provide a diagnostic tool that can  
CC define diagnosis of a disease or susceptibility to a disease which  
CC results from under-expression, over-expression or altered expression of  
CC hESF I, II and III e.g. a susceptibility to inherited asthma and  
CC endometrial cancer. They are also useful for chromosome identification.  
CC The present sequence represents a PCR primer used to amplify the hESF I  
CC cDNA sequence  
XX  
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAA 2803  
Db 27 AAAAAAAAAAAAAAAA 10  
RESULT 1595  
AAF25224/C  
ID AAF25224 standard; DNA; 27 BP.  
XX  
AC AAF25224;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE 3' primer for an endometrial specific steroid binding factor I cDNA.  
XX Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;  
KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;  
KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;  
KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US6174992-B1.  
XX  
PD 16-JAN-2001.  
XX  
PF 08-MAR-1999; 99US-00263810.  
XX  
PR 21-MAR-1996; 96US-0014724P.  
PR 21-MAR-1997; 97US-00821451.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ni J, Yu G, Gentz R;  
XX WPI; 2001-158477/16.  
XX  
XX New human endometrial specific steroid binding factors, useful for  
PT treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,  
PT airway disease, neoplasia and atopy.  
XX  
PS Example 2; Col 33; 36pp; English.  
XX  
CC PCR primers AAF25221 and AAF25224 were used to amplify cDNA encoding a

CC human endometrial specific steroid binding factor (hESF). The  
CC specification describes hESFI, hESFII, and hESFIII. hESFI, II and III  
CC polypeptides, and polynucleotides encoding them are useful for treating  
CC and preventing inflammation, asthma, rhinitis, cystic fibrosis, airway  
CC disease, neoplasia and atopy, inhibiting phospholipase A2 activity,  
CC binding polychlorinated biphenyls, reducing foreign protein antigenicity,  
CC inhibiting monocyte and neutrophil chemotaxis and phagocytosis,  
CC inhibiting platelet aggregation, regulating eicosanoid levels in the  
CC human uterus, and for controlling the growth of endometrial cells. hESF  
CC polypeptides and nucleotides are also useful for research, biological,  
CC clinical or therapeutic purposes  
XX

SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 27 AAAAAAAAAAAAAAAAAA 10

RESULT 1596  
ABL41793/C

ID ABL41793 standard; DNA; 27 BP.

XX ABL41793;

DT 29-MAY-2002 (first entry)

DE Primer for human endometrial specific steroid-binding factor I cDNA.

XX Human; endometrial specific steroid-binding factor; ESF;

KW prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma;  
KW PCR primer; ss.

XX Homo sapiens.

OS Synthetic.

XX US6338948-B1.

XX 15-JAN-2002.

PF 30-MAY-2000; 2000US-00583169.

XX 21-MAR-1996; 96US-0014724P.

PR 21-MAR-1997; 97US-00821451.

PR 08-MAR-1999; 99US-00263810.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz R;

XX WPI; 2002-215019/27.

XX New antibody specific for human endometrial specific steroid-binding  
PT factor (hESF) III, useful for detecting hESF III protein in biological  
PT sample and to isolate or identify clones expressing the protein.

PS Example 2; Col 33; 36pp; English.

XX PCR primers ABL41790 and ABL41793 were used to amplify cDNA encoding  
CC human endometrial specific steroid-binding factor (hESF) I. The primers  
CC were used to introduce restriction sites for cloning. The full length  
CC hESF I protein has a molecular weight of 9.8 kDa. The protein has  
CC homology to rat prostatic steroid-binding protein. Antibodies which bind  
CC hESF proteins, such as hESF I, hESF II, and hESF III are useful for  
CC isolating or to identify clones expressing the polypeptides or to purify  
CC the polypeptides by affinity chromatography. Agonists and antagonists of  
CC hESF proteins are useful for treating and/or preventing susceptibility to  
CC asthma  
XX

SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 27 AAAAAAAAAAAAAAAAAA 10

RESULT 1597  
ABX14927/C

ID ABX14927 standard; DNA; 27 BP.

XX ABX14927;

DT 08-APR-2003 (first entry)

DE hESF I amplifying 3' PCR primer for expression using baculovirus.

XX Human; PCR; ss; endometrial specific steroid-binding factor; hESF;  
KW Clara cell 10 kDa; CC10; secretory protein; asthma; primer;  
KW prostatic steroid-binding protein; hormone; lung; uterus; gene therapy.

XX Homo sapiens.

OS Synthetic.

XX US2002151012-A1.

PD 17-OCT-2002.

XX 06-NOV-2001; 2001US-00985911.

PR 21-MAR-1996; 96US-0014724P.

PR 21-MAR-1997; 97US-00821451.

PR 08-MAR-1999; 99US-00263810.

PR 30-MAY-2000; 2000US-00583169.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Yu G, Gentz R;

XX WPI; 2003-182506/18.

XX New human endometrial specific steroid-binding factor (hESF) proteins and  
PT genes, useful for treating or diagnosing a disease or susceptibility to a  
PT disease, particularly asthma.

PS Example 2; Page 18; 37pp; English.

XX The invention discloses isolated polypeptides, which comprise human  
CC endometrial specific steroid-binding factors I, II and III (hESF I, II  
CC and III), and the nucleic acids encoding them. The hESF polypeptide has  
CC homologues to mammalian Clara cell 10 kDa (CC10) secretory protein and  
CC rat prostatic steroid-binding protein which are factors which modulate or  
CC mediate the action of hormones involved in the regulation of functions of  
CC the lung and uterus. The nucleic acids and polypeptides can be used to  
CC identify compounds that bind to and inhibit activation, raise antibodies  
CC or develop antagonists against the isolated hESF polypeptide. The  
CC polypeptides or polynucleotides are useful for treating a patient having  
CC a need of hESF I, hESF II, hESF III or for treating a patient having a  
CC need to inhibit hESF. The polypeptide is administered by providing to the  
CC patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In  
CC particular, the disease is asthma. The hESF polypeptides or  
CC polynucleotides are also useful for diagnosing a disease or a  
CC susceptibility to the disease. The sequence presented is the 3' PCR  
CC primer which was used to amplify hESF I cDNA for expression using  
XX baculovirus expression system T

SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 27;





DT 18-JUN-1999 (first entry)  
XX Deletion sequence oligonucleotide 25.  
DE  
XX  
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;  
KW probe; cellular adhesion modulator; cellular proliferation modulator;  
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;  
KW HIV; primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9911820-A1.  
PN  
XX  
XX 11-MAR-1999.  
PD  
XX  
XX  
XX 01-SEP-1998; 98WO-US018084.  
PF  
XX  
XX 02-SEP-1997; 97US-00923771.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
XX Chen D, Srivatsa GS;  
PI  
XX  
XX WPI; 1999-205198/17.  
DR  
XX  
XX New compositions comprising sensor arrays made up of unique probe  
PT oligonucleotides - useful for characterizing a sample of target deletion  
PT oligonucleotides.  
XX  
XX Example 1; Page 98; 163pp; English.  
PS  
XX  
CC This invention describes a novel composition comprising a number of  
CC sensor arrays, where each array comprises a unique probe oligonucleotide,  
CC which is the reverse complement of part of a unique target  
CC oligonucleotide present in a mixture of target deletion sequence  
CC oligonucleotides. The compositions form a method for characterizing a  
CC sample of target deletion oligonucleotides which are labelled and  
CC hybridize with the probe oligonucleotides of the sensor arrays. Such  
CC oligonucleotides and their targets are represented in AAX23548-X23709.  
CC Oligonucleotides characterized by the method form pharmaceutical  
CC compositions that are useful for modulating cellular adhesion or  
CC proliferation, and being active against a eukaryotic pathogen, a human  
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human  
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory  
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable  
CC characterization of deletion sequence oligonucleotides having related,  
CC but different nucleobase sequences, and quantification of different  
CC species of deletion sequence ("target") oligonucleotides in a mixture.  
CC Also, if the specificity of the oligonucleotide's nucleobase sequence for  
CC its reverse complement is not modified, the method may be performed using  
CC oligodeoxynucleotides  
XX  
SQ Sequence 27 BP; 7 A; 2 C; 3 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 80.8%; Pred. No. 1.9e+03;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2776 GTTAGAATTGAAAAAAAAAAAAAAAAAAAA 2801  
Db  
26 GTTGTCTTCTTAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1601  
AAD33510  
ID AAD33510 standard; DNA; 27 BP.  
XX  
AC AAD33510;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS9-27-0001 probe for calibration of molecular array data.  
XX

KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
XX EP1186673-A2.  
PN  
XX  
PD 13-MAR-2002.  
XX  
XX 10-SEP-2001; 2001EP-00307665.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659173.  
PR  
XX  
XX (AGIL-) AGILENT TECHNOLOGIES INC.  
PA  
XX  
XX Wobler PK, Delenstarr GC;  
PI  
XX  
XX WPI; 2002-282886/33.  
DR  
XX  
XX Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
XX Disclosure; Page 14; 32pp; English.  
PS  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibration probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 27 BP; 21 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18  
RESULT 1602  
AAD33510/c  
ID AAD33510 standard; DNA; 27 BP.  
XX  
AC AAD33510;  
XX  
XX 01-JUL-2002 (first entry)  
DT  
XX  
DE T7T18Apad\_PS9-27-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
XX Unidentified.  
OS  
XX  
XX EP1186673-A2.  
PN  
XX  
XX 13-MAR-2002.  
PD  
XX  
XX 10-SEP-2001; 2001EP-00307665.  
PF  
XX  
XX 11-SEP-2000; 2000US-00659173.  
PR  
XX  
XX (AGIL-) AGILENT TECHNOLOGIES INC.  
PA  
XX  
XX Wobler PK, Delenstarr GC;  
PI  
XX  
XX WPI; 2002-282886/33.  
DR  
XX

PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations of probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 27 BP; 21 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2183  
Db 18 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 1603  
ACC83476/c  
ID ACC83476 standard; DNA; 28 BP.  
XX  
AC ACC83476;  
XX  
DT 08-SEP-2003 (first entry)  
XX  
DE Oligo dT primer.  
XX  
KW Rat; Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic;  
KW antirheumatic; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
FN WO2003044159-A2.  
XX  
PD 30-MAY-2003.  
XX  
PF 20-NOV-2002; 2002WO-IL000925.  
XX  
PR 20-NOV-2001; 2001US-0331626P.  
XX  
PA (PROC-) PROCHON BIOTECH LTD.  
XX  
PI Yayon A, Blumenstein S, Harari D;  
XX  
DR WPI; 2003-457599/43.  
XX  
PT New chondrocyte-derived zinc finger polypeptides and encoding  
PT polynucleotides, useful for detecting, diagnosing and treating Czf-1  
PT protein-related diseases, such as osteoarthritis and rheumatoid  
PT arthritis.  
XX  
PS Example 1; Page 27; 64pp; English.  
XX  
CC The present sequence is that of an oligo-dT primer, which was used in the  
CC PCR amplification of cDNA (see ACC83474) encoding a novel rat zinc finger  
CC protein, designated Czf-1 (see ABR42912). Czf-1 is expressed in  
CC osteoblasts and chondrocytes, and serves as a marker for osteoarthritis.  
CC Czf-1 polynucleotides, polypeptides and antibodies can be used in the  
CC characterisation, diagnosis and treatment of fibroblast growth factor  
CC receptor-related and skeletal diseases and disorders, such as  
CC osteoarthritis, rheumatoid arthritis, and cartilage-related diseases  
XX  
SQ Sequence 28 BP; 2 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 28 AAAAAAAAAAAAAAAAAA 11

RESULT 1604  
ABZ59816/c  
ID ABZ59816 standard; RNA; 28 BP.  
XX  
AC ABZ59816;  
XX  
DT 01-APR-2003 (first entry)  
XX  
DE Potato gene PCR primer DDT18AN.  
XX  
KW Potato; plant; mitochondrial carrier protein; elongation factor EF-2;  
KW transferrin binding protein; receptor-like protein kinase; helicase;  
KW non-long terminal repeat retroelement reverse transcriptase;  
KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN DE10114063-A1.  
XX  
PD 10-OCT-2002.  
XX  
PF 22-MAR-2001; 2001DE-01014063.  
XX  
PR 22-MAR-2001; 2001DE-01014063.  
XX  
PA (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.  
XX  
PI Buelow L, Tschardtke M, Haussuehl K;  
XX  
DR WPI; 2003-041808/04.  
XX  
PT New DNA sequences from potato, useful for producing plants with altered  
PT properties, e.g. tolerance of flooding, also related proteins, antibodies  
PT and inhibitory sequences.  
XX  
PS Example 1; Page 8; 26pp; German.  
XX  
CC The invention relates to DNA sequences (I) that encode six specific plant  
CC proteins: (i) a protein (ABP60425) with mitochondrial carrier protein  
CC activity (IIa); (ii) a protein (ABP60426) with transferrin binding  
CC protein activity (IIb); (iii) a protein (ABP60427) with receptor-like  
CC protein kinase activity (IIC); (iv) a protein (ABP60428) with elongation  
CC factor EF-2 activity (IID); (v) a protein (ABP60429) with non-long  
CC terminal repeat retroelement reverse transcriptase activity (IIE); or  
CC (vi) a protein (ABP60430) with helicase activity (IIF). (I), also related  
CC sequences, derived ribozymes and antisense sequences, expression vectors,  
CC encoded proteins and antibodies against the proteins, are used to produce  
CC plants with altered properties, including tolerance of overwatering. The  
CC antibodies are also used for isolation of the proteins and in  
CC immunoassays. Also (I) or their primer or probe fragments are used to  
CC screen for terminators and constitutively, aerobically or anaerobically  
CC inducible plant promoters, specifically for use in potatoes and the  
CC sequence that encodes (IID) is used to alter the translation profile in  
CC plants. Since (I) are derived from potato, their promoters and  
CC terminators provide high level transgene expression in potato, with  
CC improved tissue specificity and inducibility, and can also be used to  
CC control endogenous genes. The present sequence is that of a PCR primer  
CC used in the first strand synthesis of cDNAs derived from Potato  
XX  
SQ Sequence 28 BP; 3 A; 2 C; 2 G; 20 T; 0 U; 1 Other;

Query Match 0.6%; Score 18; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2e+03;







Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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QY	2785	GA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	2802
Db	28	GA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	11

  

RESULT 1607										
ID	AAV61015	standard; DNA; 28 BP.								
XX	AAV61015;									
AC										
XX										
DT	03-DEC-1998	(first entry)								
XX										
DE	HS/HIP reverse transcriptase PCR primer #4.									
XX										
KW	Human; heparan sulfate/heparin interacting protein; HIP; diagnosis;									
KW	blood coagulation; antithrombin-3; bleeding; wound; PCR primer; ss.									
XX										
OS	Synthetic.									
OS	Homo sapiens.									
XX										
PN	WO9838214-A1.									
XX										
PD	03-SEP-1998.									
XX										
PF	27-FEB-1998;	98WO-US003788.								
XX										
PR	28-FEB-1997;	97US-00810609.								
XX										
PA	(TEXA ) UNIV TEXAS A & M SYSTEM.									
XX										
PI	Carson DD, Hoeek M, Liu S;									
XX										
DR	WPI; 1998-495388/42.									
XX										
PT	Use of heparin sulphate/heparin interacting protein - for modulating									
PT	blood coagulation, e.g. for neutralising heparin, treating diseases									
PT	involving excessive bleeding or administration to wound sites.									
XX										
PS	Example 1; Page 78; 148pp; English.									
XX										
CC	A method has been developed for identifying a heparin (Hp) component that									
CC	binds to antithrombin-3 (AT-3). The method comprises: (a) contacting a Hp									
CC	sample suspected of containing a Hp component that binds to AT-3 with a									
CC	heparan sulphate (HS)/Hp interacting protein (HIP) to allow binding of									
CC	the Hp component; and (b) detecting the binding of the Hp component to									
CC	the HS/HIP. The present sequence represents a primer for reverse									
CC	transcriptase PCR of heparan sulfate/heparin interacting protein									
CC	(HS/HIP). Products from the present invention can be used for modulating									
CC	blood coagulation. They can be used for neutralising heparin, treating									
CC	diseases characterised by excessive bleeding or administration to wound									
CC	sites. The HS/HIPs can also be used for the production of antibodies and									
CC	in diagnostic applications									
XX										
SQ	Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;									

  

Query Match	0.6%;	Score 18;	DB 1;	Length 28;
Best Local Similarity	100.0%;	Pred. No. 2e+03;		
Matches	18;	Conservative	0;	Mismatches 0;
Indels				0;
Gaps				0;

  

QY	2786	AA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	2803
Db	28	AA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	11

  

RESULT 1608										
ID	AAZ61254/c	standard; DNA; 28 BP.								
XX	AAZ61254									
AC										
XX										

DE Single stranded DNA PCR primer SEQ ID NO:5.  
XX Single stranded DNA primer; PCR primer; amplification; ss.  
KW Synthetic.  
XX  
OS JP2001204472-A.  
XX  
PN 31-JUL-2001.  
XX  
PD 21-JAN-2000; 2000JP-00012535.  
XX  
PF 21-JAN-2000; 2000JP-00012535.  
XX  
PR (SUME ) SUMITOMO ELECTRIC IND CO.  
XX  
PA WPI; 2001-609513/70.  
XX  
DR New polynucleotide for the amplification of a one-side single-stranded  
XX DNA and the production of a double-stranded cDNA comprises a single-  
PT stranded DNA primer.  
PT  
PT  
XX Disclosure; Page 11; 13pp; Japanese.  
PS  
XX  
CC The present invention describes a single-stranded DNA primer comprising a  
CC single-stranded DNA having a dTn sequence, which hybridises with the  
CC polyA site of an mRNA at the 3'-terminal, and has a blocking group at the  
CC 5'-terminal in which the other part constitutes an adapter double-  
CC stranded DNA connected to the double-stranded cDNA. The terminal of the  
CC side of the DNA is not connected to the double-stranded cDNA, which  
CC consists of a base sequence having full homology to the single-stranded  
CC DNA corresponding to the 5'-terminal. A method is also described for the  
CC preparation of a double-stranded cDNA in which the above single-stranded  
CC DNA primer is hybridised with the polyA site of an mRNA and said single-  
CC stranded DNA primer is used as the primer to reverse-transcribe said mRNA  
CC and further it is converted to a double-stranded cDNA by a DNA  
CC polymerase. The primer is used for the uniform amplification of DNAs. The  
CC present sequence represents a PCR primer which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 28 BP; 3 A; 3 C; 2 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db |||||  
28 AAAAAAAAAAAAAAAAAA 11  
  
RESULT 1610  
AAD33512  
ID AAD33512 standard; DNA; 28 BP.  
XX  
AC AAD33512;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS8-28-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
OS Unidentified.  
XX  
PN EP1186673-A2.  
XX  
PD 13-MAR-2002.  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX

PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Wobler PK, Delenstarr GC;  
XX  
DR WPI; 2002-282886/33.  
XX  
PT Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 28 BP; 22 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db |||||  
1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1611  
AAA90025/c  
ID AAA90025 standard; DNA; 29 BP.  
XX  
AC AAA90025;  
XX  
DT 20-DEC-2000 (first entry)  
XX  
DE PCR primer for fatty acid binding protein (FABP) DNA amplification.  
XX  
KW Vaccine; Japanese schistosomiasis; fatty acid binding protein; FABP;  
KW PCR primer; ss.  
XX  
OS Unidentified.  
XX  
PN CN1255548-A.  
XX  
PD 07-JUN-2000.  
XX  
PF 27-NOV-1998; 98CN-00122043.  
XX  
PR 27-NOV-1998; 98CN-00122043.  
XX  
PA (SHAN-) SHANGHAI DOMESTIC ANIMAL PARASITOSIS INS.  
XX  
PI Lin J, Wu X, Liu J;  
XX  
DR WPI; 2000-524988/48.  
XX  
PT Clone of Japanese schistosome fatty acid-binding protein gene and its  
PT expression in Bombyx mori system.  
XX  
PS Claim 3; Page 1; 12pp; Chinese.  
XX  
CC The present invention relates to the preparation of a vaccine against  
CC Japanese schistosomiasis. The vaccine comprises a gene encoding a fatty  
CC acid binding protein (FABP). The FABP is expressed in a Bombyx mori  
CC system as a fusion protein of 18kD. The fusion protein has an increased  
CC immunogenicity and stronger anti-infective action than the wild-type  
CC protein. The present sequence represents a PCR primer used to amplify DNA

```
CC encoding the FAPB of the invention
XX
SQ Sequence 29 BP; 2 A; 4 C; 3 G; 20 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 29 AAAAAAAAAAAAAAAAAA 12

RESULT 1612
AAD33515
ID AAD33515 standard; DNA; 29 BP.
XX
AC AAD33515;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS6-29-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
generate signals proportional to total concentrations of labeled target
molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
molecular array. The method involves employing calibrations probes that
generate signals proportional to the total concentrations of labelled
target molecules to which the molecular array probes are directed over an
entire range of sample solutions and molecular arrays incorporating sets
of calibration probes. Method is useful for calibrating different types
of signals scanned from a molecular array, or calibrating signals scanned
from different molecular arrays. The present sequence is poly (A)
normalisation probe used in calibration of molecular array data
XX
SQ Sequence 29 BP; 23 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1613
AAI69697/c
ID AAI69697 standard; DNA; 29 BP.
XX
AC AAI69697;
PT Calibration of molecular array data by employing calibration probes that
```

```
XX
DT 10-JAN-2002 (first entry)
XX
DE Hepatitis E virus HEV-T1 sequence related PCR primer #62.
XX
KW Hepatitis E virus; HEV-T1; hepatitis infection; PCR primer; ss.
XX
OS Unidentified.
XX
PN CN1300771-A.
XX
PD 27-JUN-2001.
XX
PF 23-DEC-1999; 99CN-00125741.
XX
PR 23-DEC-1999; 99CN-00125741.
XX
PA (CHME-) CHINESE MEDICINE & BIOLOGIC PROD APPRAIS.
XX
PI Wang Y, Zhang H, Li H;
XX
DR WPI; 2001-550442/62.
XX
PT Hepatitis E virus gene sequence and its application.
XX
PS Example 1; Page 15 (Disclosure); 34pp; Chinese.
XX
CC The present invention relates to a novel nucleotide sequence and protein
of a new hepatitis E virus HEV-T1 and the application of the nucleotide
sequence and protein in diagnosing, preventing and treating hepatitis.
CC The present sequence is a PCR primer described in the exemplification of
the invention
XX
SQ Sequence 29 BP; 3 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

Query Match      0.6%; Score 18; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803
Db 29 AAAAAAAAAAAAAAAAAA 12

RESULT 1614
AAD33517
ID AAD33517 standard; DNA; 30 BP.
XX
AC AAD33517;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS5-30-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
```

PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibration probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 30 BP; 24 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1615  
AAV56638/c  
ID AAV56638 standard; DNA; 30 BP.  
XX  
AC AAV56638;  
XX  
DT 23-NOV-1998 (first entry)  
XX  
DE Feline FLAF cDNA primer #9.  
XX  
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;  
KW T lymphocyte cell; autoimmune disease; primer; ss.  
XX  
OS Synthetic.  
OS Felis catus.  
XX  
PN WO9746583-A1.  
XX  
PD 11-DEC-1997.  
XX  
PF 29-MAY-1997; 97WO-JP001824.  
XX  
PR 04-JUN-1996; 96JP-00165249.  
XX  
PA (KAGA ) CHERO-SERO-THERAPEUTIC RES INST.  
XX  
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;  
XX WPI; 1998-042118/04.  
XX  
PT Novel feline cytokine protein - useful for treating feline auto:immune  
PT diseases, e.g. those caused by feline herpes virus or feline calicivirus.  
XX  
PS Example 14; Page 66; 94pp; Japanese.  
XX  
CC AAV56637-V56640 are primers used in the amplification of novel feline  
CC cytokine proteins, FLAFp40 and FLAFp35. This protein can be used in the  
CC production of a FLAFp35/FLAFp40 heterodimer which can potentiate the  
CC cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins  
CC are used for treatment of feline autoimmune diseases e.g. as caused by  
CC feline herpes virus or feline calicivirus  
XX  
SQ Sequence 30 BP; 3 A; 3 C; 3 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 30 AAAAAAAAAAAAAAAAAA 13  
  
RESULT 1616  
AAF74908  
ID AAF74908 standard; DNA; 30 BP.  
XX  
AC AAF74908;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:5.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
DR  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 30 BP; 24 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1617  
AAD33519  
ID AAD33519 standard; DNA; 31 BP.  
XX  
AC AAD33519;  
XX  
DT 01-JUL-2002 (first entry)  
XX





FT misc\_feature 15. .18  
FT /\*tag= a  
FT /note= "characteristic sequence identifier"  
XX  
PN WO9508647-A1.  
XX  
PD 30-MAR-1995.  
XX  
XX  
PF 23-SEP-1994; 94WO-US010821.  
XX  
XX  
PR 24-SEP-1993; 93US-00126594.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
PA  
PI Soares MB, Efstratiadis A;  
XX  
XX WPI; 1995-139615/18.  
DR  
XX New normalised directional cDNA libraries - used for isolating novel  
PT cDNA's, including tissue-specific and development-specific DNA.  
PT  
XX  
XX Disclosure; Page 45; 186pp; English.  
XX  
CC Human tissues were obtained for construction of a variety of cDNA  
CC libraries, including infant brain, adult brain and adult hippocampus.  
CC Each of the cDNA libraries had a characteristic sequence identifier,  
CC provided by the oligonucleotide utilised to prime first strand cDNA  
CC synthesis (see AAQ87894-Q87907 for these primer sequences; all these  
CC primers have the PacI restriction site for directional cloning of cDNAs).  
CC Each of the libraries was propagated in the form of single-stranded (ss)  
CC circles and normalised separately by a novel method. The method  
CC comprises: generating fragments complementary to the 3' non-coding  
CC sequence of the ss circles in the library to produce partial duplexes;  
CC purifying the partial duplexes; melting and reassociating them to  
CC appropriate Cot; and purifying the unassociated ss circles to generate a  
CC normalised cDNA library. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 32 BP; 4 A; 0 C; 0 G; 28 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 32 AAAAAAAAAAAAAAAAAA 15  
  
RESULT 1620  
AAD33521  
ID AAD33521 standard; DNA; 32 BP.  
XX  
AC AAD33521;  
XX  
DT 01-JUL-2002 (first entry)  
XX  
DE T7T18Apad\_PS3-32-0001 probe for calibration of molecular array data.  
XX  
KW Molecular array; probe; ss.  
XX  
XX Unidentified.  
OS  
XX EP1186673-A2.  
PN  
XX 13-MAR-2002.  
PD  
XX  
PF 10-SEP-2001; 2001EP-00307665.  
XX  
PR 11-SEP-2000; 2000US-00659173.  
XX  
XX (AGIL-) AGILENT TECHNOLOGIES INC.  
PA  
XX Wobler PK, Delenstarr GC;  
PI

XX WPI; 2002-282886/33.  
DR  
XX Calibration of molecular array data by employing calibration probes that  
PT generate signals proportional to total concentrations of labeled target  
PT molecules, and molecular arrays incorporating sets of calibration probes.  
XX  
PS Disclosure; Page 14; 32pp; English.  
XX  
CC The invention relates to a method for calibrating data scanned from a  
CC molecular array. The method involves employing calibrations probes that  
CC generate signals proportional to the total concentrations of labelled  
CC target molecules to which the molecular array probes are directed over an  
CC entire range of sample solutions and molecular arrays incorporating sets  
CC of calibration probes. Method is useful for calibrating different types  
CC of signals scanned from a molecular array, or calibrating signals scanned  
CC from different molecular arrays. The present sequence is poly (A)  
CC normalisation probe used in calibration of molecular array data  
XX  
SQ Sequence 32 BP; 26 A; 4 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 18; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 1621  
AAT94579/c  
ID AAT94579 standard; DNA; 32 BP.  
XX  
AC AAT94579;  
XX  
DT 12-MAY-1998 (first entry)  
XX  
DE Antifungal polypeptide 3' antisense PCR primer.  
XX  
KW Antifungal polypeptide; AlyAFP; inhibition; transgenic plants; primer;  
KW phytopathogenic fungus; resistance; rapid amplification of cDNA ends;  
KW PCR; RACE; antisense; ss.  
XX  
OS Synthetic.  
OS Alyssum sp.  
XX  
PN WO9737024-A2.  
XX  
PD 09-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-US005709.  
XX  
PR 29-MAR-1996; 96US-00627706.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI Liang J, Shah D, Wu Y, Rosenberger CA;  
XX  
XX WPI; 1997-503109/46.  
DR  
XX Alyssum antifungal polypeptide and corresponding DNA - used in the  
PT production of transgenic plants resistant to phytopathogenic fungi.  
PT  
XX Example 4; Page 66; 92pp; English.  
PS  
XX Primers AAT94578-9 were used to PCR amplify the 3' end of the sequence  
CC encoding the antifungal polypeptide AlyAFP (AAW35558), by a 3' RACE  
CC (Rapid Amplification of cDNA Ends) method. This 32-mer primer anneals to  
CC the polyA tail of the sequence. The primers amplify the sequence shown in  
CC AAT94580. The polypeptide can be used to control phytopathogenic fungi,  
CC whilst the coding DNA can be used to produce transgenic plants that  
CC express the polypeptide, making them resistant to the phytopathogenic



CC binds a component of mRNP complex, separating mRNP complex by binding the  
CC ligand with a molecule specific for ligand, which is attached to the  
CC solid support and then collecting the mRNP complex by removing the  
CC complex from the support. The method is useful for in vivo partitioning  
CC of cellular mRNA protein complexes in a biological sample. The method is  
CC useful for determining the ribonomic profile of a cell which has numerous  
CC uses including monitoring of tumour development, state of growth or state  
CC of development, perturbations of a biological system such as disease,  
CC drug or toxin treatment and the state of cell aging or death,  
CC distinguishing ribonomic profiles among organisms, to discriminate  
CC between transcriptional and post-transcriptional contributions to gene  
CC expression and to track the movement of RNAs through RNP complexes,  
CC including the interactions of combinations of proteins with RNAs in RNP  
CC complexes. AAH28281-AAH28316 represent sequences derived from the 3'  
CC untranslated region (UTR) of mRNA of various genes. The sequences contain  
CC target sequences for RNA-binding proteins

SQ Sequence 32 BP; 2 A; 2 C; 2 G; 0 T; 26 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 32;  
Best Local Similarity 80.8%; Pred. No. 2.5e+03;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAATAAAAAA 2804  
||| ||||| ||||| ||||| |||||  
Db 28 AGACCAAAAAAATAAAAAA 3

RESULT 1624  
AAC90605/c  
ID AAC90605 standard; RNA; 34 BP.  
XX  
AC AAC90605;  
XX

DT 20-MAR-2001 (first entry)  
XX

DE Tomato spotted wilt virus S RNA partial sequence #9.

XX Tospovirus resistance; transgenic plant; tomato spotted wilt virus;  
KW Impatiens necrotic spot virus; TSWV; ss.  
XX

OS Tomato spotted wilt virus.  
XX

FH Key Location/Qualifiers  
FT misc\_binding 1  
FT /\*tag= a  
FT /bound\_moiety= "binds nucleotide 32 of AAC89654"  
FT 2. .10  
FT /\*tag= b  
FT /bound\_moiety= "binds nucleotides 30-22 of AAC89654"  
FT 17. .32  
FT /\*tag= c  
FT /bound\_moiety= "binds nucleotides 30-5 of AAC89564"  
FT 33. .34  
FT /\*tag= d  
FT /bound\_moiety= "binds nucleotides 1-2 of AAC89654"

US6150585-A.

21-NOV-2000.

26-NOV-1996; 96US-00757011.

03-NOV-1989; 89US-00431259.  
05-DEC-1989; 89US-00446024.  
02-MAY-1991; 91US-00694734.  
14-APR-1993; 93US-00047346.  
26-OCT-1993; 93US-00143397.  
27-JUL-1994; 94US-00280903.

PA (NOVS ) NOVARTIS FINANCE CORP.

XX Peters D, Gielen JTL, De Haan PT, Van Grinsven MQJM, Kool AJ;  
PI

PI Goldbach RW;

XX WPI; 2001-060031/07.

DR Recombinant DNA construct comprising a DNA sequence encoding an RNA  
XX sequence that codes for a tospovirus protein, useful for producing plants  
PT with reduced susceptibility to tospovirus infection.

XX Example 9; Fig 16B; 49pp; English.

PS The present invention provides DNA constructs encoding RNA sequences from  
XX a tospovirus which can be used to produce transgenic plants with immunity  
CC to tospoviruses. Examples of tospoviruses include the tomato spotted wilt  
CC virus and the Impatiens necrotic spot virus

SQ Sequence 34 BP; 4 A; 0 C; 2 G; 0 T; 28 U; 0 Other;

Query Match 0.6%; Score 18; DB 1; Length 34;  
Best Local Similarity 80.8%; Pred. No. 2.8e+03;  
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAAATAAAAAA 2803  
||| ||| ||||| ||||| |||||  
Db 27 TAAATAAAAAATAAAAAACAAAAA 2

RESULT 1625  
AAV12483/c  
ID AAV12483 standard; DNA; 39 BP.  
XX  
AC AAV12483;  
XX

DT 15-MAY-1998 (first entry)  
XX

DE Oligonucleotide SEQ ID NO:6 from US5174320 Example 2.

XX Synthesis; selection; amplification; circular oligonucleotide;  
KW rolling circle synthesis; diagnosis; therapeutic agent; ss.  
XX Synthetic.

OS US5714320-A.

XX 03-FEB-1998.

PD 23-FEB-1995; 95US-00393439.

PF 15-APR-1993; 93US-00047860.

PR (UYRP ) UNIV ROCHESTER.

XX Kool ET;

XX WPI; 1998-144278/13.

PT Rolling circle synthesis of oligo:nucleotide(s) - using primed circular  
PT template to produce oligonucleotide multimer for cleavage.

XX Example 2; Col 45; 38pp; English.

CC The present sequence represents an oligonucleotide used in an example of  
CC the present invention. The present invention describes a method for  
CC synthesising a selected oligonucleotide (I) having well defined ends. The  
CC method comprises: (a) annealing a primer to a single-stranded (ss)  
CC circular template to yield a primed circular template, where the template  
CC comprises: (i) at least one nucleotide sequence complementary to (I); and  
CC (ii) at least one nucleotide effective to produce a cleavage site in the  
CC oligonucleotide multimer; (b) combining the primed circular template with  
CC at least two types of nucleotide triphosphates and a polymerase enzyme  
CC without the addition of auxiliary proteins to yield a ss oligonucleotide  
CC multimer complementary to the circular oligonucleotide template,  
CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide  
CC multimer at the cleavage site to produce (I) having well defined ends.



```
Query Match      0.6%; Score 18; DB 1; Length 39;
Best Local Similarity 80.8%; Pred. No. 3.1e+03;
Matches 21: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

RESULT 1626  
AAX30019/c  
ID AAX30019 standard; DNA; 39 BP.

16-JUN-1999 (first entry)

XX probe: diagnosis; synthesis; detection; polymerase; ss.

AA PN W09909216-A2

13-AUG-1998.

XX (ITVRP ) INTV ROCHESTER. PA

WPT: 1999-181062/15.

Example 2: Page 41: 103pp: English.

Sequence 39 BP: 0 A; 0 C; 3 G; 36 T; 0 U; 0 Other;

05 2779 AGAATTGAAAAA 2804

AAT69640



DT 20-FEB-1998 (first entry)

Telomerase; substrate; primer; detection; 5'-region; retrovirus;  
 KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;  
 KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.  
 XX

PN DE19644302-A1.

XX DE 24-OCT-1996:

XX  
 23 (BOEE) BOHRP TNGER MANNHEIM G[illegible]

Example: page 11: 21pp: German.

[illegible]

Case	Year	Age	Sex	Score	DB 1	Length	DB 19
1	1974	10	M	17	8		
2	1974	10	F	17	8		
3	1974	10	M	17	8		
4	1974	10	F	17	8		
5	1974	10	M	17	8		
6	1974	10	F	17	8		
7	1974	10	M	17	8		
8	1974	10	F	17	8		
9	1974	10	M	17	8		
10	1974	10	F	17	8		
11	1974	10	M	17	8		
12	1974	10	F	17	8		
13	1974	10	M	17	8		
14	1974	10	F	17	8		
15	1974	10	M	17	8		
16	1974	10	F	17	8		
17	1974	10	M	17	8		
18	1974	10	F	17	8		
19	1974	10	M	17	8		
20	1974	10	F	17	8		
21	1974	10	M	17	8		
22	1974	10	F	17	8		
23	1974	10	M	17	8		
24	1974	10	F	17	8		
25	1974	10	M	17	8		
26	1974	10	F	17	8		
27	1974	10	M	17	8		
28	1974	10	F	17	8		
29	1974	10	M	17	8		
30	1974	10	F	17	8		
31	1974	10	M	17	8		
32	1974	10	F	17	8		
33	1974	10	M	17	8		
34	1974	10	F	17	8		
35	1974	10	M	17	8		
36	1974	10	F	17	8		
37	1974	10	M	17	8		
38	1974	10	F	17	8		
39	1974	10	M	17	8		
40	1974	10	F	17	8		
41	1974	10	M	17	8		
42	1974	10	F	17	8		
43	1974	10	M	17	8		
44	1974	10	F	17	8		
45	1974	10	M	17	8		
46	1974	10	F	17	8		
47	1974	10	M	17	8		
48	1974	10	F	17	8		
49	1974	10	M	17	8		
50	1974	10	F	17	8		
51	1974	10	M	17	8		
52	1974	10	F	17	8		
53	1974	10	M	17	8		
54	1974	10	F	17	8		
55	1974	10	M	17	8		
56	1974	10	F	17	8		
57	1974	10	M	17	8		
58	1974	10	F	17	8		
59	1974	10	M	17	8		
60	1974	10	F	17	8		
61	1974	10	M	17	8		
62	1974	10	F	17	8		
63	1974	10	M	17	8		

Best Local Similarity	89.5%	Pred: No. 9.1E+02;	Indels	0:	Gaps	0:
			Mismatches	0:		

[illegible]

.....

AA69640/c

AC AAT69640;

DE Telomerase Oligo-dT-Primer P3.  
XX  
KW Telomerase; substrate; primer; detection; 5'-region; retrovirus;  
KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;  
KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.  
XX  
OS Synthetic.  
XX  
PN DE19644302-A1.  
XX  
PD 05-JUN-1997.  
XX  
PF 24-OCT-1996; 96DE-01044302.  
XX  
PR 28-NOV-1995; 95DE-01044317.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Emrich T, Leying H, Hinzpeter M, Karl G;  
XX  
DR WPI; 1997-299542/28.  
XX  
PT Measuring telomerase activity, useful for tumour diagnosis and compound  
PT screening - by extending substrate primer, followed by amplification and  
PT immobilising product for detection.  
XX  
PS Example; Page 11; 21pp; German.  
XX  
CC The present sequence is a telomerase Oligo-dT-Primer, which can be used  
CC in a novel method for detecting telomerase activity. The method comprises  
CC adding to a test sample a 1st primer, that serves as telomerase  
CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow  
CC primer extension by the telomerase, amplifying the extension product,  
CC immobilising the amplification product (AP) on a solid phase and  
CC qualitative and/or quantitative detection of AP, where the substrate  
CC primer is preferably from the 5'-region of the long terminal repeat 2  
CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose  
CC tumours and screen compounds for effector activity. Immobilisation of AP  
CC provides a signal that is reproducibly representative of telomerase  
CC activity, eliminates the need for gel electrophoretic separation and  
CC provides high sensitivity. Radioactive labels are not required and the  
CC method can be automated for routine use. Specific detection is achieved  
CC by proper choice of hybridisation conditions, without separation of the  
CC telomerase extension product. A specific signal is generated by 1-10 cell  
CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 9.1e+02;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAAAAATAAAAAAAAAA 2802  
Db :|||||  
19 DKAAAAAATAAAAAAAAAA 1  
RESULT 1629  
AAQ75733/c  
ID AAQ75733 standard; DNA; 21 BP.  
XX  
AC AAQ75733;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.

XX 01-NOV-1994.  
PD  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAATAAAAAAAAAA 2801  
Db | ||| |||||||  
21 AGTTAAAAAATAAAAAAAAAA 1  
RESULT 1630  
AAQ75732/c  
ID AAQ75732 standard; DNA; 21 BP.  
XX  
AC AAQ75732;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAAATAAAAAAAAAAAAAA 2804  
Db 21 TGTATAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1631  
AAQ75648/c  
ID AAQ75648 standard; DNA; 21 BP.  
XX  
AC AAQ75648;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAAATAAAAAAAAAAAAAA 2804  
Db 21 TAACAAAAAATAAAAAAAAAAAAAA 1  
  
RESULT 1632  
AAQ75676/c  
ID AAQ75676 standard; DNA; 21 BP.  
XX  
AC AAQ75676;  
XX

DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2783 TTGAAAAAATAAAAAAAAAAAAAA 2803  
Db 21 TTATAAAAAAATAAAAAAAAAAAAAA 1  
  
RESULT 1633  
AAQ75681/c  
ID AAQ75681 standard; DNA; 21 BP.  
XX  
AC AAQ75681;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAAAAAAAA 2801  
Db 21 AAATAAAAAA AAAAAAAAAA 1  
  
RESULT 1634  
AAQ75780  
ID AAQ75780 standard; DNA; 21 BP.  
XX  
AC AAQ75780;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT  
PT  
PT  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2167 TTTTTTTTTTTTTTTTTTA 2187

Db 1 TTTTTTTTTTTTTTTCTCA 21  
  
RESULT 1635  
AAQ75660  
ID AAQ75660 standard; DNA; 21 BP.  
XX  
AC AAQ75660;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT  
PT  
PT  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2168 TTTTTTTTTTTTTTTTAA 2188  
Db 1 TTTTTTTTTTTTTTGCA 21  
  
RESULT 1636  
AAQ75652  
ID AAQ75652 standard; DNA; 21 BP.  
XX  
AC AAQ75652;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX



PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2167 TTTTTTTTTTTTTTTTTTTTAA 2187  
Db 1 TTTTTTTTTTTTTTTTGTC A 21  
RESULT 1637  
AAQ75753  
ID AAQ75753 standard; DNA; 21 BP.  
XX  
AC AAQ75753;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2170 TTTTTTTTTTTTTTTTAACT 2190  
Db 1 TTTTTTTTTTTTTTTTCAGT 21  
RESULT 1638  
AAQ75788  
ID AAQ75788 standard; DNA; 21 BP.  
XX  
AC AAQ75788;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2168 TTTTTTTTTTTTTTTTAA 2188  
Db 1 TTTTTTTTTTTTTTTTCCAA 21  
RESULT 1639  
AAQ75680/c  
ID AAQ75680 standard; DNA; 21 BP.  
XX  
AC AAQ75680;  
XX  
DT 04-AUG-1995 (first entry)



Db 21 AGTCAAAAAAAAAAAAAAAAAA 1

RESULT 1642

AAQ75644/c  
ID AAQ75644 standard; DNA; 21 BP.

XX AAQ75644;

XX 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAAAAAA 2803

Db 21 TTACAAAAAAAAAAAAAAAAA 1

RESULT 1643

AAQ75761  
ID AAQ75761 standard; DNA; 21 BP.

XX AAQ75761;

XX 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

XX

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2186

Db 1 TTTTTTTTTTTTTTTTCATT 21

RESULT 1644

AAQ75721/c  
ID AAQ75721 standard; DNA; 21 BP.

XX AAQ75721;

XX 04-AUG-1995 (first entry)

Reverse transcription primer used in cDNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The

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CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2801
Db 21 ACTTAAAAA 1

RESULT 1645
AAQ75762
ID AAQ75762 standard; DNA; 21 BP.
XX
AC AAQ75762;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2169 TTTT 2189
Db 1 TTTTTCATC 21

RESULT 1646
AAQ75760
ID AAQ75760 standard; DNA; 21 BP.
XX
AC AAQ75760;
XX
DT 04-AUG-1995 (first entry)
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
```

```
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 TTTT 2187
Db 1 TTTTTCATA 21

RESULT 1647
AAQ75754
ID AAQ75754 standard; DNA; 21 BP.
XX
AC AAQ75754;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
```



RESULT	1649
ID	AAQ75700/c
XX	AAQ75700 standard; DNA; 21 BP.
AC	AAQ75700;
XX	
DT	04-AUG-1995 (first entry)
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KW	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	
PF	16-APR-1993; 93JP-00112515.
XX	
PR	16-APR-1993; 93JP-00112515.
XX	
PA	(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
DR	WPI; 1995-018287/03.
XX	
PT	Analysis of cDNA and gene expression - by amplification of mRNA
PT	by digestion with restriction enzymes.
XX	
PS	Disclosure; Page 7; lipp; Japanese.
XX	
CC	A method for the analysis of cDNA comprises (a) preparing an ag
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plu
CC	labelled reverse transcription primers (GENESEQ files AAQ75547-
CC	and using the aggregate of mRNAs as the template for each reve
CC	transcription primer; (b) digesting each of the prepared aggreg
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate la
CC	method can be used to analyse gene expression rapidly and easi
XX	
SQ	Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
	Query Match                  0.6%; Score 17.8; DB 1; Length 21;
	Best Local Similarity      90.5%; Pred. No. 1.2e+03;
	Matches    19; Conservative    0; Mismatches    2; Indels     0;
QY	2783 TTGAAAAA..... 2803
Dd	21 TGGTAAAAA..... 1
RESULT	1650
AAQ75742	
ID	AAQ75742 standard; DNA; 21 BP.
XX	
AC	AAQ75742;
XX	
DT	04-AUG-1995 (first entry)
XX	
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KW	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	



```

PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2169 TTTTTTTTTTTTTTTTTTAAAC 2189
DB 1 TTTTTTTTTTTTTTTTCCAC 21
RESULT 1655
AAQ75645/c
ID AAQ75645 standard; DNA; 21 BP.
XX
AC AAQ75645;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
KW
XX Synthetic.
OS
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 2782 ATTGAAAAAATAAAAAAAAAA 2802
DB 21 ATACAAAAAATAAAAAAAAAA 1

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XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

XX

PS Disclosure; Page 6; 1lpp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate o  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type o  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 2166 TTTT-----  
Db 1 TTTT-----TGCT 21

RESULT 1658  
AAQ75677/C

ID AAQ75677 standard; DNA; 21 BP.

AC AAQ75677;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PP 16-APR-1993; 93JP-00112515.

PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

PX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

PS Disclosure; Page 7; 1lpp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

XX





XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2803  
Db 21 TCGTAAAAA 1

RESULT 1662  
AAQ75713/c  
ID AAQ75713 standard; DNA; 21 BP.  
XX  
AC AAQ75713;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2801  
Db 21 AACTAAAAA 1

RESULT 1663  
AAQ75769  
ID AAQ75769 standard; DNA; 21 BP.  
XX  
AC AAQ75769;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTT 2186  
Db 1 TTTTCTGT 21

RESULT 1664  
AAQ75797  
ID AAQ75797 standard; DNA; 21 BP.  
XX  
AC AAQ75797;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX

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PR    16-APR-1993;   93JP-00112515.  
XX  
PA    (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR    WPI; 1995-018287/03.  
XX  
PT    Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.  
XX  
PS    Disclosure; Page 9; 1lpp; Japanese.  
XX  
CC    A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily
```

	Sequence	21 BP;	0 A;	3 C;	0 G;	18 T;	0 U;	● Other;
	Query Match	0.6%; Score 17.8; DB 1; Length 21;						
	Best Local Similarity	90.5%; Pred. No. 1.2e+03;						
	Matches	19;	Conservative	0;	Mismatches	2;	Indels	0; Gaps 0;

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QY      2170 TTTT'TTTTTTTTTTAACCT 2190  
         |||||  
DB       1 TTTT'TTTTTTTTTTC CCT 21
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RESULT 1665  
AAQ75672/c  
ID     AQ75672 standard; DNA; 21 BP.  
XX  
AC     AQ75672;  
XX  
DT     04-AUG-1995 (first entry)
```

Reverse transcription primer used in cdNA analysis technique.

Analysis; gene expression; reverse transcription; primer; cdNA;  
aggregate; restriction enzyme; ss.

Synthetic.

PJ06303997-A.
01-NOV-1994.
16-APR-1993;    93JP-00112515.
16-APR-1993;    93JP-00112515.

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
WPI; 1995-018287/03.

Analysis of cdNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.

Disclosure; Page 7; 1lpp; Japanese.

A method for the analysis of cdNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily

Sequence	21 BP;	2 A;	0 C;	1 G;	18 T;	0 U;	○ Other;
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AAQ75709/c  
ID AAQ75709 standard; DNA; 21 BP.  
XX  
AC AAQ75709;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAAA AAAAAAAAAA 2802  
Db 21 ATCTAAAAA AAAAAAAAAA 1  
  
RESULT 1671  
AAQ75744  
ID AAQ75744 standard; DNA; 21 BP.  
XX  
AC AAQ75744;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.

(NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
WPI; 1995-018287/03.  
Analysis of cDNA and gene expression - by amplification of mRNA followed  
by digestion with restriction enzymes.  
Disclosure; Page 8; 11pp; Japanese.  
A method for the analysis of cDNA comprises (a) preparing an aggregate of  
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
and using the aggregate of mRNAs as the template for each reverse  
transcription primer; (b) digesting each of the prepared aggregates of  
the double-stranded cDNAs with restriction enzyme and; (c)  
electrophoresing the digested aggregate of cDNAs in separate lanes. The  
method can be used to analyse gene expression rapidly and easily  
Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2167 TTTTTTTTT TTTTTTTTTT 2187  
Db 1 TTTTTTTTT TTTTTTCGTA 21  
  
RESULT 1672  
AAQ75792  
ID AAQ75792 standard; DNA; 21 BP.  
XX  
AC AAQ75792;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;



CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAAATAAAAAAAAAAAAAA 2804  
Db 21 TGCCAAAAAATAAAAAAAAAAAAA 1  
  
RESULT 1676  
AAQ75626  
ID AAQ75626 standard; DNA; 21 BP.  
XX  
AC AAQ75626;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2169 TTTTATTTTATTTTATTTTAAAC 2189  
Db 1 TTTTATTTTATTTTATTTTGAGC 21  
  
RESULT 1677  
AAQ75664

ID AAQ75664 standard; DNA; 21 BP.  
XX  
AC AAQ75664;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 21;  
Best Local Similarity 90.5%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2167 TTTTATTTTATTTTATTTTAA 2187  
Db 1 TTTTATTTTATTTTATTTTGCTA 21  
  
RESULT 1678  
AAQ75664/c  
ID AAQ75664 standard; DNA; 21 BP.  
XX  
AC AAQ75664;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX











```

AC AAQ75656;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2783 TTGAAAAA AAAAAAAAAA 2803
Db 21 TCGCAAAA AAAAAAAAAA 1

RESULT 1692
AAQ75617
ID AAQ75617 standard; DNA; 21 BP.
AC AAQ75617;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
```







Db	1	TTTTTTTGTGTTTTGTTTT	21
RESULT 1699			
ABS77577			
ID	ABS77577	standard; DNA; 22 BP.	
XX			
AC	ABS77577;		
XX			
DT	13-DEC-2002	(first entry)	
XX			
DE	Angiogenesis inhibitory oligonucleotide #61.		
XX			
KW	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;		
KW	tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;		
KW	diabetic retinopathy; retinopathy of prematurity; macular degeneration;		
KW	corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;		
KW	rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;		
KW	plaque neovascularisation; telangiectasia; haemophiliac joint;		
KW	angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;		
KW	scleroderma; hypertrophic scar.		
XX			
OS	Synthetic.		
XX			
PN	WO200253141-A2.		
XX			
PD	11-JUL-2002.		
XX			
PF	14-DEC-2001; 2001WO-US048458.		
XX			
PR	14-DEC-2000; 2000US-0255534P.		
XX			
PA	(COLE-) COLEY PHARM GROUP INC.		
XX			
PI	Bratzler RL;		
XX			
DR	WPI; 2002-566690/60.		
XX			
PT	Inhibiting angiogenesis in a subject, involves administering at least one		
PT	antiangiogenic nucleic acid molecule to the subject.		
XX			
PS	Claim 2; Page 20; 276pp; English.		
XX			
CC	The invention relates to inhibiting angiogenesis in a subject, comprising		
CC	administering at least one antiangiogenic nucleic acid molecule. Also		
CC	included is a kit comprising a first container housing the antiangiogenic		
CC	nucleic acids, and instructions for administering them to a subject		
CC	having a condition characterised by unwanted angiogenesis. The method is		
CC	useful for inhibiting angiogenesis associated with solid tumour growth,		
CC	tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,		
CC	diabetic retinopathy, retinopathy of prematurity, macular degeneration,		
CC	corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,		
CC	rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque		
CC	neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, and		
CC	wound granulation, intestinal adhesions, atherosclerosis, scleroderma and		
CC	hypertrophic scars. The present sequence is an antiangiogenic nucleic		
CC	acid of the invention		
XX			
SQ	Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;		
Query Match 0.6%; Score 17.8; DB 1; Length 22;			
Best Local Similarity 90.5%; Pred. No. 1.3e+03;			
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	2166	TTTTTTTTTTTTTTTTTTTTTTT	2186
Db	1	TTTTTTTGTGTTTTTGTGTTT	21
RESULT 1700			
ACD99369			
ID	ACD99369	standard; DNA; 22 BP.	

XX AC ACD99369;  
XX DT 25-SEP-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #55.  
XX KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX OS Synthetic.  
XX PN US2003050268-A1.  
XX PD 13-MAR-2003.  
XX PF 29-MAR-2002; 2002US-00112653.  
XX PR 29-MAR-2001; 2001US-0279642P.  
XX PA (KRIE/) KRIEG A M.  
XX PA (BERG/) BERG D J.  
XX PI Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX DT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX PS Disclosure; Page 10; 229pp; English.  
XX CC The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186  
Db 1 TTTT TTTT GTTT TTTT GTTT TTTT 21  
RESULT 1701  
ADB36438  
ID ADB36438 standard; DNA; 22 BP.  
XX AC ADB36438;  
XX DT 04-DEC-2003 (first entry)  
XX DE Immunostimulatory nucleic acid #52.  
XX KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX OS Synthetic.  
XX PN US2003087848-A1.  
XX PD 08-MAY-2003.

XX PF 02-FEB-2001; 2001US-00776479.  
XX PR 03-FEB-2000; 2000US-0179991P.  
XX PA (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
XX PA (FOUR/) FOURON Y.  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX WPI; 2003-657977/62.  
XX PT Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX PS Claim 10; Page 6; 221pp; English.  
XX CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 22;  
Best Local Similarity 90.5%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2186  
Db 1 TTTT TTTT GTTT TTTT GTTT TTTT 21  
RESULT 1702  
AAH91823  
ID AAH91823 standard; DNA; 23 BP.  
XX AC AAH91823;  
XX DT 09-OCT-2001 (first entry)  
XX DE Human inflammatory bowel disease associated polymorphic site #898.  
XX KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT misc\_feature 11 /\*tag= a  
FT /note= "SNP, optionally T or A at this position"  
XX WO200142511-A2.  
XX PD 14-JUN-2001.  
XX PF 11-DEC-2000; 2000WO-US033632.  
XX PR 10-DEC-1999; 99US-0170257P.  
PR 10-APR-2000; 2000US-0196046P.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX WPI; 2001-367874/38.  
XX DR















DE XX SNP specific SNPE primer SEQ ID 995.

KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;

KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;

KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;

KW inflammation; forensic investigation; paternity analysis; primer; ss.

XX

OS Homo sapiens.

XX

PN WO200129262-A2.

XX

PD 26-APR-2001.

XX

PF 13-OCT-2000; 2000WO-US028436.

XX

PR 15-OCT-1999; 99US-0160096P.

XX

XX (ORCH-) ORCHID BIOSCIENCES INC.

XX

PA Picoult-Newburg L, Pohl M;

XX

PI WPI; 2001-290930/30.

XX

DR New genotyping oligonucleotide, useful for detecting the presence,

XX

PT absence or identity of single polynucleotide polymorphism in a nucleic

PT acid sample.

XX

PS Claim 1; Page 55; 83pp; English.

XX

CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide

CC primer extension (SNPE) primers, and the sequences of regions flanking

CC sites of single nucleotide polymorphisms SNPs. The present invention

CC includes kits for determining the presence or absence of a SNP, using the

CC oligonucleotides of the invention. The PCR primers are used to amplify a

CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.

CC The oligonucleotides are useful for genotyping a nucleic acid sample by

CC performing a single-nucleotide primer extension reaction. The

CC oligonucleotides are useful for determining the presence, absence or

CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to

CC assess by association analysis the genotype of an individual or group of

CC individuals, having a pathological phenotypic trait suspected of being

CC caused by one or more SNPs. Phenotypic traits include diseases e.g.

CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular

CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,

CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic

CC traits also include symptoms of or susceptibility to multifactorial

CC disease of which a component is or may be genetic such as autoimmune

CC diseases, including, rheumatoid arthritis, multiple sclerosis,

CC inflammation, cancer, nervous system diseases and infection by pathogenic

CC microorganism. The method is also useful in forensic investigations and

CC paternity analysis. The present sequence represents a single nucleotide

CC primer extension (SNPE) primer specific for a human SNP containing DNA

CC sequence

XX

SQ Sequence 25 BP; 1 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;

Best Local Similarity 90.5%; Pred. No. 1.7e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTTT 2186

Db 5 TTTTCTTTTCTTTTCTTTT 25

RESULT 1716

ABS98709

ID ABS98709 standard; DNA; 25 BP.

XX

AC ABS98709;

XX

DT 18-DEC-2002 (first entry)

XX

DE Human p53 PCR primer #5.

XX

KW PCR; ss; primer; electronic microarray; primer extension;

KW RNA polymerase recognition site; oncogenesis; cell growth;

KW differentiation.

XX

OS Homo sapiens.

XX

PN US2002119484-A1.

XX

PD 29-AUG-2002.

XX

PF 12-FEB-2002; 2002US-00075579.

XX

PR 07-JUL-1994; 94US-00271882.

PR 24-JAN-2000; 2000US-00490965.

PR 09-NOV-2000; 2000US-00710200.

XX

XX (NANO-) NANOGEN INC.

PA

XX Weidenhammer EM, Xu X, Heller MJ, Kahl BF;

PI

XX WPI; 2002-750052/B1.

DR

XX Determining mRNA expression in sample, by producing shortened amplicons

PT from mRNA isolated from sample, electronically hybridizing amplicons to

PT probes bound to a support, and detecting the amount of hybridized

PT amplicons.

XX

PS Example 6; Page 13; 37pp; English.

XX

CC The invention relates to detecting (M1) relative amounts of at least 2

CC mRNA sequences in a biological sample (BS), comprises isolating mRNA from

CC BS, amplifying at least 2 mRNA transcripts, from each BS to produce

CC amplicons (A) less than about 300 bases in length, electronically

CC hybridising (A) to at least 2 probes bound to a support at predetermined

CC locations, and detecting amounts of each (A) hybridised to the bound

CC probes. Also included are (1) preserving (M2) and reusing a nucleic acid

CC library produced from a patient biological sample, by: (a) isolating mRNA

CC from a patient biological sample; (b) reverse-transcribing the mRNA to

CC produce a cDNA library; (c) amplifying the cDNA library by a DNA

CC polymerase reaction utilising at least one chimaeric primer comprising a

CC RNA polymerase recognition site upstream of a sequence specific for a

CC mRNA transcript of interest and a fill-in primer for the complementary

CC nucleic acid strand chosen from sequence specific primers and random

CC primers (at least 1 of the primers used is chosen from 5' affinity-moiety

CC labeled chimaeric primers and 5' affinity-moiety labeled sequence

CC specific fill-in primers); (d) binding the amplification products to a

CC solid support coated with an affinity-binding moiety; (e) utilising the

CC bound amplification products as a template for an in vitro transcription

CC reaction; (f) separating the in vitro transcription products from the

CC amplification products bound to the solid support; and (g) utilising the

CC bound amplification products from step (h) as a template for at least one

CC additional in vitro transcription reaction (the amount of in vitro

CC transcription product produced is not significantly less than that

CC produced in step (e)); (2) detecting (M3) the extent of hybridisation of

CC a nucleic acid in a sample to a probe nucleic acid sequence; and (3)

CC providing (M4) an internal control for an individual test site in a

CC nucleic acid hybridisation reaction assay to determine the presence of at

CC least one nucleic acid sequence of interest in at least one nucleic acid

CC containing sample (the nucleic acid hybridisation assay is performed on

CC an electronically controlled microarray comprising at least two test

CC sites). M1 is useful for detecting the relative amounts of at least two

CC mRNA sequences in a biological sample. M1 is useful for determining the

CC level of mRNA expression in the cells of a biological sample, for

CC gathering data to correlate difference in expression patterns with

CC specific physiological and/or pathological states, for studying

CC expression of genes in organisms under various physiological conditions,

CC for studying the role of gene expression in diseases and oncogenesis,

CC physio-chemical cellular responses to stimuli, and cell growth and

CC differentiation, for titrating the amount of amplified mRNA present in a

CC sample, and to compare, side by side, the expression levels of mRNA in a  
CC cell type that has undergone two physical or chemical stimuli. The method  
CC uses primer extension and an active electronic microarray. The present  
CC sequence is a gene specific primer used in the method of the invention  
XX  
SQ Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 487 GAGCCAGGAGGAGCGGGGCT 507  
Db 1 GAGCCAGGAGGAGCGGGGCT 21

RESULT 1717  
AAD44166  
ID AAD44166 standard; DNA; 25 BP.  
XX  
AC AAD44166;  
XX  
DT 13-DEC-2002 (first entry)  
DE Probe 261 targetted to human tumour suppressor p53 gene.  
XX  
KW Target nucleotide; analyte; signal; drug discovery; human; probe; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002051973-A1.  
XX  
PD 02-MAY-2002.  
XX  
PF 17-SEP-1999; 99US-00398399.  
XX  
PR 17-SEP-1999; 99US-00398399.  
XX  
PA (DELE/) DELENSTARR G C.  
PA (LEFK/) LEFKOWITZ S M.  
PA (LUEB/) LUEBKE K J.  
PA (OVER/) OVERMAN L B.  
PA (SAMP/) SAMPRAS N M.  
PA (SAMP/) SAMPSON J R.  
PA (WOLB/) WOLBER P K.  
XX  
PI Delenstarr GC, Lefkowitz SM, Luebke KJ, Overman LB, Sampras NM;  
PI Sampson JR, Wolber PK;  
XX  
DR WPI; 2002-443693/47.  
XX  
PT Detecting a target nucleotide sequence in an analyte, for use in e.g.  
PT drug discovery, comprises using a set of features having  
PT oligophosphodiester probes, and subtracting a background signal from an  
PT observed signal.  
XX  
PS Claim 5; Page 19; 35pp; English.  
XX  
CC The invention relates to a method for detecting the presence and/or  
CC amount of a target nucleotide sequence in an analyte. The method  
CC comprising: contacting an aliquot of an analyte suspected of containing  
CC the target sequence with a set of features comprising oligophosphodiester  
CC probes; and subtracting a background signal from an observed signal to  
CC determine the presence and/or amount of the target sequence in the  
CC analyte. The method is used to detect the presence and/or amount of a  
CC target sequence in an analyte. The method is used for estimating  
CC background noise in a nucleic acid hybridisation assay and for validating  
CC a test-background feature. The method is useful in chemical, biological  
CC medical and diagnostic techniques, and for drug discovery. The present  
CC sequence is a probe targetted to human tumour suppressor p53 gene  
XX  
SQ Sequence 25 BP; 5 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 487 GAGCCAGGAGGAGCGGGGCT 507  
Db 2 GAGCCAGGAGGAGCGGGGCT 22

RESULT 1718  
ABS76275  
ID ABS76275 standard; DNA; 25 BP.  
XX  
AC ABS76275;  
XX  
DT 27-DEC-2002 (first entry)  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1801.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX  
DR WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 312; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 3 A; 4 C; 7 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2310 AAGCAATTTGTTGCTGCTGT 2330  
Db 2 AAGCCAGTTGTTGCTGCTGT 22

RESULT 1719  
ABS76276  
ID ABS76276 standard; DNA; 25 BP.

XX ABS76276;  
AC 27-DEC-2002 (first entry)  
XX  
DT Human PAPP-E exon 7 associated 25-mer SEQ ID 1802.  
XX  
DE PAPP-E; human; pregnancy associated plasma protein E; abortive;  
XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
KW  
XX Homo sapiens.  
OS  
XX US2002102252-A1.  
PN  
XX 01-AUG-2002.  
PD  
XX 06-APR-2001; 2001US-00827998.  
PF  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX WPI; 2002-697817/75.  
DR  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
PT  
XX Example 2; Page 312; 353pp; English.  
PS  
XX This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 3 A; 5 C; 7 G; 10 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2310 AAGCAATTGTTGCTGCTTGT 2330  
Db 1 AAGCCAGTTGTTGCTGCTTGT 21  
RESULT 1720  
ABS76274  
ID ABS76274 standard; DNA; 25 BP.  
XX  
AC ABS76274;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1800.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
XX dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.

XX US2002102252-A1.  
PN  
XX 01-AUG-2002.  
PD  
XX 06-APR-2001; 2001US-00827998.  
PF  
XX 26-MAY-2000; 2000US-0207456P.  
PR (GUY/) GU Y.  
XX (SHAN/) SHANNON M E.  
PA  
XX Gu Y, Shannon ME;  
PI  
XX WPI; 2002-697817/75.  
DR  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
PT  
XX Example 2; Page 312; 353pp; English.  
PS  
XX This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 4 A; 4 C; 7 G; 10 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2310 AAGCAATTGTTGCTGCTTGT 2330  
Db 3 AAGCCAGTTGTTGCTGCTTGT 23  
RESULT 1721  
ABS76273  
ID ABS76273 standard; DNA; 25 BP.  
XX  
AC ABS76273;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1799.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX



PI Gu Y, Shannon ME;  
XX WPI; 2002-697817/75.  
DR  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
XX Example 2; Page 311; 353pp; English.  
XX  
XX This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2310 AAGCAATTGCTGCTGCTGT 2330  
Db 4 AAGCCAGTTGTTGCTGCTGT 24  
  
RESULT 1722  
ABS76272  
ID ABS76272 standard; DNA; 25 BP.  
XX  
AC ABS76272;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1798.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUYY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX  
DR WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
XX Example 2; Page 311; 353pp; English.  
XX  
XX This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive

CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 4 A; 5 C; 6 G; 10 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2310 AAGCAATTGCTGCTGCTGT 2330  
Db 5 AAGCCAGTTGTTGCTGCTGT 25  
  
RESULT 1723  
ABK99538  
ID ABK99538 standard; DNA; 25 BP.  
XX  
AC ABK99538;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human p53 gene hybridisation probe #8.  
DE  
XX Nucleic acid microarray; probe; ss.  
KW  
XX Homo sapiens.  
OS  
XX US2002068293-A1.  
PN  
XX 06-JUN-2002.  
PD  
XX 02-JUL-2001; 2001US-00899381.  
PF  
XX 17-SEP-1999; 99US-00398399.  
PR  
XX (DELE/) DELENSTARR G C.  
PA (WOLB/) WOLBER P K.  
PA (SANA/) SANA T R.  
XX  
PI Delenstarr GC, Wolber PK, Sana TR;  
XX  
DR WPI; 2002-582474/62.  
XX  
XX Nucleic acid arrays for qualitatively or quantitatively determining the  
PT presence of analyte target nucleic acid in a sample comprises both  
PT hybridization features and background features.  
XX  
XX Claim 8; Page 15; 38pp; English.  
PS  
XX The invention relates to a nucleic acid array (I) comprising at least one  
CC hybridisation feature and at least one background feature. (I) is useful  
CC for detecting the presence of an analyte nucleic acid in a sample. The  
CC detection comprises contacting the nucleic acid array with the sample  
CC under stringent hybridisation conditions, subtracting the background  
CC signal from the hybridisation signal to obtain a background corrected  
CC hybridisation signal and relating the background corrected hybridisation  
CC signal to the presence of the analyte target nucleic acid in the sample  
CC The method further comprises a labeling step comprising labeling any  
CC analyte target nucleic acids present in the sample with a member of a  
CC signal producing system prior to contacting the array with the sample.  
CC ABK99529-ABK99544 and ABK99549-ABK99578 represent nucleic acid probes of  
CC the invention  
XX  
SQ Sequence 25 BP; 5 A; 6 C; 13 G; 1 T; 0 U; 0 Other;

```

Query Match      0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 487 GAGCCAGGAGGGAGCGGGGCT 507
Db 2 GAGCCAGGAGGGAGCGAGGGCT 22

RESULT 1724
AAD39915
ID AAD39915 standard; DNA; 25 BP.
XX
AC AAD39915;
XX
DT 22-OCT-2002 (first entry)
DE Human PCR primer #5 used for amplifying p53 target gene.
XX
KW Human; amplicon; electronic hybridisation; gene expression; oncogenesis;
KW physio-chemical cellular response; stimuli; cell growth; differentiation;
KW PCR; primer; p53; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Biotinylated"
XX
PN US6379897-B1.
XX
PD 30-APR-2002.
XX
PF 09-NOV-2000; 2000US-00710200.
XX
PR 09-NOV-2000; 2000US-00710200.
XX
PA (NANO-) NANOGEN INC.
XX
PI Weidenhammer EM, Wang L, Xu X, Heller MJ, Kahl BF;
XX WPI; 2002-424785/45.
XX
PT Detecting relative amounts of at least two different mRNAs in biological
PT samples by electronically hybridizing amplicons to probes, useful to
PT monitor gene expression in disease and in cell response studies.
XX
PS Example 6; Col 45; 36pp; English.
XX
CC The invention relates to a method for detecting the relative amounts of
CC at least two different mRNA sequences in biological samples. The method
CC comprising isolating sample mRNA, amplifying at least two mRNAs to
CC produce amplicons of not more than 300 bases, electronically hybridising
CC the amplicons to probes bound to a support at predetermined locations and
CC detecting amounts of hybridised amplicons. The method may be used to
CC monitor gene expression in the study of disease and oncogenesis, physio-
CC chemical cellular responses to stimuli and cell growth and
CC differentiation. The present sequence is a human PCR primer used for
CC amplifying p53 target gene
XX
SQ Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;

Query Match      0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 487 GAGCCAGGAGGGAGCGGGGCT 507
Db 1 GAGCCAGGAGGGAGCAGGGCT 21
```

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RESULT 1725
ACD00131
ID ACD00131 standard; DNA; 25 BP.
XX
AC ACD00131;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #604.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO2003031621-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032599.
XX
PR 12-OCT-2001; 2001US-0329000P.
XX
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
PI Zhang J;
XX
DR WPI; 2003-381720/36.
XX
PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,
PT investigating and/or treating disorders associated with aberrant
PT expression or activity of GPCR-A-1, such as tumors and cancers.
XX
PS Example 2; SEQ ID NO 628; 156pp; English.
XX
CC The invention describes an isolated nucleic acid encoding a G protein
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a
CC 409 residue amino acid sequence, all given in the specification, with or
CC without conservative amino acid substitutions, or complements of the
CC sequence of them. The encoding nucleic acid is not more than 100 kbse in
CC length. The methods and compositions of the present invention are useful
CC for diagnosing, investigating and/or treating disorders associated with
CC aberrant expression or activity of GPCR-A-1, such as tumours and cancers.
CC This sequence represents an oligonucleotide used to analyse the gene
CC encoding human G-protein coupled receptor GPCR-A-1
XX
SQ Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;

Query Match      0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2105 GGGGCGCTTCTGGTTTAGGA 2125
Db 4 GGGGACCTTCTGGTCTTAGGA 24

RESULT 1726
ACD00133
ID ACD00133 standard; DNA; 25 BP.
XX
AC ACD00133;
XX
DT 28-JUL-2003 (first entry)
XX
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #606.
XX
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.
XX
OS Homo sapiens.
```

XX WO2003031621-A2.  
PN 17-APR-2003.  
XX 11-OCT-2002; 2002WO-US032599.  
XX 12-OCT-2001; 2001US-0329000P.  
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX Zhang J;  
XX WPI; 2003-381720/36.  
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
PT investigating and/or treating disorders associated with aberrant  
PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX Example 2; SEQ ID NO 630; 156pp; English.  
PS The invention describes an isolated nucleic acid encoding a G protein  
XX coupled receptor (GPCR), mutations of which cause cancer, comprising a  
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
CC 409 residue amino acid sequence, all given in the specification, with or  
CC without conservative amino acid substitutions, or complements of the  
CC sequence of them. The encoding nucleic acid is not more than 100 kbase in  
CC length. The methods and compositions of the present invention are useful  
CC for diagnosing, investigating and/or treating disorders associated with  
CC aberrant expression or activity of GPCR-A-1, such as tumours and cancers.  
CC This sequence represents an oligonucleotide used to analyse the gene  
CC encoding human G-protein coupled receptor GPCR-A-1  
XX Sequence 25 BP; 5 A; 4 C; 10 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2105 GGGGGCCTTCTGGTTTATAGGA 2125  
Db ||||| ||||| ||||| ||||| |||||  
2 GGGGACCTTCTGGTCTTAGGA 22

RESULT 1727  
ACD00132  
ID ACD00132 standard; DNA; 25 BP.  
XX ACD00132;  
AC 28-JUL-2003 (first entry)  
XX G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #605.  
DE Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
OS Homo sapiens.  
XX WO2003031621-A2.  
PN 17-APR-2003.  
XX 11-OCT-2002; 2002WO-US032599.  
XX 12-OCT-2001; 2001US-0329000P.  
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX Zhang J;  
XX WPI; 2003-381720/36.  
XX

PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
PT investigating and/or treating disorders associated with aberrant  
PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX Example 2; SEQ ID NO 629; 156pp; English.  
XX The invention describes an isolated nucleic acid encoding a G protein  
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
CC 409 residue amino acid sequence, all given in the specification, with or  
CC without conservative amino acid substitutions, or complements of the  
CC sequence of them. The encoding nucleic acid is not more than 100 kbase in  
CC length. The methods and compositions of the present invention are useful  
CC for diagnosing, investigating and/or treating disorders associated with  
CC aberrant expression or activity of GPCR-A-1, such as tumours and cancers.  
CC This sequence represents an oligonucleotide used to analyse the gene  
CC encoding human G-protein coupled receptor GPCR-A-1  
XX Sequence 25 BP; 4 A; 4 C; 10 G; 7 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2105 GGGGGCCTTCTGGTTTATAGGA 2125  
Db ||||| ||||| ||||| ||||| |||||  
3 GGGGACCTTCTGGTCTTAGGA 23

RESULT 1728  
ACD00130  
ID ACD00130 standard; DNA; 25 BP.  
XX ACD00130;  
AC 28-JUL-2003 (first entry)  
XX G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #603.  
DE Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
XX G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
OS Homo sapiens.  
XX WO2003031621-A2.  
PN 17-APR-2003.  
XX 11-OCT-2002; 2002WO-US032599.  
XX 12-OCT-2001; 2001US-0329000P.  
PR (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX Zhang J;  
XX WPI; 2003-381720/36.  
XX New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
PT investigating and/or treating disorders associated with aberrant  
PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX Example 2; SEQ ID NO 627; 156pp; English.  
XX The invention describes an isolated nucleic acid encoding a G protein  
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
CC 409 residue amino acid sequence, all given in the specification, with or  
CC without conservative amino acid substitutions, or complements of the  
CC sequence of them. The encoding nucleic acid is not more than 100 kbase in  
CC length. The methods and compositions of the present invention are useful  
CC for diagnosing, investigating and/or treating disorders associated with  
CC aberrant expression or activity of GPCR-A-1, such as tumours and cancers.  
CC









CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 TCAAAAAAAAAAAAAAAAAAGAA 1

RESULT 1736  
ADB04571  
ID ADB04571 standard; DNA; 25 BP.  
XX  
AC ADB04571;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5557.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EPI281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5557; 103pp; English.  
XX

CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross

CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. No. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 TTTTTTTTTTTTTTTTTTA 2187  
Db 3 TTCTTTTTTTTTTTTTTTGA 23

RESULT 1737  
ADB04571/C  
ID ADB04571 standard; DNA; 25 BP.  
XX  
AC ADB04571;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5557.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EPI281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5557; 103pp; English.  
XX

CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX

SQ Sequence 25 BP; 3 A; 1 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 25;

```
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAAGAAAAAAGAAAAAAGAAAAA 2804
Db 23 TCAAGAAAAAAGAAAAAAGAAAAA 3

RESULT 1738
ADB04570
ID ADB04570 standard; DNA; 25 BP.
XX
AC ADB04570;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 5556.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5556; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2167 TTTTNTTTTTTTTTTTTTTTTGA 2187
Db 4 TTCTTTTTTTTTTTTTTTTGA 24

Best Local Similarity 90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAAGAAAAAAGAAAAAAGAAAAA 2804
Db 23 TCAAGAAAAAAGAAAAAAGAAAAA 3

RESULT 1740
ABX79024
ID ABX79024 standard; DNA; 25 BP.
XX
AC ABX79024;
XX
DT 15-APR-2003 (first entry)
XX
```



DE Electronic microarray associated p53 oligonucleotide #5.  
XX Electronic microarray; utilising gene expression experimental model;  
KW oncogenesis; physio-chemical cellular response; cell growth;  
KW cell differentiation; ss.  
XX Homo sapiens.  
OS US2002150917-A1.  
PN 17-OCT-2002.  
XX 10-OCT-2001; 2001US-00975408.  
PF 09-NOV-2000; 2000US-00710200.  
XX (NANO-) NANOGEN INC.  
PA Weidenhammer EM, Wang L, Xu X, Heller MJ, Kahl BF;  
XX WPI; 2003-198284/19.  
DR Detecting relative amounts of at least two mRNA utilizing microelectronic  
XX arrays in a sample, useful for studying disease and oncogenesis, physio-  
PT chemical cellular responses to stimuli, and cell growth and  
PT differentiation.  
XX Example 6; Page 14; 39pp; English.  
PS The invention describes a method of detecting the relative amounts of at  
XX least two mRNA sequences in at least one biological sample, comprising:  
CC (a) isolating mRNA from the sample; (b) amplifying at least two mRNA  
CC transcripts to produce amplicons; (c) electronically hybridising the  
CC amplicons produced to at least two probes bound to a support at  
CC predetermined locations; and (d) detecting the amounts of each amplicon  
CC hybridised to the bound probes at the predetermined locations. The  
CC methods and compositions are useful for utilising gene expression  
CC experimental models for use in studying disease and oncogenesis, physio-  
CC chemical cellular responses to stimuli, and cell growth and  
CC differentiation. This sequence represents an oligonucleotide targeted to  
CC a human gene and used to demonstrate the methods described in the  
CC invention  
XX  
SQ Sequence 25 BP; 5 A; 6 C; 12 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 25;  
Best Local Similarity 90.5%; Pred. NO. 1.7e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 487 GAGCCAGGAGGAGGGGGGCT 507  
Db 1 GAGCCAGGAGGAGGGGGCT 21  
RESULT 1741  
AAAL3806/C  
ID AAAL3806 standard; DNA; 26 BP.  
XX AAAL3806;  
AC  
XX 27-JUL-2000 (first entry)  
DT  
XX Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.  
DE  
XX Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;  
KW bread; oxidative stress; osmotic pressure; stress; glucose starvation;  
KW PCR primer; ss.  
XX Saccharomyces cerevisiae.  
OS  
XX JP2000078977-A.  
PN  
XX 21-MAR-2000.  
PD

XX 04-SEP-1998; 98JP-00251390.  
PF 04-SEP-1998; 98JP-00251390.  
XX (TAIF ) MARUHA CORP.  
PA WPI; 2000-285929/25.  
XX A stress-responsive gene promotor.  
DR Example 3; Page 10; 12pp; Japanese.  
XX The present invention describes a stress responsive gene promoter  
CC isolated from Saccharomyces cerevisiae (yeast). Also described in the  
CC present invention are: (1) a promoter containing a DNA hybridising with  
CC the above DNA under a stringent condition and having stress-responsive  
CC promoter activity; (2) a gene expression cassette containing the above  
CC promoter; (3) an expression vector containing the above gene expression  
CC cassette; (4) a recombinant vector in which a gene encoding an optional  
CC polypeptide is recombined to the above expression vector; (5) a method  
CC transformant containing the above recombinant vector; and (6) a method  
CC for the preparation of the above polypeptide in which the above  
CC transformant is cultured and the polypeptide is collected from the  
CC resultant culture. Saccharomyces cerevisiae is used for the brewing of  
CC beer, wine and sake and production of bread. The gene is responsive to  
CC the stresses such as oxidative stress, osmotic pressure stress and  
CC glucose starvation stress. The present sequence represents a PCR primer  
CC for the yeast DOG2 stress responsive gene, which is used in an example  
CC from the present invention  
XX  
SQ Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.8; DB 1; Length 26;  
Best Local Similarity 90.5%; Pred. NO. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2784 TCAAAAAAAAAAAAAAAAAAAAAA 2804  
Db 24 TCAAAAAAAAAAAAAAAAAAAAAA 4  
RESULT 1742  
AAQ05023  
ID AAQ05023 standard; DNA; 27 BP.  
XX AAQ05023;  
AC  
XX 25-MAR-2003 (revised)  
DT 31-OCT-1990 (first entry)  
XX  
DE Sequence binding to and inhibiting the Beta-globin gene.  
XX C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;  
KW epidermal growth factor; GSTpi; HMGCoA; thalassemia;  
KW Herpes simplex virus; nerve growth factor receptor; globin; ss.  
XX Synthetic.  
XX EP375408-A.  
PN 27-JUN-1990.  
XX 20-DEC-1989; 89EP-00313391.  
PF 20-DEC-1988; 88US-00287359.  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (HOGA/) HOGAN M E.  
XX Hogan ME, Kessler DJ;  
PI WPI; 1990-195509/26.  
XX

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CC oligonucleotides may be used, targetted against the 5' enhancer or the
CC promoter/coding domain, in this case from base 874 to 900 (numbering is
CC relative to the principal mRNA start site). A suitable parallel
CC oligonucleotide is GL6par (3'-5'). See also AAQ36219-362. (Updated on 25-
CC MAR-2003 to correct PF field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.8; DB 1; Length 27;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2166 TTTTTTTTTTTTTTTTTTTT 2186
Db 6 TTTGTTTTTTTGTTTTTTTT 26

RESULT 1744
ABK52620/c
ID ABK52620 standard; DNA; 27 BP.
XX
AC ABK52620;
XX
DT 27-AUG-2002 (first entry)
XX
DE Minority genome method VFA-MUT-11 DNA sequence.
XX
KW Minority genome method; viral quasi-species; majority genome;
KW genetic diagnosis; viral infection; human immune deficiency virus;
KW hepatitis B; hepatitis C; antiviral therapy; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_difference 1
FT /*tag= a
FT /label= unknown
FT /note= "C6 aminolinker sequence"
XX
PN WO200183815-A1.
XX
PD 08-NOV-2001.
XX
PF 27-APR-2001; 2001WO-ES000165.
XX
PR 27-APR-2000; 2000ES-00001068.
XX
PA (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
XX
PI Arias Esteban A, Baranowski E, Briones Llorente C;
PI Domingo Solans E, Escarmis Homs C, Gomez Castilla J;
PI Martin Ruiz- Jarabo C, Parro Garcia V;
XX
DR WPI; 2002-147445/19.
XX
PT Detecting minority genomes in viral quasi-species, useful for identifying
PT mutants responsible for drug resistance and to individualize therapy.
XX
PS Example 1; Page 53; 107pp; Spanish.
XX
CC The present invention relates to a new method for detecting minority
CC genomes, present at less than 50%, in a population of nucleic acids of a
CC viral quasi-species and having at least one mutation with respect to the
CC majority genome. The invention can be used for genetic diagnosis of viral
CC infections, especially human immune deficiency virus and hepatitis B or
CC C, particularly to detect memory minority genomes that are implicated in
CC failure of antiviral therapy, so the method may make possible design of
CC therapies customised for individual patients. The present nucleic acid
CC sequence represents the VFA-MUT-11 DNA sequence that was used in the
CC methods of the invention
XX
SQ Sequence 27 BP; 2 A; 4 C; 2 G; 18 T; 0 U; 1 Other;

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Query Match 0.6%; Score 17.8; DB 1; Length 27;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2799  
DB 22 AGGATTAAAAA 2

RESULT 1745  
ABA05517  
ID ABA05517 standard; DNA; 24 BP.  
XX  
AC ABA05517;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Human Tre carcinogenic gene protein 10.56 PCR primer 2.  
XX  
KW Human; Tre carcinogenic gene protein 10.56; cytostatic; haemostatic;  
KW virucide; immunomodulatory; antiinflammatory; gene therapy; cancer;  
KW haemopathy; human immunodeficiency virus; HIV; infection;  
KW immunological disease; inflammatory disorder; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200190131-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 21-MAY-2001; 2001WO-CN000833.  
XX  
PR 24-MAY-2000; 2000CN-00115824.  
XX  
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-083078/11.  
XX  
PT Human tre carcinogenic gene protein 10.56 and encoding polynucleotide,  
PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection; immunological diseases and  
PT inflammation.  
XX  
PS Example 2; Page 17; 36pp; Chinese.  
XX  
CC The invention relates to an isolated polypeptide of human tre  
CC carcinogenic gene protein 10.56 comprising a 96 residue amino acid  
CC sequence, fully defined in the specification, or its fragment, analogue  
CC or derivative. The polypeptide is useful in the diagnosis and treatment  
CC of malignant tumors, haemopathy, human immunodeficiency virus (HIV)  
CC infection, immunological diseases and various inflammatory disorders. The  
CC present sequence is a primer used to amplify a polynucleotide encoding  
CC the polypeptide of the invention  
XX  
SQ Sequence 24 BP; 0 A; 3 C; 0 G; 21 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2157 TTTTCTCCTTTT 2180  
DB 1 TTTTCTTCTTCTTCTTCTTCTT 24

RESULT 1746  
ABQ73262  
ID ABQ73262 standard; DNA; 24 BP.  
XX  
AC ABQ73262;  
XX

DT 30-SEP-2002 (first entry)  
XX  
DE Human ribosomal protein L312.54 PCR primer 2 SEQ ID NO:4.  
XX  
KW Human; ribosomal protein L312.54; malignant tumour; inflammation;  
KW development disorder; immunological disease; haemopathy; HIV infection;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1339454-A.  
XX  
PD 13-MAR-2002.  
XX  
PF 23-AUG-2000; 2000CN-00119720.  
XX  
PR 23-AUG-2000; 2000CN-00119720.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-455356/49.  
XX  
PT New polypeptide-ribosomal protein L312.54 and polynucleotide for encoding  
PT said polypeptide.  
XX  
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.  
XX  
CC The present invention describes human ribosomal protein L312.54 (I). Also  
CC described is a process for producing (I) using DNA recombination  
CC technology. (I) and the polynucleotide encoding it can be used for  
CC treating various diseases, such as malignant tumour, inflammations,  
CC development disorder, immunological diseases, haemopathy and HIV  
CC infection. The present sequence represents a PCR primer for (I), which is  
CC used in an example from the present invention  
XX  
SQ Sequence 24 BP; 3 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2161 TCTCCTTTT 2184  
DB 1 TATCCTTTTAAATGTTT 24

RESULT 1747  
ABQ04183  
ID ABQ04183 standard; DNA; 24 BP.  
XX  
AC ABQ04183;  
XX  
DT 11-JUN-2002 (first entry)  
XX  
DE Oligonucleotide adapter/capture probe 4174.  
XX  
KW Oligonucleotide array; adapter sequence; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO200216649-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026519.  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
XX  
PA 29-AUG-2000; 2000US-0228854P.  
XX  
PA (ILLU-) ILLUMINA INC.

PI Gunderson K;  
XX WPI; 2002-292068/33.  
DR  
XX  
PT Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
PS Claim 1; Page 141; 261pp; English.  
XX  
CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
SQ Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1086 AAGGTGAAGCTGTTTCATTGGCTA 1109  
Db 1 AAGGTGGTGCCATTCATTGGCTA 24  
  
RESULT 1748  
ABQ00107  
ID ABQ00107 standard; DNA; 24 BP.  
AC ABQ00107;  
XX  
DT 11-JUN-2002 (first entry)  
DE Oligonucleotide adapter/capture probe 98.  
XX  
KW Oligonucleotide array; adapter sequence; probe; ss.  
OS Synthetic.  
XX  
PN WO200216649-A2.  
XX  
PD 28-FEB-2002.  
XX  
PF 27-AUG-2001; 2001WO-US026519.  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
PA (ILLU-) ILLUMINA INC.  
XX  
PI Gunderson K;  
XX  
DR WPI; 2002-292068/33.  
XX  
PT Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
PS Claim 1; Page 46; 261pp; English.  
XX  
CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of

CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
SQ Sequence 24 BP; 5 A; 4 C; 7 G; 8 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1086 AAGGTGAAGCTGTTTCATTGGCTA 1109  
Db 1 AAGGTGGTGCCATTCATTGGCTA 24  
  
RESULT 1749  
ABQ04224/c  
ID ABQ04224 standard; DNA; 24 BP.  
XX  
AC ABQ04224;  
XX  
DT 11-JUN-2002 (first entry)  
XX  
DE Oligonucleotide adapter/capture probe 4215.  
DE  
XX Oligonucleotide array; adapter sequence; probe; ss.  
KW  
XX  
OS Synthetic.  
OS  
XX WO200216649-A2.  
XX  
PN  
XX  
PD 28-FEB-2002.  
PD  
XX  
PF 27-AUG-2001; 2001WO-US026519.  
PF  
XX  
PR 25-AUG-2000; 2000US-0227948P.  
PR 29-AUG-2000; 2000US-0228854P.  
XX  
PA (ILLU-) ILLUMINA INC.  
XX  
PI Gunderson K;  
XX  
DR WPI; 2002-292068/33.  
XX  
PT Array comprising adapter sequences useful for immobilizing or detecting a  
PT target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes.  
XX  
PS Claim 1; Page 141; 261pp; English.  
XX  
CC The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-  
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid  
CC and contacting the modified target nucleic acid with (I). The steps of  
CC above method is useful for detecting a target nucleic acid, which further  
CC comprises detecting the presence of the modified target nucleic acid  
XX  
SQ Sequence 24 BP; 8 A; 7 C; 4 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1086 AAGGTGAAGCTGTTTCATTGGCTA 1109  
Db 24 AAGGTGGTGCCATTCATTGGCTA 1  
  
RESULT 1750  
ABA99264  
ID ABA99264 standard; DNA; 24 BP.





XX Example 11; Page 37; 139pp; English.  
PS Primers for 5'RACE (see AAV27256 and AAV27258), for nested 5'RACE (see  
XX AAV27259), for 3'RACE (see AAV27255) and for nested 3'RACE (see AAV27257)  
CC are based on previously obtained 5' and 3'RACE products of sodium  
CC salicylate-treated sunflower cv. zebulon leaf cDNA (see AAV27252-54).  
CC They were used to obtain further sequence information related to the  
CC novel antifungal protein MS59. 4 Partial cDNA clones were obtained, and  
CC these were used to produce a full-length sequence (see AAV27260) for  
CC sunflower leaf antifungal MS59 protein (see AAW55053). Claimed antifungal  
CC proteins, including MS59, have a mol.wt. of 55-65 kDa (SDS-PAGE), have  
CC carbohydrate oxidase (especially glucose oxidase) activity, show anti-  
CC phytophthora and/or anti-pythium activity, can be expressed in transgenic  
CC plants to reduce susceptibility to infection by fungi, or expressed in  
CC host cells for use in antifungal compositions. Plants engineered to  
CC express the antifungal proteins require reduced treatments with  
CC fungicides and have a longer shelf-life  
XX  
SQ Sequence 25 BP; 6 A; 2 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1004 GAGAACTTGGACAGATCGGGTTG 1027  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 GGGAAAGTTGCAGAGATTGGGTTG 25

RESULT 1753  
AAA68966  
ID AAA68966 standard; DNA; 25 BP.  
XX  
AC AAA68966;

DT 15-SEP-2003 (revised)  
DT 06-AUG-2003 (revised)  
DT 27-OCT-2000 (first entry)  
XX

DE Bacteriophage 96 ORF RBS sequence 96ORF358.

XX Bacteriophage; antimicrobial; genome; identification; antibacterial;  
KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;  
KW bacterial infection; ss.  
XX

OS Staphylococcus aureus; bacteriophage 96.

XX WO2000032825-A2.

XX 08-JUN-2000.

XX 03-DEC-1999; 99WO-IB002040.

XX 03-DEC-1998; 98US-0110992P.  
PR 03-JUN-1999; 99US-00326144.  
PR 28-SEP-1999; 99US-00407804.  
PR 30-SEP-1999; 99US-0157218P.  
PR 01-DEC-1999; 99US-0168777P.  
PR 02-DEC-1999; 99US-00454252.  
XX

PA (PHAG-) PHAGETECH INC.

XX Pelletier J, Gros P, Dubow M;

XX WPI; 2000-412361/35.

XX Identifying a bacteriophage coding region for treating bacterial  
PT infections comprises identifying a nucleic acid encoding a product that  
PT inhibits bacteria when a bacteriophage infects a bacterium.  
XX

PS Disclosure; Page 204; 456pp; English.

XX

CC The present invention describes a method for identifying a bacteriophage  
CC coding region encoding a product active on an essential bacterial target.  
CC The method comprises identifying a nucleic acid sequence encoding a gene  
CC product that provides a bacteria-inhibiting function when an  
CC uncharacterised bacteriophage infects a pathogenic bacterium. The  
CC compound active on a target of a bacteriophage inhibitor protein in a  
CC bacteria is used to treat or prevent a bacterial infection in an animal.  
CC AAA68243 to AAA69442 and AAB16523 to AAB16954 represent bacteriophage  
CC nucleotide and protein sequences which are used in the exemplification of  
CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)  
XX (Updated on 15-SEP-2003 to standardise OS field)

SQ Sequence 25 BP; 8 A; 2 C; 3 G; 12 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2760 TAATAAAAGTATTCTTGTAGAAT 2783  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 TCATAAAAGTATTCTTGTAGTAT 25

RESULT 1754  
AAC96038/c  
ID AAC96038 standard; DNA; 25 BP.  
XX  
AC AAC96038;

DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #5.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX Homo sapiens.

XX WO200065088-A2.

XX 02-NOV-2000.

XX 20-APR-2000; 2000WO-EP003636.

XX 26-APR-1999; 99EP-00303215.

XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.

XX Ulfendahl P, Wong K;

XX WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 44; 66pp; English.

XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX

SQ Sequence 25 BP; 4 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

**XX** DNA sequence analysis; sequencing; protein sequence; protein structure;  
**KW**

Wong K: 11 fendahl p.

xx DNA sequence analysis; sequencing; protein sequence; protein structure;  
xw

DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 51; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2779 AGAATTGAAAAA 2802  
Db 24 AGAAGGGAGGAAAAA 1  
  
RESULT 1758  
AAC95726/c  
ID AAC95726 standard; DNA; 25 BP.  
XX  
AC AAC95726;  
XX  
DT 26-FEB-2001 (first entry)  
DE HLA DQA1 gene PCR primer #23.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
AC AAC95726;  
XX  
DT 26-FEB-2001 (first entry)  
DE HLA DQA1 gene PCR primer #23.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 39; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX

SQ Sequence 25 BP; 0 A; 6 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2779 AGAATTGAAAAA 2802  
Db 24 AGAAGGGAGGAAAAA 1  
  
RESULT 1759  
AAC96237/c  
ID AAC96237 standard; DNA; 25 BP.  
XX  
AC AAC96237;  
XX  
DT 26-FEB-2001 (first entry)  
DE 16s rRNA gene PCR primer #204.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 47; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 5 A; 2 C; 4 G; 14 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2776 GTTACAATTGAAAAA 2799  
Db 24 GTTCTACTTGCAAAAAA 1  
  
RESULT 1760  
AAC96446/c  
ID AAC96446 standard; DNA; 25 BP.  
XX  
AC AAC96446;  
XX





XX PR 16-MAR-2001; 2001US-0276759P.  
XX PA (AFFY-) AFFYMETRIX INC.  
XX PI Mittmann MP;  
XX PI WPI; 2003-567953/53.  
DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
PT  
XX  
PS Claim 1; SEQ ID NO 108331; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 4 A; 11 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 53 GCGGGGGCGCGCGCAGCGCCTG 76  
Db ||||| ||| ||||| |||||  
25 GGCAGGGGTGGCTTCAGACGCCTG 2  
RESULT 1763  
ACI33260  
ID ACI33260 standard; DNA; 25 BP.  
XX  
AC ACI33260;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 33251.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.  
XX PI Mittmann MP;  
XX PI WPI; 2003-567953/53.  
DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
PT  
XX  
PS Claim 1; SEQ ID NO 33251; 9pp; English.  
XX  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 7 A; 6 C; 4 G; 8 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 180 TAACCGATAATGTCAAGTACGAAG 203  
Db ||||| ||||| ||||| |||||  
2 TAACCCCTCATGTCTATGTACGAAG 25  
RESULT 1764  
ACK08351/c  
ID ACK08351 standard; DNA; 25 BP.  
XX  
AC ACK08351;  
XX  
DT 14-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 108332.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;  
PI WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 108332; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 3 A; 11 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 53 GCGGGGGGGCGGCAGACGCTG 76  
||| |||| ||| ||||| |||||  
Db 25 GGCAGGGGTGGCATCAGACGCTG 2  
  
RESULT 1765  
AAV12482  
ID AAV12482 standard; DNA; 26 BP.  
XX  
AC AAV12482;  
XX  
DT 15-MAY-1998 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO:5 from US5174320 Example 2.  
XX  
KW Synthesis; selection; amplification; circular oligonucleotide;  
KW rolling circle synthesis; diagnosis; therapeutic agent; ss.  
XX  
OS Synthetic.  
XX  
PN US5714320-A.  
XX  
PD 03-FEB-1998.  
XX  
PF 23-FEB-1995; 95US-00393439.  
XX  
PR 15-APR-1993; 93US-00047860.  
XX  
PA (UVRP ) UNIV ROCHESTER.  
XX  
PI Kool ET;  
XX

DR WPI; 1998-144278/13.  
XX Rolling circle synthesis of oligo:nucleotide(s) - using primed circular  
PT template to produce oligonucleotide multimer for cleavage.  
XX  
PS Example 2; Col 45; 38pp; English.  
XX  
CC The present sequence represents an oligonucleotide used in an example of  
CC the present invention. The present invention describes a method for  
CC synthesising a selected oligonucleotide (I) having well defined ends. The  
CC method comprises: (a) annealing a primer to a single-stranded (ss)  
CC circular template to yield a primed circular template, where the template  
CC comprises: (i) at least one nucleotide sequence complementary to (I); and  
CC (ii) at least one nucleotide effective to produce a cleavage site in the  
CC oligonucleotide multimer; (b) combining the primed circular template with  
CC at least two types of nucleotide triphosphates and a polymerase enzyme  
CC without the addition of auxiliary proteins to yield a ss oligonucleotide  
CC multimer complementary to the circular oligonucleotide template,  
CC comprising multiple copies of (I); and (c) cleaving the oligonucleotide  
CC multimer at the cleavage site to produce (I) having well defined ends.  
CC The method is used for the large-scale synthesis of DNA and RNA oligomers  
CC for use, e.g. as probes and diagnostic agents and/or therapeutic agents  
XX  
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 26;  
Best Local Similarity 83.3%; Pred. No. 2e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAAATAAAAAAAAAAAAAA 2804  
|| ||||| ||||| ||||| |||||  
Db 2 AAAAAAAAAAAAAACAAAAAATAAAAA 25  
  
RESULT 1766  
AAV59215  
ID AAV59215 standard; DNA; 26 BP.  
XX  
AC AAV59215;  
XX  
DT 14-DEC-1998 (first entry)  
XX  
DE Circular template for linear oligomer dT12.  
XX  
KW ss; circular; cyclic; RNA oligonucleotide; probe; standard; diagnostic;  
KW therapeutic agent.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding 1 /\*tag= a  
FT /\*note= "Position 1 optionally bound to position 26"  
FT misc\_binding 26 /\*tag= b  
FT /\*note= "Position 26 optionally bound to position 1"  
XX  
PN WO9838300-A1.  
XX  
PD 03-SEP-1998.  
XX  
PF 26-FEB-1998; 98WO-US003784.  
XX  
PR 26-FEB-1997; 97US-00805631.  
XX  
PA (UVRP ) UNIV ROCHESTER.  
XX  
PI Kool ET;  
XX  
DR WPI; 1998-481202/41.  
XX  
PT Synthesis of oligo:nucleotide(s) - using a single-stranded circular  
PT oligo:nucleotide template ribonucleotide tri:phosphate(s) and a



PT polymerase to form multimer(s) which can be cleaved.  
XX  
PS Example 2; Page 36; 100pp; English.  
XX  
CC The circular template was used for the synthesis of the oligomer dt12 in  
CC an example of the method of the invention for synthesising an RNA  
CC oligonucleotide, comprising combining a single-stranded circular  
CC oligonucleotide template comprising at least one copy of a nucleotide  
CC sequence complementary to the sequence of the desired RNA oligonucleotide  
CC with at least 2 types of ribonucleotide triphosphate and a polymerase  
CC enzyme to yield a single-stranded RNA oligonucleotide multimer  
CC complementary to the circular oligonucleotide template, where the RNA  
CC oligonucleotide multimer comprises multiple copies of the desired RNA  
CC oligonucleotide. The methods can be used for producing RNA  
CC oligonucleotides having a specific sequence and well defined ends. The  
CC RNA oligonucleotides produced can be used as probes, standards and  
CC diagnostic or therapeutic agents. They can be used for modifying the  
CC structure or function of a target molecule. They can also be used to  
CC cleave disease-associated RNA, DNA or protein  
XX  
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 26;  
Best Local Similarity 83.3%; Pred. No. 2e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAA AAAA 2804  
|| ||||| |||||  
Db 2 AAAAAA AAAA CAAAAA AAAA 25  
  
RESULT 1767  
AAX30018  
ID AAX30018 standard; DNA; 26 BP.  
XX  
AC AAX30018;  
XX  
DT 16-JUN-1999 (first entry)  
XX  
DE Precircle DNA oligonucleotide SEQ ID NO:5.  
XX  
KW Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.  
XX  
OS Synthetic.  
XX  
PN WO9909216-A2.  
XX  
PD 25-FEB-1999.  
XX  
PF 13-AUG-1998; 98WO-US016776.  
XX  
PR 13-AUG-1997; 97US-00910632.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Kool ET;  
XX  
DR WPI; 1999-181062/15.  
XX  
PT New detectably labelled oligonucleotide multimer, comprising multiple  
PT contiguous copies of a repeated oligonucleotide - useful for detecting  
PT target molecules in diagnosis and medicinal applications.  
XX  
PS Example 2; Page 41; 103pp; English.  
XX  
CC The present invention describes a detectably labelled oligonucleotide  
CC multimer, comprising multiple contiguous copies of a repeated  
CC oligonucleotides. The detectably labelled oligonucleotide multimer is  
CC useful for detecting a target molecule. Oligonucleotide multimers may be  
CC produced in sufficient quantity to be useful for diagnostic and medical  
CC applications. The multimers are useful for affinity labelling of  
CC proteins, and for signal amplification in highly sensitive affinity  
CC capture and sequence identification applications. The method provides a

CC faster, cheaper and simpler way for large-scale production of DNA and RNA  
CC oligomers and multimers. The incorporation of labels enables the  
CC oligonucleotide multimers to be useful in diagnostics and medicine. The  
CC present sequence represents an oligonucleotide used in an example from  
XX the present invention  
SQ Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 26;  
Best Local Similarity 83.3%; Pred. No. 2e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA AAAA AAAA 2804  
|| ||||| |||||  
Db 2 AAAAAA AAAA CAAAAA AAAA 25  
  
RESULT 1768  
ADC65872  
ID ADC65872 standard; DNA; 26 BP.  
XX  
AC ADC65872;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE DNA oligonucleotide #5.  
XX  
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;  
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;  
KW cation-mediated delivery; bacterial infection; viral infection;  
KW drug resistant infection; double stranded DNA oligomer; ss.  
XX  
OS Synthetic.  
XX  
PN US2003087241-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 30-NOV-2001; 2001US-00997931.  
XX  
PR 15-APR-1993; 93US-00047860.  
PR 23-FEB-1995; 95US-00393439.  
PR 26-FEB-1997; 97US-00805631.  
PR 11-MAY-2000; 2000US-00569344.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Kool ET;  
XX  
DR WPI; 2003-755141/71.  
XX  
PT Synthesizing RNA oligonucleotide involves combining single-stranded  
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase  
PT enzyme to yield desired RNA complementary to circular oligonucleotide  
PT template.  
XX  
PS Example 2; SEQ ID NO 5; 78pp; English.  
XX  
CC The invention relates to a method for synthesising an RNA  
CC oligonucleotide, comprising combining a single-stranded circular  
CC oligonucleotide template with at least two types of ribonucleotide  
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA  
CC oligonucleotide multimer complementary to the circular oligonucleotide  
CC template, where the RNA oligonucleotide multimer comprises multiple  
CC copies of the desired RNA oligonucleotide. The method is useful for  
CC synthesising an RNA oligonucleotide with well-defined ends. The circular  
CC oligonucleotide is introduced into the cell using direct injection,  
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or  
CC cation-mediated delivery. The method is useful for treating bacterial  
CC and/or viral infections in mammals, particularly drug resistant  
CC infections, and for producing double stranded DNA oligomers. The method  
CC is performed in the absence of an oligonucleotide primer, or without the  
CC addition of auxiliary proteins. This sequence represents an



CC	oligonucleotide used in the method of the invention.	CC	HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
XX		CC	activated receptor 2 (PAR2), paired-like homeodomain transcription factor
SQ	Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;	CC	2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
		CC	SDC4) or a MINT31 sequence
		XX	
	Query Match 0.6%; Score 17.6; DB 1; Length 26;	SQ	Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;
	Best Local Similarity 83.3%; Pred. No. 2e+03;		
	Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
			Query Match 0.6%; Score 17.6; DB 1; Length 26;
			Best Local Similarity 94.4%; Pred. No. 2e+03;
			Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	2781 AATTGAAAAA 2804	QY	2785 GAAAAA 2802
			:
Db	2 AAAAAA 25	Db	3 RAAAAA 20
RESULT 1769		RESULT 1770	
AAS01617		AAS01577	
ID	AAS01617 standard; DNA; 26 BP.	ID	AAS01577 standard; DNA; 26 BP.
XX		XX	
AC	AAS01617;	AC	AAS01577;
XX		XX	
DT	18-JUL-2001 (first entry)	DT	18-JUL-2001 (first entry)
XX		XX	
DE	Human MINT31/CACNA1G region 6 bisulfite GM6 reverse PCR primer.	DE	Human T-type calcium channel CACNA1G R6 3'-bisulfite PCR primer.
XX		XX	
KW	Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;	KW	Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
KW	cellular proliferative disorder; colorectal cancer; age related disease;	KW	cellular proliferative disorder; colorectal cancer; age related disease;
KW	apolipoprotein B; APOB; caudal type homeobox transcription factor 2;	KW	apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
KW	CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;	KW	CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;
KW	G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';	KW	G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
KW	HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;	KW	HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
KW	PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;	KW	PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
KW	patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;	KW	patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
KW	chromosome 17; PCR primer; ss.	KW	chromosome 17; PCR primer; ss.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	WO200119845-A1.	PN	WO200119845-A1.
XX		XX	
PD	22-MAR-2001.	PD	22-MAR-2001.
XX		XX	
PF	14-SEP-2000; 2000WO-US025479.	PF	14-SEP-2000; 2000WO-US025479.
XX		XX	
PR	15-SEP-1999; 99US-00398522.	PR	15-SEP-1999; 99US-00398522.
XX		XX	
PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.	PA	(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX		XX	
PI	Issa J;	PI	Issa J;
XX		XX	
DR	WPI; 2001-244777/25.	DR	WPI; 2001-244777/25.
XX		XX	
PT	New nucleic acid molecule for use as a marker for screening cancer,	PT	New nucleic acid molecule for use as a marker for screening cancer,
PT	comprises the coding region for a T-type calcium channel and regulatory	PT	comprises the coding region for a T-type calcium channel and regulatory
PT	sequences associated with the channel.	PT	sequences associated with the channel.
XX		XX	
PS	Claim 21; Page 35; 125pp; English.	PS	Claim 21; Page 34; 125pp; English.
XX		XX	
CC	The present sequence for bisulfite GM6 reverse PCR primer is used to	CC	The present sequence for 3'-bisulfite PCR primer is used to study the
CC	study the methylation state of region 6 in human MINT31/T-type calcium	CC	methylation state of region R6 in a novel human T-type calcium channel
CC	channel CACNA1G which map to chromosome 17. The methylation state of	CC	CACNA1G which maps to chromosome 17. The methylation state of specific
CC	specific regions within CpG islands associated with the CACNA1G gene	CC	CACNA1G which maps to chromosome 17. The methylation state of specific
CC	correlate with several cancerous phenotypes involving various tissue and	CC	regions within CpG islands associated with the CACNA1G gene correlate
CC	cell types. Since aberrant methylation of normally unmethylated CpG	CC	with several cancerous phenotypes involving various tissue and cell
CC	islands is often observed in immortalised and transformed cells, CACNA1G	CC	types. Since aberrant methylation of normally unmethylated CpG islands is
CC	is implicated in cellular proliferative disorders e.g. leukaemia,	CC	often observed in immortalised and transformed cells, CACNA1G is
CC	colorectal, lung, breast and other cancers. The nucleic acid coding for	CC	implicated in cellular proliferative disorders e.g. leukaemia,
CC	CACNA1G is useful as a marker for screening cancer and age related	CC	colorectal, lung, breast and other cancers. The nucleic acid coding for
CC	diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for	CC	CACNA1G is useful as a marker for screening cancer and age related
CC	amplification of a CpG-containing nucleic acid, where the primer	CC	diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC	hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can	CC	CACNA1G is useful as a marker for screening cancer and age related
CC	be used for detecting aberrant methylation. The CpG island sequences	CC	diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for
CC	(AAS01677-AAS01692) are selected from genes encoding CACNA1G,	CC	amplification of a CpG-containing nucleic acid, where the primer
CC	apolipoprotein B (APOB), caudal type homeobox transcription factor 2	CC	hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can
CC	(CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G	CC	be used for detecting aberrant methylation. The CpG island sequences
CC	protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';	CC	(AAS01677-AAS01692) are selected from genes encoding CACNA1G,

CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2  
CC (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G  
CC protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';  
CC HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-  
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor  
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;  
CC SDC4) or a MINT31 sequence  
XX  
SQ Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 26;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAATAAAAAAAAAA 2802  
Db :|||||  
3 RAAAAAAAAAAAAAAAAA 20  
  
RESULT 1771  
AAS01670/c  
ID AAS01670 standard; DNA; 26 BP.  
XX  
AC AAS01670;  
XX  
DT 18-JUL-2001 (first entry)  
XX  
DE Human MINT31/CACNA1G region 6 reverse target sequence for bisulfite PCR.  
XX  
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;  
KW cellular proliferative disorder; colorectal cancer; age related disease;  
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;  
KW chromosome 17; ds.  
XX  
OS Homo sapiens.  
XX WO200119845-A1.  
PN  
XX  
PD 22-MAR-2001.  
XX  
PF 14-SEP-2000; 2000WO-US025479.  
XX  
PR 15-SEP-1999; 99US-00398522.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Issa J;  
XX  
DR WPI; 2001-244777/25.  
XX  
PT New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.  
XX  
PS Claim 20; Page 36; 125pp; English.  
XX  
CC The present sequence for human MINT31/T-type calcium channel CACNA1G  
CC region 6 reverse target sequence is used to study the methylation state  
CC of region 6 in MINT31/CACNA1G which map to chromosome 17. The methylation  
CC state of specific regions within CpG islands associated with the CACNA1G  
CC gene correlate with several cancerous phenotypes involving various tissue  
CC and cell types. Since aberrant methylation of normally unmethylated CpG  
CC islands is often observed in immortalised and transformed cells, CACNA1G  
CC is implicated in cellular proliferative disorders e.g. leukaemia,  
CC colorectal, lung, breast and other cancers. The nucleic acid coding for  
CC CACNA1G is useful as a marker for screening cancer and age related  
CC diseases. A diagnostic kit containing primers (AAS01574-AAS01623) for  
CC amplification of a CpG-containing nucleic acid, where the primer

CC hybridises with a target polynucleotide sequence (AAS01627-AAS01676), can  
CC be used for detecting aberrant methylation. The CpG island sequences  
CC (AAS01677-AAS01692) are selected from genes encoding CACNA1G,  
CC apolipoprotein B (APOB), caudal type homeobox transcription factor 2  
CC (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBN1), G  
CC protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';  
CC HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-  
CC activated receptor 2 (PAR2), paired-like homeodomain transcription factor  
CC 2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;  
CC SDC4) or a MINT31 sequence  
XX  
SQ Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 17.6; DB 1; Length 26;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAATAAAAAAAAAA 2802  
Db :|||||  
24 RAAAAAAAAAAAAAAAAA 7  
  
RESULT 1772  
AAS01630  
ID AAS01630 standard; DNA; 26 BP.  
XX  
AC AAS01630;  
XX  
DT 18-JUL-2001 (first entry)  
XX  
DE Human CACNA1G R6 3'-target sequence for bisulfite PCR.  
XX  
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;  
KW cellular proliferative disorder; colorectal cancer; age related disease;  
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;  
KW chromosome 17; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119845-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 14-SEP-2000; 2000WO-US025479.  
XX  
PR 15-SEP-1999; 99US-00398522.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Issa J;  
XX  
DR WPI; 2001-244777/25.  
XX  
PT New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.  
XX  
PS Claim 20; Page 37; 125pp; English.  
XX  
CC The present sequence for human T-type calcium channel R6 3'-target  
CC sequence (complementary to the 3'-bisulfite PCR primer) is used to study  
CC the methylation state of R6 of CACNA1G which maps to chromosome 17. The  
CC methylation state of specific regions within CpG islands associated with  
CC the CACNA1G gene correlate with several cancerous phenotypes involving  
CC various tissue and cell types. Since aberrant methylation of normally  
CC unmethylated CpG islands is often observed in immortalised and  
CC transformed cells, CACNA1G is implicated in cellular proliferative  
CC disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The





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RESULT 1775
ADC65873/c
ID ADC65873 standard; DNA; 29 BP.
XX
AC ADC65873;
XX
DT 18-DEC-2003 (first entry)
XX
DE DNA oligonucleotide #6.
XX
KW RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW cation-mediated delivery; bacterial infection; viral infection;
KW drug resistant infection; double stranded DNA oligomer; ss.
XX
OS Synthetic.
XX
PN US2003087241-A1.
XX
PD 08-MAY-2003.
XX
PF 30-NOV-2001; 2001US-00997931.
XX
PR 15-APR-1993; 93US-00047860.
PR 23-FEB-1995; 95US-00393439.
PR 26-FEB-1997; 97US-00805631.
PR 11-MAY-2000; 2000US-00569344.
XX
PA (UYRP ) UNIV ROCHESTER.
XX
PI Kool ET;
XX
DR WPI; 2003-755141/71.
XX
PT Synthesizing RNA oligonucleotide involves combining single-stranded
PT circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT enzyme to yield desired RNA complementary to circular oligonucleotide
PT template.
XX
PS Example 2; SEQ ID NO 6; 78pp; English.
XX
CC The invention relates to a method for synthesising an RNA
CC oligonucleotide, comprising combining a single-stranded circular
CC oligonucleotide template with at least two types of ribonucleotide
CC triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC oligonucleotide multimer complementary to the circular oligonucleotide
CC template, where the RNA oligonucleotide multimer comprises multiple
CC copies of the desired RNA oligonucleotide. The method is useful for
CC synthesising an RNA oligonucleotide with well-defined ends. The circular
CC oligonucleotide is introduced into the cell using direct injection,
CC electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC cation-mediated delivery. The method is useful for treating bacterial
CC and/or viral infections in mammals, particularly drug resistant
CC infections, and for producing double stranded DNA oligomers. The method
CC is performed in the absence of an oligonucleotide primer, or without the
CC addition of auxiliary proteins. This sequence represents an
CC oligonucleotide used in the method of the invention.
XX
SQ Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAATAAAAAAAAAA 2804
Db 29 AAAAAAAAAAACAAAAA 6

RESULT 1776
AAF74918
ID AAF74918 standard; DNA; 29 BP.
```

```
XX AAF74918;
AC
XX 23-MAY-2001 (first entry)
DT
XX
DE CD40L poly-A tract sequence SEQ ID NO:15.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAATAAAAAAAAAA 2804
Db 1 AAAAAAAAAAACAAAAA 24

RESULT 1777
AAF74907
ID AAF74907 standard; DNA; 29 BP.
XX
AC AAF74907;
XX
XX 23-MAY-2001 (first entry)
DT
XX
DE CD40L poly-A tract sequence SEQ ID NO:4.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
```



XX 22-MAR-2001.  
XX 13-SEP-2000; 2000WO-US024966.  
XX 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX Example 1; Fig 3; 90pp; English.  
XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC anti-rheumatic, immunosuppressive and anti-inflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.6; DB 1; Length 29;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAA AAAAAAAAAA 2804  
DB 1 AAAAAA AAAAAAAAAA CAAAAA 24  
RESULT 1778  
AAF74935  
ID AAF74935 standard; DNA; 29 BP.  
XX AAF74935;  
XX 23-MAY-2001 (first entry)  
XX CD40L poly-A tract sequence SEQ ID NO:32.  
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; anti-rheumatic; immunosuppressive;  
KW anti-inflammatory; inflammatory disease; autoimmune disease; ds.  
XX Homo sapiens.  
XX WO200119844-A1.  
XX 22-MAR-2001.  
XX 13-SEP-2000; 2000WO-US024966.  
XX 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX Crow MK, Li Y;  
XX WPI; 2001-244775/25.  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT

PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX Example 1; Fig 3; 90pp; English.  
XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC anti-rheumatic, immunosuppressive and anti-inflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.6; DB 1; Length 29;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAA AAAAAAAAAA 2804  
DB 1 AAAAAA AAAAAAAAAA CAAAAA 24  
RESULT 1779  
AAF74921  
ID AAF74921 standard; DNA; 29 BP.  
XX AAF74921;  
XX 23-MAY-2001 (first entry)  
XX CD40L poly-A tract sequence SEQ ID NO:18.  
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; anti-rheumatic; immunosuppressive;  
KW anti-inflammatory; inflammatory disease; autoimmune disease; ds.  
XX Homo sapiens.  
XX WO200119844-A1.  
XX 22-MAR-2001.  
XX 13-SEP-2000; 2000WO-US024966.  
XX 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX Example 1; Fig 3; 90pp; English.  
XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC anti-rheumatic, immunosuppressive and anti-inflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
SQ

```
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA
Db 1 AAAAAA

RESULT 1780
AAF74928
ID AAF74928 standard; DNA; 29 BP.
XX
AC AAF74928;
XX
DT 23-MAY-2001 (first entry)
XX
DE CD40L poly-A tract sequence SEQ ID NO:25.
XX
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO200119844-A1.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-US024966.
XX
PR 13-SEP-1999; 99US-0153625P.
XX
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI Crow MK, Li Y;
XX
DR WPI; 2001-244776/25.
XX
PT New altered CD40L promoter for use in the study, diagnosis and treatment
PT of a variety of inflammatory disorders and autoimmune diseases, such as
PT rheumatoid arthritis.
XX
PS Example 1; Fig 3; 90pp; English.
XX
CC The present invention describes an isolated, purified nucleic acid, which
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC residues 331-455 of the sequence comprising 455 nucleotides given in
CC AAF74905 where A in the wild type sequence at position 331 (corresponding
CC to position -125) is replaced with C. (I) has antiarthritic,
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC be used in gene therapy. (I) is useful in the study, diagnosis and
CC treatment of inflammatory and autoimmune diseases, as well as diseases in
CC which elevated expression of CD40L is a factor, e.g., rheumatoid
CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.6; DB 1; Length 29;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA
Db 1 AAAAAA

CC arthritis. The present sequence represents a CD40L poly-A tract sequence
CC which is used in an example from the present invention
XX
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.6; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA
Db 31 AAAAAA

RESULT 1781
ABA97621/c
ID ABA97621 standard; DNA; 31 BP.
XX
AC ABA97621;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly j nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 31 BP; 4 A; 1 C; 0 G; 26 T; 0 U; 0 Other;

Query Match          0.6%; Score 17.6; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA
Db 31 AAAAAA

RESULT 1782
AAQ75552/c
ID AAQ75552 standard; DNA; 19 BP.
XX
AC AAQ75552;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
```



KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAATAAAAAAAAAA 2803  
Db 19 GTAAAAAATAAAAAAAAAA 1  
  
RESULT 1786  
AAQ75557  
ID AAQ75557 standard; DNA; 19 BP.  
XX  
AC AAQ75557;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTCTTTTCTTTTCTTTT 2184  
Db 1 TTTTCTTTTCTTTTCTTTT 19  
  
RESULT 1787  
AAQ75549  
ID AAQ75549 standard; DNA; 19 BP.  
XX  
AC AAQ75549;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTCTTTTCTTTTCTTTT 2184  
Db 1 TTTTCTTTTCTTTTCTTTT 19





Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAAAA 2802  
Db 19 TCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1791  
AAQ75550/c  
ID AAQ75550 standard; DNA; 19 BP.  
XX  
AC AAQ75550;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1792  
ADE29541  
ID ADE29541 standard; RNA; 19 BP.  
XX  
AC ADE29541;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.  
XX  
KW short interfering nucleic acid; siNA; downregulation; inhibition;

KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
KW cytotostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;  
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;  
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
KW psoriasis; inflammatory bowel disease; drug screening;  
KW genetic engineering; pharmacogenomic; gene mapping; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003072590-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-JAN-2003; 2003WO-US002510.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;  
XX  
XX WPI; 2003-689980/65.  
DR  
XX  
PT New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of cancer, downregulates expression of mitogen-activated  
PT protein kinase genes.  
XX  
PS Example 3; SEQ ID NO 163; 164pp; English.  
XX

CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of a mitogen-activated protein kinase  
CC (MAPK) genes by RNA interference. Also described: (1) a method for  
CC modulating expression of MAPK genes in cells, tissue explants or  
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,  
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
CC disease). They can also be used for drug screening; diagnosis; target  
CC identification and validation; genetic engineering; pharmacogenomics;  
CC studying gene function and gene mapping (e.g. of single-nucleotide  
CC polymorphisms). The present sequence represents a MAPK siNA which is used  
CC in the exemplification of the present invention.  
XX

SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAAAAAAAAAAAAAAAAA 2801  
Db 1 UUCAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1793  
ADE29541/c  
ID ADE29541 standard; RNA; 19 BP.  
XX  
AC ADE29541;  
XX



Db 1 UUUUUUUUUUUUUUUUGAA 19  
RESULT 1795  
ADE29704/c  
ID ADE29704 standard; RNA; 19 BP.  
XX  
AC ADE29704;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.  
XX  
KW short interfering nucleic acid; siNA; downregulation; inhibition;  
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;  
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;  
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;  
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
KW psoriasis; inflammatory bowel disease; drug screening;  
KW genetic engineering; pharmacogenomic; gene mapping; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003072590-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 28-JAN-2003; 2003WO-US002510.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;  
XX  
XX WPI; 2003-689980/65.  
DR  
XX  
PT New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of cancer, downregulates expression of mitogen-activated  
PT protein kinase genes.  
XX  
PS Example 3; SEQ ID NO 326; 164pp; English.  
XX  
CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of a mitogen-activated protein kinase  
CC (MAPK) genes by RNA interference. Also described: (1) a method for  
CC modulating expression of MAPK genes in cells, tissue explants or  
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,  
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
CC disease). They can also be used for drug screening; diagnosis; target  
CC identification and validation; genetic engineering; pharmacogenomics;  
CC studying gene function and gene mapping (e.g. of single-nucleotide  
CC polymorphisms). The present sequence represents a MAPK siNA which is used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 19 BP; 2 A; 0 C; 1 G; 0 T; 16 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2801  
Db 19 TTCAAAAA 1  
RESULT 1796  
AAQ75582/c  
ID AAQ75582 standard; DNA; 20 BP.  
XX  
AC AAQ75582;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2801  
Db 19 TTAAAAAA 1  
RESULT 1797  
AAQ75579/c  
ID AAQ75579 standard; DNA; 20 BP.  
XX  
AC AAQ75579;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.



XX Synthetic.  
XX  
XX  
PN JP06303997-A.  
XX  
XX 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2801  
Db 19 TTA 1  
RESULT 1798  
AAQ75597  
ID AAQ75597 standard; DNA; 20 BP.  
XX  
XX AAQ75597;  
AC  
XX  
XX 04-AUG-1995 (first entry)  
DT  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2801  
Db 19 TTA 1  
RESULT 1798  
AAQ75597  
ID AAQ75597 standard; DNA; 20 BP.  
XX  
XX AAQ75597;  
AC  
XX  
XX 04-AUG-1995 (first entry)  
DT  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2169 TTTT 2187  
Db 1 TTTT 19  
RESULT 1799  
AAQ75595  
ID AAQ75595 standard; DNA; 20 BP.  
XX  
XX AAQ75595;  
AC  
XX 04-AUG-1995 (first entry)  
DT  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2169 TTTT 2187  
Db 1 TTTT 19  
RESULT 1800  
AAA91207



PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||  
Db 20 AACAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 1803  
AAQ75584/c  
ID AAQ75584 standard; DNA; 20 BP.  
XX  
AC AAQ75584;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804

Db 19 ATAAAAAAAAAAAAAAAAAAAA 1  
|  
RESULT 1804  
AAQ75585/c  
ID AAQ75585 standard; DNA; 20 BP.  
XX  
AC AAQ75585;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
CC Analysis of cDNA and gene expression - by amplification of mRNA followed  
CC by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||  
Db 20 AATAAAAAAAAAAAAAAAAAAAAA 2  
  
RESULT 1805  
AAQ75568/c  
ID AAQ75568 standard; DNA; 20 BP.  
XX  
AC AAQ75568;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX

PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1806  
AAQ75570  
ID AAQ75570 standard; DNA; 20 BP.  
XX  
AC AAQ75570;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1806  
AAQ75570  
ID AAQ75570 standard; DNA; 20 BP.  
XX  
AC AAQ75570;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1806  
AAQ75590/c  
ID AAQ75590 standard; DNA; 20 BP.  
XX  
AC AAQ75590;  
XX  
DT 04-AUG-1995 (first entry)

CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2184  
Db 1 TTTTTTTTTTTTTTTTGT 19  
RESULT 1807  
AAQ75589/c  
ID AAQ75589 standard; DNA; 20 BP.  
XX  
AC AAQ75589;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1808  
AAQ75590/c  
ID AAQ75590 standard; DNA; 20 BP.  
XX  
AC AAQ75590;  
XX  
DT 04-AUG-1995 (first entry)



XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; Gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803

Db 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1809

AAQ75602

ID AAQ75602 standard; DNA; 20 BP.

XX

AC AAQ75602;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

XX Analysis; Gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184

Db 1 TTTTTTTTTTTTTTTTCT 19

RESULT 1810

ABZ85534

ID ABZ85534 standard; DNA; 20 BP.

XX

AC ABZ85534;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX

PS Claim 15; SEQ ID NO 776; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAAAAAAAAAAGAAAA 19

RESULT 1811  
ABZ88938  
ID ABZ88938 standard; DNA; 20 BP.

XX AC ABZ88938;

XX DT 17-OCT-2003 (first entry)

DE DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4180; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAAAAAAAAA 2802  
| | | | | | | | | | | | | | | | | |  
Db 2 TCAAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1812  
ABZ88813/c  
ID ABZ88813 standard; DNA; 20 BP.

XX AC ABZ88813;

XX DT 17-OCT-2003 (first entry)

DE DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4055; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

QY 2786 AAAAAA AAAAAA AAAAAA 2804

FD 01-NOV-1994:

XX 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
  
RESULT 1816  
ABZ89703  
ID ABZ89703 standard; DNA; 20 BP.  
XX  
AC ABZ89703;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; lung; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A., Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX

PS Disclosure; SEQ ID NO 4945; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGA AAAAA AAAAA AAAAA AAAAA AAAAA 2801  
Db 2 TTTA AAAAA AAAAA AAAAA AAAAA AAAAA 20  
  
RESULT 1817  
AAQ75574/c  
ID AAQ75574 standard; DNA; 20 BP.  
XX  
AC AAQ75574;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX







PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 1824  
AAQ75567/c  
ID AAQ75567 standard; DNA; 20 BP.  
XX  
AC AAQ75567;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 19 ACAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1825  
AAQ75571/c  
ID AAQ75571 standard; DNA; 20 BP.  
XX  
AC AAQ75571;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2803  
Db 19 GCAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1826  
AAF99943/c  
ID AAF99943 standard; DNA; 20 BP.  
XX  
AC AAF99943;  
XX  
DT 12-JUL-2001 (first entry)  
XX  
DE Synthetic oligonucleotide #9.





XX  
PS Claim 15: SEO ID NO 911; 872pp; English.

XX  
PS Disclosure: SEO ID NO 6071; 872pp; English.

XX  
PS Claim 15: SEO ID NO 911; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 8 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1486 AACCTGCAGAAATGGAG 1504  
| | | | | | | | | | | | | | | | | | | |  
Db 2 AACCTGCAGAAATGGAG 20

RESULT 1831  
ABZ89301  
ID ABZ89301 standard; DNA; 20 BP.

XX AC ABZ89301;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4543; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAA 2802  
| | | | | | | | | | | | | | | | | | | |  
Db 2 TCACAAAAAAAAAAAAA 20

RESULT 1832  
ABZ89301/c  
ID ABZ89301 standard; DNA; 20 BP.

XX AC ABZ89301;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX DR WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4543; 872pp; English.

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTT 2187  
Db 20 TTTTTTTTTTTTTTTGA 2

RESULT 1833  
AAQ75731/C  
ID AAQ75731 standard; DNA; 21 BP.

XX AC AAQ75731;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2801  
Db 19 TTAAAAA 1

RESULT 1834  
AAQ75734/C

ID AAQ75734 standard; DNA; 21 BP.

XX AC AAQ75734;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2801  
Db 19 TTAAAAA 1

RESULT 1835  
AAQ75649/C

ID AAQ75649 standard; DNA; 21 BP.

XX AC AAQ75649;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX



KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS JP06303997-A.  
XX  
XX  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAACAAAAAAAAAAAAAAAAAAAA 3  
RESULT 1836  
AAQ75701/c  
ID AAQ75701 standard; DNA; 21 BP.  
XX  
XX AAQ75701;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
XX JP06303997-A.  
XX  
XX 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1837  
AAF24290/c  
ID AAF24290 standard; DNA; 21 BP.  
XX  
XX AAF24290;  
AC AAF24290;  
XX  
XX 03-APR-2001 (first entry)  
XX  
XX Complementary nucleic acid detection method related sequence #5.  
DE Complementary nucleic acid; gene analysis; polymorphism; variation;  
XX DNA chip; primer; ss.  
KW Unidentified.  
XX  
OS EP1065278-A2.  
XX  
PD 03-JAN-2001.  
XX  
XX 07-JUN-2000; 2000EP-00112235.  
PF  
XX 07-JUN-1999; 99JP-00159339.  
PR (FUJF ) FUJI PHOTO FILM CO LTD.  
XX  
XX Makino Y, Abe Y, Ogawa M, Takagi M, Takenaka S, Yamashita K;  
XX WPI; 2001-140003/15.  
DR  
XX Determining complementarity of nucleotide fragment for gene analysis, by  
PT comparing flow of electric current from or to electroconductive substrate  
PT through DNA fragment, with reference obtained from its complement.  
XX  
XX Example 1; Page 12; 28pp; English.  
XX  
XX The present invention provides a method for analysing a nucleic acid  
CC strand to determine the degree of complementarity between two sequences.  
CC This involves the measurement of an electric current along the annealed  
CC strands compared to a standard. This is useful in the analysis of genetic  
CC polymorphisms and variation between genes  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAATAAAAAAAAAAAAA 3



RESULT 1838  
ABX79794/c  
ID ABX79794 standard; cDNA; 21 BP.  
XX  
AC ABX79794;  
XX  
DT 17-APR-2003 (first entry)  
XX  
DE EST polymorphic DNA repeat polynucleotide #119.  
XX  
KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;  
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;  
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;  
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;  
KW Fredreich's ataxia; myotonic dystrophy; hyperandrogenaemia;  
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.  
XX  
OS Homo sapiens.  
XX  
PN US6472154-B1.  
XX  
PD 29-OCT-2002.  
XX  
PF 31-DEC-1999; 99US-00475947.  
XX  
PR 31-DEC-1999; 99US-00475947.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Garner HR, Wren JD, Minna JD, Fondon JW;  
XX  
DR WPI; 2003-208818/20.  
XX  
PT Identifying a candidate polymorphic repeat within a coding sequence, for  
PT understanding or treating genetic disease, comprises detecting tandem  
PT repeats in a target coding sequence and scoring the repeats for  
PT polymorphic probability.  
XX  
PS Example; Col 495; 588pp; English.  
XX  
CC The invention discloses a method for identifying a candidate polymorphic  
CC repeat within a coding sequence (expressed sequence tag, EST), which  
CC comprises detecting tandem repeats in a target coding sequence, scoring  
CC the repeats for polymorphic probability and generating a dataset  
CC correlating the repeats with polymorphic probability to identify a  
CC candidate polymorphic repeat. The computational methods (polymorphic  
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are  
CC useful for identifying and detecting candidate polymorphic repeats in  
CC human genes, which can be used to understand, treat or eliminate genetic  
CC diseases, predispositions or adverse drug-treatment reactions. Examples  
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River  
CC syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxia,  
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and  
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are  
CC the polymorphic repeats identified for a search of human ESTs  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 21 AAAAAAAAAATAAAAAAAAAAA 3  
  
RESULT 1839  
AAQ75752  
ID AAQ75752 standard; DNA; 21 BP.  
XX  
AC AAQ75752;  
XX

DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2169 TTTTTTTTTTTTTTTTTTA 2187  
Db 1 TTTTTTTTTTTTTTTTTTCA 19  
  
RESULT 1840  
AAQ75719/c  
ID AAQ75719 standard; DNA; 21 BP.  
XX  
AC AAQ75719;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX





XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX Disclosure; Page 7; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAA 1  
RESULT 1847  
AAQ75675/c  
ID AAQ75675 standard; DNA; 21 BP.  
XX  
AC AAQ75675;  
XX  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT

PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 ATAAAAAAAAAAAAAAAAA 1  
RESULT 1848  
AAQ75643/c  
ID AAQ75643 standard; DNA; 21 BP.  
XX  
AC AAQ75643;  
XX  
XX 04-AUG-1995 (first entry)  
DT Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX Disclosure; Page 6; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 ATAAAAAAAAAAAAAAAAA 1



Db 19 ACAAAAAAAAAAAAAAAAAA 1

RESULT 1849

AAQ75695/C  
ID AAQ75695 standard; DNA; 21 BP.

XX AC AAQ75695;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2803

Db 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1850

AAQ75646/C  
ID AAQ75646 standard; DNA; 21 BP.

XX AC AAQ75646;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.

XX

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804

Db 19 ACAAAAAAAAAAAAAAAAAA 1

RESULT 1851

AAQ75678/C  
ID AAQ75678 standard; DNA; 21 BP.

XX AC AAQ75678;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
PS double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803  
DB 19 GTAAAAAAAAAAAAAAAAA 1

RESULT 1855  
AAQ75635/c  
ID AAQ75635 standard; DNA; 21 BP.  
XX AAQ75635;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2802  
DB 19 TCAAAAAAAAAAAAAAAAAA 1

PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 7; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AATAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 1858  
AAQ75638/c  
ID AAQ75638 standard; DNA; 21 BP.  
XX  
AC AAQ75638;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 6; 11pp; Japanese.  
PS  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2802  
Db 19 TCAAAAAAAAAAAAAAAAAAAAAA 1  
RESULT 1859  
AAQ75647/c  
ID AAQ75647 standard; DNA; 21 BP.  
XX  
AC AAQ75647;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
DR  
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PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AACAAAAAAAAAAAAAAAAAAAAA 2  
RESULT 1860  
AAQ75654  
ID AAQ75654 standard; DNA; 21 BP.  
XX  
AC AAQ75654;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.





RESULT 1863  
AAQ75687/C  
ID AAQ75687 standard; DNA; 21 BP.  
XX AC  
XX AAQ75687;  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAA 1  
  
RESULT 1864  
AAQ75690/c  
ID AAQ75690 standard; DNA; 21 BP.  
XX AC  
XX AAQ75690;  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX

XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAA 1  
  
RESULT 1865  
AAQ75767  
ID AAQ75767 standard; DNA; 21 BP.  
XX  
AC AAQ75767;  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 1866  
AAQ75689/c  
ID AAQ75689 standard; DNA; 21 BP.  
XX  
AC AAQ75689;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 1867  
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ID AAQ75673 standard; DNA; 21 BP.  
XX  
AC AAQ75673;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX

SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 1866  
AAQ75689/c  
ID AAQ75689 standard; DNA; 21 BP.  
XX  
AC AAQ75689;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19  
RESULT 1867  
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ID AAQ75673 standard; DNA; 21 BP.  
XX  
AC AAQ75673;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2803  
Db 19 GTAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1867  
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ID AAQ75673 standard; DNA; 21 BP.  
XX  
AC AAQ75673;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAA AAAAAA AAAAAA AAAAAA 2803  
Db 19 GTAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1867  
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ID AAQ75673 standard; DNA; 21 BP.  
XX  
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XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 19 ATAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1868  
AAQ75770  
ID AAQ75770 standard; DNA; 21 BP.  
XX  
AC AAQ75770;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
PF 16-APR-1993; 93JP-00112515.  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 19 ATAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1868  
AAQ75770  
ID AAQ75770 standard; DNA; 21 BP.  
XX  
AC AAQ75770;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
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KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
PF 16-APR-1993; 93JP-00112515.  
PR 16-APR-1993; 93JP-00112515.  
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CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
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SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 19 ATAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 1868  
AAQ75770  
ID AAQ75770 standard; DNA; 21 BP.  
XX  
AC AAQ75770;  
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DT 04-AUG-1995 (first entry)  
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DE Reverse transcription primer used in cDNA analysis technique.  
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KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
PF 16-APR-1993; 93JP-00112515.  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX





PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 6; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TCAAAAAAAAAAAAAAAAAA 2802  
Db 19 TCAAAAAAAAAAAAAAAAAA 1  
RESULT 1872  
AAQ75665/c  
ID AAQ75665 standard; DNA; 21 BP.  
XX  
AC AAQ75665;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAAAAAA 2803  
Db 19 GCAAAAAAAAAAAAAAAAAA 1  
RESULT 1873  
AAQ75641/c  
ID AAQ75641 standard; DNA; 21 BP.  
XX  
AC AAQ75641;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 ACAAAAAAAAAAAAAAAAAA 1  
RESULT 1874  
AAQ75632/c  
ID AAQ75632 standard; DNA; 21 BP.  
XX  
AC AAQ75632;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAAGAAAAAAGAAAAA 2802  
Db | ||||| ||||| |||||  
19 TCAAGAAAAAAGAAAAA 1  
  
RESULT 1875  
AAQ75670/c  
ID AAQ75670 standard; DNA; 21 BP.  
XX  
AC AAQ75670;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
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PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
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PS Disclosure; Page 7; 11pp; Japanese.  
XX

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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2803  
Db | ||||| ||||| |||||  
19 GCAAGAAAAAAGAAAAA 1  
  
RESULT 1876  
AAQ75657/c  
ID AAQ75657 standard; DNA; 21 BP.  
XX  
AC AAQ75657;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
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PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2803  
Db | ||||| ||||| |||||  
19 GCAAGAAAAAAGAAAAA 1  
  
RESULT 1877



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Query Match      0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTCTTTCTTTCTTTCTTTCTTT 2184
Db 1 TTTTCTTTCTTTCTTTCTTTCTTTCTTTGT 19

RESULT 1880
AAQ75639/c
ID AAQ75639 standard; DNA; 21 BP.
XX AC
XX AAQ75639;
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 1lpp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
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CC the double-stranded cDNAs with restriction enzyme and; (c)
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CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match      0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1881
AAQ75667/c
ID AAQ75667 standard; DNA; 21 BP.
XX AC
XX AAQ75667;
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

Query Match      0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTCTTTCTTTCTTTCTTTCTTT 2184
Db 1 TTTTCTTTCTTTCTTTCTTTCTTTCTTTGT 19

RESULT 1880
AAQ75639/c
ID AAQ75639 standard; DNA; 21 BP.
XX AC
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DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
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XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
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XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match      0.6%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 AAAAAAAAAAAAAAAAAAAAAA 2804
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1881
AAQ75667/c
ID AAQ75667 standard; DNA; 21 BP.
XX AC
XX AAQ75667;
DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 6; 1lpp; Japanese.
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
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DR WPI; 1995-018287/03.  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
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CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db | ||||| ||||| ||||| |||||  
19 GCAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1886  
AAQ75624  
ID AAQ75624 standard; DNA; 21 BP.  
XX  
AC AAQ75624;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2802  
Db | ||||| ||||| ||||| |||||  
19 TCAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1888  
AAQ75666/c  
ID AAQ75666 standard; DNA; 21 BP.  
XX  
AC AAQ75666;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2169 TTTTTTTTTTTTTTTTTTA 2187  
Db | ||||| ||||| ||||| |||||  
1 TTTTTTTTTTTTTTTTGA 19  
  
RESULT 1887  
AAQ75624/c  
ID AAQ75624 standard; DNA; 21 BP.  
XX  
AC AAQ75624;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2802  
Db | ||||| ||||| ||||| |||||  
19 TCAAAAAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1888  
AAQ75666/c  
ID AAQ75666 standard; DNA; 21 BP.  
XX  
AC AAQ75666;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX



XX AAQ75658;  
AC  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX Reverse transcription primer used in cDNA analysis technique.  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
XX JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-00112515.  
XX  
XX PR 16-APR-1993; 93JP-00112515.  
XX  
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX DR WPI; 1995-018287/03.  
XX  
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX PS Disclosure; Page 6; 11pp; Japanese.  
XX  
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAAAAAA 2803  
Db 19 GCAAAAAAAAAAAAAAAAAA 1

RESULT 1892  
ADE80976  
ID ADE80976 standard; DNA; 21 BP.  
XX  
XX AC ADE80976;  
XX  
XX DT 29-JAN-2004 (first entry)  
XX  
XX DE Human papillomavirus L1 gene type-specific PCR primer SEQ ID NO:26.  
XX  
XX KW detection; human papillomavirus; HPV; genotype;  
KW HPV genus-specific primer; HPV genus-specific probe; amplification;  
KW hybridisation; genotyping; L1 gene; PCR primer; ss.  
XX  
XX OS Synthetic.  
OS Human papillomavirus.  
XX  
XX PN WO2003076667-A1.  
XX  
XX PD 18-SEP-2003.  
XX  
XX PF 10-MAR-2003; 2003WO-HU000020.  
XX  
XX PR 14-MAR-2002; 2002HU-00000981.

XX (JENE/) JENEY C.  
PA (TAKA/) TAKACS T.  
XX  
XX PI Jeney C, Takacs T;  
XX  
XX DR WPI; 2003-902774/82.  
XX  
XX PT Use of amplification primer-mixture and human papillomavirus genus-  
PT specific hybridization probes, for detecting and genotyping human  
PT papillomavirus in biological samples.  
XX  
XX PS Claim 2; SEQ ID NO 26; 61pp; English.  
XX  
XX CC The present invention describes a method for detecting many human  
CC papillomavirus (HPV) genotypes from biological samples. The method  
CC comprises amplifying and hybridising the extracted nucleic acid molecules  
CC with HPV genus-specific primers and probes designed from HPV genomic  
CC regions. Amplification primer-mixtures, consensus primers, type-specific  
CC primers, hybridisation probes, and reagent kits of the present invention  
CC can be used for detecting and genotyping HPV. The primer mixture is  
CC useful for the amplification of the 3, 4, 6, 7, 9, 10, 11, 12, 13, 14,  
CC 16, 18, 20, 24, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 40, 41,  
CC 42, 44, 45, 51, 52, 53, 54, 55, 56, 58, 49, 60, 61, 66, 67, 68, 72, 74 or  
CC 77 genotypes of HPV. The HPV genomic regions are useful for designing HPV  
CC genus-specific and HPV genotype-specific hybridisation probes. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 21 BP; 8 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2533 ATACAGGGTATTAGAAATT 2551  
Db 3 ATACAGGGTATTAGAAATT 21

RESULT 1893  
AAT33702  
ID AAT33702 standard; DNA; 23 BP.  
XX  
XX AC AAT33702;  
XX  
XX DT 19-MAY-1997 (first entry)  
XX  
XX DE Primer #2 for tissue or cell derived RNA.  
XX  
XX KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;  
KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;  
KW viral infection; hereditary disease; agricultural gene; ss.  
XX  
XX OS Synthetic.  
XX  
XX FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= .a  
FT /note= "hydroxylated"  
XX  
XX PN EP735144-A1.  
XX  
XX PD 02-OCT-1996.  
XX  
XX PF 26-MAR-1996; 96EP-00104817.  
XX  
XX PR 28-MAR-1995; 95JP-00069695.  
PR 20-JUL-1995; 95JP-00184006.  
PR 12-SEP-1995; 95JP-00234122.  
XX  
XX PA (SHKJ ) RES DEV CORP JAPAN.  
XX  
XX PI Kato K;



XX WPI; 1996-435619/44.  
DR Molecular indexing of DNA - using restriction enzymes, PCR amplification  
XX and electrophoresis to analyse DNA fragments.  
PT Claim 3; Page 14; 20pp; English.  
XX  
PS AAT33701-T33703 represent amplification primers used in the reverse-  
XX transcription of tissue or cell derived mRNA, in the method of the  
CC invention. The method of the invention is a molecular indexing method,  
CC and comprises digesting the cDNA amplified by these sequences with a  
CC class IIS restriction enzyme. Each resultant cDNA fragment is then  
CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors  
CC cohesive to all possible overhangs), and digesting the products with two  
CC further class IIS restriction enzymes. These steps are repeated (but the  
CC enzyme used for the first step is different in each) to produce two  
CC further cDNA samples. The ligation samples are then recovered using  
CC streptavidin-coated paramagnetic beads, removing the strand complementary  
CC to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer  
CC (such as this sequence) are then used to amplify the cDNA samples. The  
CC amplified products are separated, and the sizes of the fragments obtained  
CC is recorded. The method can be used for the analysis and diagnosis or  
CC diseases such as cancers or viral infections, for the search and  
CC isolation of the genes of physiologically active substances that are  
CC potential pharmaceuticals, or causative genes of hereditary diseases, as  
CC well as for the isolation of genes for improving agricultural products.  
CC Using this method, it is possible to classify (index) DNA into groups in  
CC a short period of time without duplication  
XX  
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2165 CTTTCTTTTCTTTTCTTTTCTTTT 2183  
Db 4 CTGTTTCTTTTCTTTTCTTTTCTTTT 22  
  
RESULT 1894  
AAT33702/c  
ID AAT33702 standard; DNA; 23 BP.  
XX  
AC AAT33702;  
XX  
DT 19-MAY-1997 (first entry)  
XX  
DE Primer #2 for tissue or cell derived RNA.  
XX  
KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;  
KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;  
KW viral infection; hereditary disease; agricultural gene; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= a  
FT /note= "hydroxylated"  
XX  
PN EP735144-A1.  
XX  
PD 02-OCT-1996.  
XX  
PF 26-MAR-1996; 96EP-00104817.  
XX  
FX 28-MAR-1995; 95JP-00069695.  
PR 20-JUL-1995; 95JP-00184006.  
PR 12-SEP-1995; 95JP-00234122.  
XX  
PA (SHKJ ) RES DEV CORP JAPAN.

XX Kato K;  
PI WPI; 1996-435619/44.  
XX  
DR Molecular indexing of DNA - using restriction enzymes, PCR amplification  
XX and electrophoresis to analyse DNA fragments.  
PT Claim 3; Page 14; 20pp; English.  
XX  
PS AAT33701-T33703 represent amplification primers used in the reverse-  
XX transcription of tissue or cell derived mRNA, in the method of the  
CC invention. The method of the invention is a molecular indexing method,  
CC and comprises digesting the cDNA amplified by these sequences with a  
CC class IIS restriction enzyme. Each resultant cDNA fragment is then  
CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors  
CC cohesive to all possible overhangs), and digesting the products with two  
CC further class IIS restriction enzymes. These steps are repeated (but the  
CC enzyme used for the first step is different in each) to produce two  
CC further cDNA samples. The ligation samples are then recovered using  
CC streptavidin-coated paramagnetic beads, removing the strand complementary  
CC to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer  
CC (such as this sequence) are then used to amplify the cDNA samples. The  
CC amplified products are separated, and the sizes of the fragments obtained  
CC is recorded. The method can be used for the analysis and diagnosis or  
CC diseases such as cancers or viral infections, for the search and  
CC isolation of the genes of physiologically active substances that are  
CC potential pharmaceuticals, or causative genes of hereditary diseases, as  
CC well as for the isolation of genes for improving agricultural products.  
CC Using this method, it is possible to classify (index) DNA into groups in  
CC a short period of time without duplication  
XX  
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 23 GAAAAAAAAAAAAAAAAAAAAA 5  
  
RESULT 1895  
AAV61555  
ID AAV61555 standard; DNA; 23 BP.  
XX  
AC AAV61555;  
XX  
DT 08-DEC-1998 (first entry)  
XX  
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
XX  
KW Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;  
KW gene expression; internal standard; calibration curve; ss.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
PN EP870842-A2.  
XX  
PD 14-OCT-1998.  
XX  
PF 07-APR-1998; 98EP-00302726.  
XX  
PR 07-APR-1997; 97JP-00088495.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Kato K;  
XX  
DR WPI; 1998-523164/45.

XX Determination of gene expression levels - using combinations of different  
PT cDNA samples tagged with different PCR adaptors.  
PT  
XX  
PS Example 2; Page 9; 22pp; English.  
XX  
CC The present sequence represents a primer which was used to synthesize  
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers  
CC AAV61554 and AAV61556 were added to both mouse liver-derived and mouse  
CC kidney-derived total RNA to generate single-stranded cDNA. These primers  
CC were used in the method of the invention to determine the amount ratio  
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA  
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-  
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to  
CC be quantitatively determined, and because internal standards are not  
CC required to prepare a calibration curve, it is a quicker and less  
CC laborious process  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTTTTTT 2183  
Db |||||  
4 CTGTTTTTTTTTTTTTTTTT 22  
  
RESULT 1896  
AAA07787/c  
ID AAA07787 standard; DNA; 23 BP.  
XX  
AC AAA07787;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Structure of a fragment of duplex A target strand.  
XX  
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US019029.  
XX  
PR 22-AUG-1998; 98US-0097712P.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi

CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections (see AAA07786 for details of other  
CC uses for which the oligomers are suitable for). Oligomers comprising the  
CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to  
CC target nucleic acid sequences, are physiologically stable, non-toxic and  
CC able to penetrate into cells while maintaining stringent base pair  
CC fidelity for target DNA sequences. The oligomers demonstrate significant  
CC single- or double-stranded target nucleic acid binding activity to form  
CC duplexes, triplexes or other forms of stable association  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2784 TGAAAAAATAAAAAAAAAA 2802  
Db |||||  
23 TGAGAAAAAATAAAAAAAAAA 5  
  
RESULT 1897  
AAA07786  
ID AAA07786 standard; DNA; 23 BP.  
XX  
AC AAA07786;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Structure of a fragment of duplex A target strand.  
XX  
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US019029.  
XX  
PR 22-AUG-1998; 98US-0097712P.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory

CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections. The oligomers are suitable for use  
CC in both in vivo and ex vivo therapeutic applications including treatment  
CC of cells such as bone marrow or peripheral blood in conditions such as  
CC leukemia or viral infections, genes as target for cancer treatments  
CC including oncogenes such as ras, k-ras, bcl-2, c-myc, c-abl  
CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6  
CC (Kaposi's sarcoma), HER-2 and translocations such as bcr/abl or RNAs  
CC encoded by such genes, as well as viral gene sequences such as polymerase  
CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1  
CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,  
CC human papilloma virus, varicella zoster virus, influenza virus or  
CC rhinovirus. They can also be used to modulate inflammatory responses by  
CC modulating expression of genes such as IL-1 receptor, IL-1, ICAM-1 or E-  
CC selectin in mediating inflammation and modulation of cellular  
CC proliferation in conditions such as arterial occlusion (restenosis) after  
CC angioplasty by modulating the expression of growth or mitogenic factors  
CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor  
CC or fibroblast growth factor or their receptors or cell proliferation  
CC factor such as c-myc, other extracellular proliferation factors such as  
CC transforming growth factor alpha, IL-6, approx.g-interferon, protein  
CC kinase C for treatment of psoriasis or other conditions, and epithelial  
CC growth factor, transforming growth factor or MHC alleles in autoimmune  
CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex  
CC DNA stability when hybridizing to target nucleic acid sequences, are  
CC physiologically stable, non-toxic and able to penetrate into cells while  
CC maintaining stringent base pair fidelity for target DNA sequences. The  
CC oligomers demonstrate significant single- or double-stranded target  
CC nucleic acid binding activity to form duplexes, triplexes or other forms  
CC of stable association  
XX  
SQ Sequence 23 BP; 18 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAGAAAAA 2802  
DB 1 TCAGAAAAA 19

RESULT 1898  
AAA08408  
ID AAA08408 standard; DNA; 23 BP.  
XX  
AC AAA08408;  
XX  
DT 13-JUL-2000 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO:2.  
XX  
KW Detection; primer; adapter; probe; hybridisation; gene cluster;  
KW fractionation; ss.  
XX  
OS Synthetic.  
XX  
PN JP2000055914-A.  
XX  
PD 25-FEB-2000.  
XX  
PF 13-AUG-1998; 98JP-00228944.  
XX  
PR 13-AUG-1998; 98JP-00228944.  
XX  
PA (TAIS ) TAISHO PHARM CO LTD.  
XX  
DR WPI; 2000-368733/32.  
XX  
PT Gene detection method involves hybridizing probe opposite to objective  
PT gene out of fractional gene cluster.  
XX  
PS Example 1; Page 9; 11pp; Japanese.

XX The present invention describes a gene detection method which comprises  
CC fractionating using a probe opposite to the objective gene which is  
CC hybridised out of fractioned gene cluster. The objective gene detected  
CC belongs to the group of objective genes contained in the sample. The  
CC method is used for gene detection by fractionation of cDNA by molecular  
CC index method using specific primer. It provides high detection  
CC sensitivity of objective gene. AAA08407 to AAA08414 represent  
CC oligonucleotides used in the exemplification of the present invention  
XX  
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTCTTTT 2183  
DB 4 CTGTTTTT 22

RESULT 1899  
AAA08408/c  
ID AAA08408 standard; DNA; 23 BP.  
XX  
AC AAA08408;  
XX  
DT 13-JUL-2000 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO:2.  
XX  
KW Detection; primer; adapter; probe; hybridisation; gene cluster;  
KW fractionation; ss.  
XX  
OS Synthetic.  
XX  
PN JP2000055914-A.  
XX  
PD 25-FEB-2000.  
XX  
PF 13-AUG-1998; 98JP-00228944.  
XX  
PR 13-AUG-1998; 98JP-00228944.  
XX  
PA (TAIS ) TAISHO PHARM CO LTD.  
XX  
DR WPI; 2000-368733/32.  
XX  
PT Gene detection method involves hybridizing probe opposite to objective  
PT gene out of fractional gene cluster.  
XX  
PS Example 1; Page 9; 11pp; Japanese.  
XX  
CC The present invention describes a gene detection method which comprises  
CC fractionating using a probe opposite to the objective gene which is  
CC hybridised out of fractioned gene cluster. The objective gene detected  
CC belongs to the group of objective genes contained in the sample. The  
CC method is used for gene detection by fractionation of cDNA by molecular  
CC index method using specific primer. It provides high detection  
CC sensitivity of objective gene. AAA08407 to AAA08414 represent  
CC oligonucleotides used in the exemplification of the present invention  
XX  
SQ Sequence 23 BP; 1 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAA 2803  
DB 23 GAAAAA 5

PT Gene detection method involves hybridizing probe opposite to objective  
PT gene out of fractional gene cluster.  
XX  
PS Example 1; Page 9; 11pp; Japanese.

RESULT 1900  
AAH24266/c  
ID AAH24266 standard; DNA; 24 BP.  
AC AAH24266;  
XX  
DT 11-SEP-2001 (first entry)  
XX  
DE Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.  
XX  
KW Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue;  
KW recombinant production; malignant tumour; cancer; blood disease;  
KW HIV infection; human immunodeficiency virus; immune disorder;  
KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;  
KW immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138385-A1.  
XX  
PD 31-MAY-2001.  
XX  
PF 20-NOV-2000; 2000WO-CN000459.  
XX  
PR 22-NOV-1999; 99CN-00124059.  
XX  
PA (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-355903/37.  
XX  
PT Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis  
PT and treatment of malignant tumor, hemopathy, HIV infection, immunological  
PT diseases and various inflammation.  
XX  
PS Example 3; Page 12; 38pp; Chinese.  
XX  
CC The invention relates to human phosphatase 79 (AAB73700), nucleic acids  
CC encoding it (AAH24264), and a method for the recombinant production of  
CC human phosphatase 79. The present invention additionally discloses an  
CC agonist of phosphatase 79 for therapeutic use, and an antibody which  
CC specifically binds to human phosphatase 79. Human phosphatase 79, and  
CC nucleotides which encode it may be used for treating a variety of  
CC diseases, such as malignant tumours, blood diseases, HIV (human  
CC immunodeficiency virus) infection, immune disorders and inflammatory  
CC conditions. The protein may also be used to screen for modulators of its  
CC activity or for peptide fingerprinting identification. The polynucleotide  
CC can be used as a primer for nucleic acid amplification reaction or as a  
CC probe for hybridisation reactions, or in producing gene chips or  
CC microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-  
CC PCR (RT-PCR) primers used in an exemplification of the invention to  
CC isolate human phosphatase 79 cDNA  
XX  
SQ Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 24 AAAAAAAAAAAAAAAAAATA 6  
  
RESULT 1901  
AAH44623/c  
ID AAH44623 standard; DNA; 24 BP.  
XX  
AC AAH44623;  
XX  
DT 16-NOV-2001 (first entry)  
XX

DE Human FD 17 PCR primer 2 SEQ ID NO:4.  
XX  
KW Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic;  
KW antiinflammatory; gene therapy; malignant tumour; haemopathy;  
KW human immunodeficiency virus infection; HIV infection;  
KW immunological disease; inflammation; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200164729-A1.  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-CN000221.  
XX  
PR 02-MAR-2000; 2000CN-00111868.  
XX  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-550164/61.  
XX  
PT New human polypeptide FD 17 for diagnosing and treating malignant tumor,  
PT hemopathy, human immunodeficiency virus (HIV) infection, immunological  
PT diseases and inflammations.  
XX  
PS Example 2; Page 11; 36pp; Chinese.  
XX  
CC The present invention describes the human FD 17 protein (I). (I) has  
CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic  
CC activities. The polynucleotide encoding (I) can be used in gene therapy.  
CC (I) and the polynucleotide encoding it are applicable in the diagnosis  
CC and treatment of malignant tumour, haemopathy, human immunodeficiency  
CC virus (HIV) infection, immunological diseases and various inflammations.  
CC The present sequence represents a PCR primer for human FD 17, which is  
CC used in an example from the present invention  
XX  
SQ Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 23 AAAAAAAAAAGAAAAA 5  
  
RESULT 1902  
ABK13715/c  
ID ABK13715 standard; DNA; 24 BP.  
XX  
AC ABK13715;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.  
XX  
KW Human; transcriptional activation subunit 14; malignant neoplasm;  
KW haematopathy; cytostatic; HIV infection; human immunodeficiency virus;  
KW immunological disease; inflammation; virucide; immunomodulatory;  
KW antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200194403-A1.  
XX  
PD 13-DEC-2001.  
XX  
PF 14-MAY-2001; 2001WO-CN000753.  
XX  
PR 16-MAY-2000; 2000CN-00115720.



XX (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.  
PI Mao Y, Xie Y;  
XX WPI; 2002-090139/12.  
XX Human transcriptional activation subunit 14 and encoding polynucleotide,  
PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX  
PS Example 2; Page 17; 36pp; Chinese.  
XX  
CC The present invention relates to the isolation of human transcriptional  
CC activation subunit 14, and the polynucleotide encoding it. Also described  
CC is the process for preparing the protein by DNA recombination and the  
CC application of the polypeptide and polynucleotide in treating various  
CC diseases such as malignant neoplasms, haematopathy, human  
CC immunodeficiency virus (HIV) infection, immunological diseases, and  
CC various inflammations. Antagonists against the polypeptide can also be  
CC used in treating such diseases. The present sequence for reverse  
CC transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714)  
CC for isolating cDNA encoding human transcriptional activation subunit 14  
XX  
SQ Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 22 AAAAAAAAAAGAGAAAA 4  
  
RESULT 1903  
AAL47515/c  
ID AAL47515 standard; DNA; 24 BP.  
XX  
AC AAL47515;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
XX Human cyclophilin-40-12-54 coding sequence PCR primer #2.  
DE  
XX Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.  
KW  
XX Homo sapiens.  
OS  
XX CN1331162-A.  
PN  
XX 16-JAN-2002.  
PD  
XX 28-JUN-2000; 2000CN-00116823.  
PF  
XX 28-JUN-2000; 2000CN-00116823.  
PR  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-305482/35.  
DR  
XX Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.  
PT  
XX  
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC cyclophilin-40-12.54. The sequences can be used in the treatment of  
CC immunopathy and cancer. The present sequence is a PCR primer for the  
CC coding sequence of the invention  
XX

SQ Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 19 AAAAAAAAAAGAGAAAA 1  
  
RESULT 1904  
AAH76998/c  
ID AAH76998 standard; DNA; 24 BP.  
XX  
AC AAH76998;  
XX  
DT 15-DEC-2001 (first entry)  
XX  
DE Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.  
XX  
KW Human; amyloid precursor protein 9; recombinant production;  
KW malignant tumour; cancer; blood disease; HIV infection;  
KW human immunodeficiency virus; immune disorder; inflammatory condition;  
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator;  
KW reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200174878-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 23-MAR-2001; 2001WO-CN000391.  
XX  
PR 24-MAR-2000; 2000CN-00115106.  
XX  
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-626386/72.  
XX  
XX New human amyloid precursor protein 9 and encoded polynucleotide,  
PT applicable in diagnosis and treatment of cancer, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and various  
PT inflammations.  
PT  
XX Example 2; Page 16; 37pp; Chinese.  
PS  
XX  
CC The invention relates to human amyloid precursor protein 9 (AAG66809),  
CC nucleic acids encoding it (AAH76996), and a method for the recombinant  
CC production of amyloid precursor protein 9. The protein has a molecular  
CC weight of 9 kD. The present invention additionally discloses an  
CC antagonist of amyloid precursor protein 9 for therapeutic use, and an  
CC antibody which specifically binds to amyloid precursor protein 9. Amyloid  
CC precursor protein 9, and nucleotides which encode it may be used for  
CC treating a variety of diseases, such as malignant tumours, blood  
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders  
CC and inflammatory conditions. The protein may also be used to screen for  
CC modulators of its activity or for peptide fingerprinting identification.  
CC The polynucleotide can be used as a primer for nucleic acid amplification  
CC reactions or as a probe for hybridisation reactions, or in producing gene  
CC chips or microarrays. Sequences AAH76997-AAH76998 represent reverse  
CC transcription-PCR (RT-PCR) primers used in an exemplification of the  
CC invention to isolate human amyloid precursor protein 9 cDNA  
XX  
SQ Sequence 24 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
Db 19 GTAAAAAAAAAAAAAAAAAAAA 1

RESULT 1905  
AAC96267/c  
ID AAC96267 standard; DNA; 25 BP.  
XX AC  
XX AAC96267;  
XX 26-FEB-2001 (first entry)  
XX HLA DPA1 gene PCR primer #24.  
XX DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX OS Homo sapiens.  
XX WO200065088-A2.  
XX 02-NOV-2000.  
XX 20-APR-2000; 2000WO-EP003636.  
XX 26-APR-1999; 99EP-00303215.  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX Ulfendahl P, Wong K;  
XX WPI; 2000-679677/66.  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX Claim 14; Page 48; 66pp; English.  
XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX SQ Sequence 25 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAA 2799  
Db 19 AATTCAAAAAAAAAAAAAAAAAA 1

RESULT 1906  
AAF74925  
ID AAF74925 standard; DNA; 25 BP.  
XX AC  
XX AAF74925;  
XX 23-MAY-2001 (first entry)  
XX CD40L poly-A tract sequence SEQ ID NO:22.  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
diagnosis; antiarthritic; antirheumatic; immunosuppressive;

antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX OS Homo sapiens.  
XX PN WO200119844-A1.  
XX PD 22-MAR-2001.  
XX PF 13-SEP-2000; 2000WO-US024966.  
XX PR 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX Example 1; Fig 3; 90pp; English.  
XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX SQ Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1907  
AAF74930  
ID AAF74930 standard; DNA; 25 BP.  
XX AC  
XX AAF74930;  
XX 23-MAY-2001 (first entry)  
XX CD40L poly-A tract sequence SEQ ID NO:27.  
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX OS Homo sapiens.  
XX PN WO200119844-A1.  
XX PD 22-MAR-2001.  
XX 13-SEP-2000; 2000WO-US024966.  
XX PR 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PI Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
DR  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 25 BP; 19 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2e+03; Length 25;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAACAAAAA 19  
  
RESULT 1908  
AAH38315/c  
ID AAH38315 standard; DNA; 25 BP.  
XX  
AC AAH38315;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific SNPE primer SEQ ID 1111.  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200129262-A2.  
XX  
XX 26-APR-2001.  
XX  
XX 13-OCT-2000; 2000WO-US028436.  
XX  
XX 15-OCT-1999; 99US-0160096P.  
XX  
XX (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
XX Picoult-Newburg L, Pohl M;  
XX  
XX WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
XX Claim 1; Page 55; 83pp; English.  
PS  
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC

CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a single nucleotide  
CC primer extension (SNPE) primer specific for a human SNP containing DNA  
CC sequence  
XX  
SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 25 AAAAAAAAAAAAAAAAAAAAAA 7  
  
RESULT 1909  
AAC95727  
ID AAC95727 standard; DNA; 25 BP.  
XX  
AC AAC95727;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DQA1 gene PCR primer #24.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200065088-A2.  
XX  
XX 02-NOV-2000.  
XX  
XX 20-APR-2000; 2000WO-EP003636.  
XX  
XX 26-APR-1999; 99EP-00303215.  
XX  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
XX Ulfendahl P, Wong K;  
XX  
XX WPI; 2000-679677/66.  
XX  
XX Identifying extendible primers for use in identification, or  
XX classification of a nucleic acid of an organism, allele or gene such as  
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of  
XX specific length.  
XX  
XX Claim 14; Page 39; 66pp; English.  
PS  
XX The present invention provides a method for identifying a set of  
CC





XX	Homo sapiens.
OS	WO200129262-A2.
XX	26-APR-2001.
XX	13-OCT-2000; 2000WO-US028436.
PF	15-OCT-1999; 99US-0160096P.
XX	(ORCH-) ORCHID BIOSCIENCES INC.
PA	Picoult-Newburg L, Pohl M;
PI	WPI; 2001-290930/30.
XX	New genotyping oligonucleotide, useful for detecting the presence,
PT	absence or identity of single polynucleotide polymorphism in a nucleic
PT	acid sample.
XX	Claim 1; Page 63; 83pp; English.
PS	Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX	primer extension (SNPE) primers, and the sequences of regions flanking
CC	sites of single nucleotide polymorphisms SNPs. The present invention
CC	includes kits for determining the presence or absence of a SNP, using the
CC	oligonucleotides of the invention. The PCR primers are used to amplify a
CC	SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC	The oligonucleotides are useful for genotyping a nucleic acid sample by
CC	performing a single-nucleotide primer extension reaction. The
CC	oligonucleotides are useful for determining the presence, absence or
CC	identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC	assess by association analysis the genotype of an individual or group of
CC	individuals, having a pathological phenotypic trait suspected of being
CC	caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC	agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC	dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC	osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC	traits also include symptoms of or susceptibility to multifactorial
CC	disease of which a component is or may be genetic such as autoimmune
CC	diseases, including, rheumatoid arthritis, multiple sclerosis,
CC	inflammation, cancer, nervous system diseases and infection by pathogenic
CC	microorganism. The method is also useful in forensic investigations and
CC	paternity analysis. The present sequence represents a single nucleotide
CC	primer extension (SNPE) primer specific for a human SNP containing DNA
CC	sequence
XX	Sequence 25 BP; 19 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
SQ	Query Match 0.6%; Score 17.4; DB 1; Length 25;
	Best Local Similarity 94.7%; Pred. No. 2e+03;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2786 AAAAAAAAAAAAAAAA 2804
Db	1 AAAAAAAAAACGAAAAAA 19
RESULT 1913	
AAH39903/c	
ID	AAH39903 standard; DNA; 25 BP.
XX	
AC	AAH39903;
DT	
XX	14-AUG-2001 (first entry)
DE	SNP specific SNPE primer SEQ ID 2699.
XX	
KW	Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW	SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW	Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW	polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;

KW	acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW	inflammation; forensic investigation; paternity analysis; primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200129262-A2.
PD	
XX	26-APR-2001.
XX	
PF	13-OCT-2000; 2000WO-US028436.
XX	
PR	15-OCT-1999; 99US-0160096P.
XX	
PA	(ORCH-) ORCHID BIOSCIENCES INC.
XX	
PI	Picoult-Newburg L, Pohl M;
XX	
DR	WPI; 2001-290930/30.
XX	
PT	New genotyping oligonucleotide, useful for detecting the presence,
PT	absence or identity of single polynucleotide polymorphism in a nucleic
PT	acid sample.
XX	
PS	Claim 1; Page 63; 83pp; English.
XX	
CC	Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC	primer extension (SNPE) primers, and the sequences of regions flanking
CC	sites of single nucleotide polymorphisms SNPs. The present invention
CC	includes kits for determining the presence or absence of a SNP, using the
CC	oligonucleotides of the invention. The PCR primers are used to amplify a
CC	SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC	The oligonucleotides are useful for genotyping a nucleic acid sample by
CC	performing a single-nucleotide primer extension reaction. The
CC	oligonucleotides are useful for determining the presence, absence or
CC	identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC	assess by association analysis the genotype of an individual or group of
CC	individuals, having a pathological phenotypic trait suspected of being
CC	caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC	agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC	dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC	osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC	traits also include symptoms of or susceptibility to multifactorial
CC	disease of which a component is or may be genetic such as autoimmune
CC	diseases, including, rheumatoid arthritis, multiple sclerosis,
CC	inflammation, cancer, nervous system diseases and infection by pathogenic
CC	microorganism. The method is also useful in forensic investigations and
CC	paternity analysis. The present sequence represents a single nucleotide
CC	primer extension (SNPE) primer specific for a human SNP containing DNA
CC	sequence
XX	
SQ	Sequence 25 BP; 19 A; 3 C; 2 G; 1 T; 0 U; 0 Other;
	Query Match 0.6%; Score 17.4; DB 1; Length 25;
	Best Local Similarity 94.7%; Pred. No. 2e+03;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2166 TTTTTCCTTTTTTTTTTTT 2184
Dd	19 TTTTTCCTTTTTTTTTTTT 1
RESULT 1914	
AAC90736/c	
ID AAC90736 standard; DNA; 25 BP.	
XX	
AC AAC90736;	
XX	
DT 14-MAR-2001 (first entry)	
XX	
DE Human secretory protein TGC-715 PCR primer SEQ ID NO:51.	
XX	
KW Human; secretory protein; cancer; immune disease; infectious disease;	
KW lung function disorder; liver function disorder; antiinflammatory;	





CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 2 A; 1 C; 4 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 24 AAAAAAAAAAAAAAAAAAGAA 6  
  
RESULT 1919  
AAF16616  
ID AAF16616 standard; DNA; 26 BP.  
XX  
AC AAF16616;  
XX  
DT 13-MAR-2001 (first entry)  
XX  
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 103.  
XX  
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;  
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;  
KW DNA-RNA hybrid; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200071164-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 24-MAY-2000; 2000WO-AU0000498.  
XX  
PR 24-MAY-1999; 99AU-000000510.  
XX  
PA (TACH/) TACHAS G.  
XX  
PI Tachas G;  
XX  
DR WPI; 2001-025093/03.  
XX  
PT Treating gastric acid disturbance by administering an oligonucleotide  
PT which modulates the activity of a polypeptide involved in gastric acid  
PT production or secretion.  
XX  
PS Example 3; Page 150; 164pp; English.  
XX  
CC The present invention provides oligonucleotides, and methods for their  
CC use, which are useful in modulating the action of proteins involved in  
CC gastric acid production. The target protein is preferably the histamine  
CC H2 receptor or one of the proteins which form part of the gastric proton  
CC pump. The sequences and methods of the invention are useful in the  
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,  
CC duodenal ulcers and other gastric acid disturbances, most of which are  
CC caused by Helicobacter pylori  
XX  
SQ Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 26;  
Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAGAAAAAAAAA 19  
  
RESULT 1920  
AAF74913

ID AAF74913 standard; DNA; 26 BP.  
XX  
AC AAF74913;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:10.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 26 BP; 20 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 26;  
Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAACAAAA 19  
  
RESULT 1921  
AAF74926  
ID AAF74926 standard; DNA; 27 BP.  
XX  
AC AAF74926;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:23.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX



PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
RESULT 1922  
AAF74932  
ID AAF74932 standard; DNA; 27 BP.  
XX  
AC AAF74932;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:29.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
AC AAF74932;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:29.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX

PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAA 19  
RESULT 1923  
AAF74931  
ID AAF74931 standard; DNA; 27 BP.  
XX  
AC AAF74931;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:28.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

CC which elevated expression of CD40L is a factor, e.g., rheumatoid arthritis. The present sequence represents a CD40L poly-A tract sequence which is used in an example from the present invention

XX

SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1924  
AAF74934  
ID AAF74934 standard; DNA; 27 BP.  
XX  
AC AAF74934;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:31.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis; diagnosis; antiarthritic; antirheumatic; immunosuppressive; antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment of a variety of inflammatory disorders and autoimmune diseases, such as rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX

The present invention describes an isolated, purified nucleic acid, which is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having residues 331-455 of the sequence comprising 455 nucleotides given in AAF74905 where A in the wild type sequence at position 331 (corresponding to position -125) is replaced with C. (I) has antiarthritic, antirheumatic, immunosuppressive and antiinflammatory activities, and can be used in gene therapy. (I) is useful in the study, diagnosis and treatment of inflammatory and autoimmune diseases, as well as diseases in which elevated expression of CD40L is a factor, e.g., rheumatoid arthritis. The present sequence represents a CD40L poly-A tract sequence which is used in an example from the present invention

XX

SQ Sequence 27 BP; 21 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||

Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1925  
AAQ05023/c  
ID AAQ05023 standard; DNA; 27 BP.  
XX  
AC AAQ05023;  
XX  
DT 25-MAR-2003 (revised)  
DT 31-OCT-1990 (first entry)  
XX  
DE Sequence binding to and inhibiting the Beta-globin gene.  
XX  
KW C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF; epidermal growth factor; GSTpi; HMGCoA; thalassemia;  
KW Herpes simplex virus; nerve growth factor receptor; globin; ss.  
XX  
OS Synthetic.  
XX  
PN EP375408-A.  
XX  
PD 27-JUN-1990.  
XX  
PF 20-DEC-1989; 89EP-00313391.  
XX  
PR 20-DEC-1988; 88US-00287359.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA (HOGA/) HOGAN M E.  
XX  
PI Hogan ME, Kessler DJ;  
XX  
DR WPI; 1990-195509/26.  
XX  
PT Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-linear triplex to control transcription process in gene-specific fashion.  
XX  
PS Claim 47; Page 31; 40pp; English.  
XX

Sequence forms triplex with the double stranded target sequence with G binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel orientation and when targeted to a specific sequence will deactivate it. This allows for growth inhibition in cancerous cells; manipulation of cellular structural protein content; inhibition of IL-2 chain receptor; disbursting plaque formation in Alzheimer's disease; inhibiting EGF gene; modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF gene expression; arresting HSV-I replication and suppressing Beta- globin expression in thalassaemia and sickle cell anaemia patients. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||

Db 27 AAAAAAAAAACAAAAAAAA 9

RESULT 1926  
AAQ36361/c  
ID AAQ36361 standard; DNA; 27 BP.  
XX  
AC AAQ36361;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-JUN-1993 (first entry)  
XX  
DE GL6par, targetted to human beta globin sequence.  
XX  
KW Heamoglobin; beta thalassemia; sickle cell anaemia; delta protein;

KW triplex; target; duplex; promoter; coding domain; 3'-5'; ss.  
XX Synthetic.  
OS US5176996-A.  
XX  
PN 05-JAN-1993.  
PD  
XX 22-DEC-1989; 89US-00453532.  
PF  
XX 20-DEC-1988; 88US-00287359.  
PR  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA  
XX Hogan ME, Kessler DJ;  
PI  
XX WPI; 1993-035718/04.  
DR  
XX Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -  
PT which bind to target sequence in duplex DNA forming colinear triplex by  
PT binding to major groove.  
XX  
PS Example 13; Col 35; 29pp; English.  
XX  
CC The beta globin gene encodes on of the proteins comprising human adult  
CC haemoglobin. Mutation in this gene is responsible for beta thalassemia  
CC and sickle cell anaemia. Expression of the gene may be prevented by the  
CC formation of a triplex between the duplex target DNA sequence and an anti  
CC parallel or parallel synthetic oligonucleotide. The triplex  
CC oligonucleotides are designed to inhibit the beta globin gene in  
CC thalassemics and in patients with sickle cell anaemia, to be replaced by  
CC the naturally occurring delta protein. Two classes of triplex  
CC oligonucleotides may be used, targeted against the 5' enhancer or the  
CC promoter/coding domain, in this case from base 874 to 900 (numbering is  
CC relative to the principal mRNA start site). A suitable parallel  
CC oligonucleotide is GL6par (3'-5'). See also AAQ36219-362. (Updated on 25-  
CC MAR-2003 to correct PF field.)  
XX  
SQ Sequence 27 BP; 0 A; 0 C; 6 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 27;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 27 AAAAAAAAAACAAAAAAAAA 9

RESULT 1927  
AAF74920  
ID AAF74920 standard; DNA; 28 BP.  
XX  
AC AAF74920;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:17.  
XX

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX

PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX

PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
PI Crow MK, Li Y;  
XX  
DR WPI; 2001-244776/25.  
XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX  
PS Example 1; Fig 3; 90pp; English.  
XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAACAA 19

RESULT 1928  
AAF74906

ID AAF74906 standard; DNA; 28 BP.

XX  
AC AAF74906;

XX  
DT 23-MAY-2001 (first entry)

XX  
DE CD40L poly-A tract sequence SEQ ID NO:3.

XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX

OS Homo sapiens.

XX  
PN WO200119844-A1.

XX  
PD 22-MAR-2001.

XX  
PF 13-SEP-2000; 2000WO-US024966.

XX  
PR 13-SEP-1999; 99US-0153625P.

XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

XX  
PI Crow MK, Li Y;

XX  
DR WPI; 2001-244776/25.

XX  
PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
XX

PS Example 1; Fig 3; 90pp; English.

XX  
CC The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having

CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1929

AAF74916  
ID AAF74916 standard; DNA; 28 BP.

AC AAF74916;

DT 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:13.

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PA Crow MK, Li Y;

XX WPI; 2001-244776/25.

PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1930

AAF74927  
ID AAF74927 standard; DNA; 28 BP.

AC AAF74927;

XX 23-MAY-2001 (first entry)

DE CD40L poly-A tract sequence SEQ ID NO:24.

KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.

OS Homo sapiens.

XX WO200119844-A1.

XX 22-MAR-2001.

PF 13-SEP-2000; 2000WO-US024966.

PR 13-SEP-1999; 99US-0153625P.

XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.

PA Crow MK, Li Y;

XX WPI; 2001-244776/25.

PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.

PS Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX

SQ Sequence 28 BP; 22 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1931

AAQ52308/c  
ID AAQ52308 standard; cDNA; 28 BP.

XX AAQ52308;

DT 25-MAR-2003 (revised)



PT Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -  
PT which bind to target sequence in duplex DNA forming colinear triplex by  
PT binding to major groove.  
XX  
XX Example 13; Col 36; 29pp; English.  
PS  
XX The beta globin gene encodes on of the proteins comprising human adult  
CC haemoglobin. . Mutation in this gene is responsible for beta thalassemia  
CC and sickle cell anaemia. Expression of the gene may be prevented by the  
CC formation of a triplex between the duplex target DNA sequence and an anti  
CC parallel or parallel synthetic oligonucleotide. The triplex  
CC oligonucleotides are designed to inhibit the beta globin gene in  
CC thalassemics and in patients with sickle cell anaemia, to be replaced by  
CC the naturally occurring delta protein. Two classes of triplex  
CC oligonucleotides may be used, targetted against the 5' enhancer or the  
CC promoter/coding domain, in this case from base 874 to 900 (numbering is  
CC relative to the principal mRNA start site). A suitable antiparallel  
CC oligonucleotide is GL6anti. See also AAQ36219-361. (Updated on 25-MAR-  
CC 2003 to correct PF field.)  
XX  
SQ Sequence 28 BP; 0 A; 0 C; 6 G; 22 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db ||||| ||||| ||||| |||||  
28 AAAAAAAAAAACCAAAAAA 10  
  
RESULT 1933  
AAT70113  
ID AAT70113 standard; DNA; 28 BP.  
AC AAT70113;  
XX  
DT 24-SEP-1997 (first entry)  
XX  
DE PolyAB primer 2.  
XX primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
KW  
XX Synthetic.  
OS  
XX WO9640998-A1.  
PN  
XX 19-DEC-1996.  
PD  
XX  
XX 05-JUN-1996; 96WO-US008582.  
PF  
XX 07-JUN-1995; 95US-00481687.  
PR  
XX (PION-) PIONEER HI-BRED INT INC.  
PA  
XX Wang X, Duvick JP, Briggs SP;  
PI  
XX WPI; 1997-087067/08.  
DR  
XX Method for prodn. of cDNA libraries with anchored ends - useful for  
PT subtractive cloning of sequences of interest.  
PT  
XX Claim 1; Page 28; 56pp; English.  
PS  
XX The invention provides a PCR-based method for generating a full-length  
CC cDNA library with anchored ends. The method uses lock-docking primers  
CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
CC second primer, polyGH (H = A, C or T) locks onto the polyC tail added by  
CC terminal deoxynucleotidyl transferase (TdT). In the final step, AAT70112-  
CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to  
CC amplify the first strand and produce a cDNA library with anchored ends.

DT 03-JUN-1994 (first entry)  
XX  
DE FKBP12C PCR primer VX10801.  
XX  
KW Transplant rejection; monitoring; FK506 immunosuppressant therapy;  
KW tissue specific; polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX  
PN WO9323548-A2.  
XX  
PD 25-NOV-1993.  
XX  
XX 20-MAY-1993; 93WO-US004916.  
PF  
XX 20-MAY-1992; 92US-00886611.  
PR  
XX (VERT-) VERTEX PHARM INC.  
PA  
XX Peattie DA;  
PI  
XX WPI; 1993-386579/48.  
DR  
XX New cDNA for tissue specific FK506 binding proteins - and detection of  
XX its mRNA to monitor transplant rejection and effect or FK506  
PT immunosuppressant therapy.  
PT  
XX Example 4; Page 36; 54pp; English.  
PS  
XX The sequence is that of a PCR primer VX10801 which was used to amplify  
CC DNA specific to FKBP12C. (Updated on 25-MAR-2003 to correct PN field.)  
CC  
XX Sequence 28 BP; 5 A; 1 C; 4 G; 18 T; 0 U; 0 Other;  
SQ  
  
Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAAAAAAAAAAAAAA 2800  
Db ||||| ||||| ||||| |||||  
19 ATTCAAAAAAAAAAAAAAAAAA 1  
  
RESULT 1932  
AAQ36362/c  
ID AAQ36362 standard; DNA; 28 BP.  
XX  
AC AAQ36362;  
XX  
XX 25-MAR-2003 (revised)  
DT 07-JUN-1993 (first entry)  
XX  
XX GL6anti, targetted to human beta globin sequence.  
DE  
XX Hemoglobin; beta thalassemia; sickle cell anaemia; delta protein;  
KW triplex; target; duplex; promoter; coding domain; ss.  
KW  
XX Synthetic.  
OS  
XX US5176996-A.  
PN  
XX 05-JAN-1993..  
PD  
XX 22-DEC-1989; 89US-00453532.  
PF  
XX 20-DEC-1988; 88US-00287359.  
PR  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA  
XX Hogan ME, Kessler DJ;  
PI  
XX WPI; 1993-035718/04.  
DR  
XX

CC cDNA libraries produced may be used to identify new (unique) nucleotide  
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
CC method produces discreet sized PCR products which would not necessarily  
CC require further subcloning/screening. The method also produces full-  
CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 18 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 28;  
Best Local Similarity 94.7%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803  
| | | | | | | | | | | | | | | | | | | | | |  
Db 9 GCAAAAAAAAAAAAAAAAAA 27

RESULT 1934  
ADA26181/C  
ID ADA26181 standard; DNA; 30 BP.  
XX  
AC ADA26181;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:26.  
XX

KW genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;  
KW characteristic; single nucleotide polymorphism; SNP; genotyping;  
KW chromosome 1; gene; ds.  
XX

OS Synthetic.  
OS Oryza sativa.

XX WO2003070934-A1.  
XX  
PD 28-AUG-2003.

XX 07-FEB-2003; 2003WO-JP001317.  
XX

XX 25-FEB-2002; 2002JP-00048115.  
XX

XX (PLAN-) PLANT GENOME CENT CO LTD.  
XX

PI Minobe Y, Monna L, Kitazawa N, Yoshino R, Suzuki J;  
XX

DR WPI; 2003-697617/66.  
XX

XX Judging the genotype of a region around a plant sd-1 gene with  
PT polymorphism-obtained markers isolated by positional cloning, useful in  
PT genotyping for examination of semi-dwarf character of rice.  
XX

PS Disclosure; Page 15; 104pp; Japanese.  
XX

CC The present invention describes a method for judging the genotype of a  
CC region around a plant semi-dwarf (sd-1) gene in which polymorphisms are  
CC present, by detecting the polymorphisms. Also described: (1) examining  
CC semi-dwarf characteristics of a plant using the judgment method with  
CC detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA  
CC regions, which are primers for judging the genotype of a region around a  
CC plant sd-1 gene; (3) reagents for judging the genotype of a region around a  
CC a plant sd-1 gene containing these oligonucleotides; and (4) reagents for  
CC examining the semi-dwarf character of a plant containing the  
CC oligonucleotides. The method is for judging the genotype of a region  
CC around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS  
CC ((derived) cleaved amplified polymorphic sequence) for examination of the  
CC semi-dwarf character of rice to identify desirable strains e.g. with high  
CC crop yield, pest resistance and resistance to flooded water. The method  
CC is easy and quick, in which a seedling is required for studying single  
CC nucleotide polymorphisms (SNPs) for genotyping, without needing

CC cultivation of seedling to fully-grown plant for judging heterozygote and  
CC distinguishing morphology. The present sequence represents a rice sd-1  
CC DNA fragment, which is given in the exemplification of the present  
CC invention. Rice sd-1 is located on chromosome 1.  
XX

SQ Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 AAAAAAAAAAGAGAAAAA 12

RESULT 1935  
ABL56893/C  
ID ABL56893 standard; DNA; 30 BP.  
XX  
AC ABL56893;  
XX

DT 26-JUL-2002 (first entry)  
XX

DE Synthetic deoxyribonucleotide poly f.  
XX

KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.  
XX

OS Synthetic.  
XX

PN EP1046717-A2.  
XX

PD 25-OCT-2000.  
XX

XX 20-APR-2000; 2000EP-00108643.  
XX

XX 20-APR-1999; 99JP-00111601.  
XX

XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
XX

XX (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
XX

XX (KANK-) KANKYO ENG CO LTD.  
XX

PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX

DR WPI; 2000-657765/64.  
XX

PT Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX

PS Example 5; Page 21; 55pp; English.  
XX

CC The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC conventional PCR conditions can be used). The specificity of PCR is kept  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a synthetic

CC deoxyriboligonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAA 12  
RESULT 1936  
ABA97617/C  
ID ABA97617 standard; DNA; 30 BP.  
XX  
AC ABA97617;  
XX  
DT 11-APR-2002 (first entry)  
XX  
DE Poly f nucleotide sequence.  
XX  
KW ss; fluorochrome; nucleic acid probe; fluorescence.  
XX  
OS Unidentified.  
XX  
PN JP2001286300-A.  
XX  
PD 16-OCT-2001.  
XX  
PF 20-APR-2000; 2000JP-00120097.  
XX  
PR 20-APR-1999; 99JP-00111601.  
PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX  
PA (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
XX  
DR WPI; 2002-134193/18.  
XX  
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of  
PT the obtained data.  
XX  
PS Example 5; Page 17; 34pp; Japanese.  
XX  
CC This invention relates to a method for measuring nucleic acids using a  
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
CC decreases the fluorescence of the fluorochrome when hybridised with a  
CC target nucleic acid, the decrease in the fluorescence is measured. The  
CC method can be used for measuring a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAA 12  
RESULT 1937  
ABL95890/C  
ID ABL95890 standard; DNA; 30 BP.  
XX  
AC ABL95890;  
XX

DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly f for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
CC Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
CC their polymorphism and mutation, particularly useful in science and  
CC medicine for e.g. analytical applications, disease diagnosis and  
CC microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAA 12  
RESULT 1938  
ABL56894/C  
ID ABL56894 standard; DNA; 30 BP.  
XX  
AC ABL56894;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Synthetic deoxyriboligonucleotide poly 9.  
XX  
KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN EP1046717-A2.  
XX

PD 25-OCT-2000.  
XX  
PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
XX  
PT Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX  
PS Example 5; Page 21; 55pp; English.  
XX  
CC The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAAA 12  
  
RESULT 1939  
ABL56895/C  
ID ABL56895 standard; DNA; 30 BP.  
XX  
AC ABL56895;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Synthetic deoxyribonucleotide poly h.  
XX  
KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN EP1046717-A2.  
XX  
PD 25-OCT-2000.  
XX

PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
XX  
PT Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX  
PS Example 5; Page 21; 55pp; English.  
XX  
CC The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAAA 12  
  
RESULT 1940  
ABA97619/c  
ID ABA97619 standard; DNA; 30 BP.  
XX  
AC ABA97619;  
XX  
DT 11-APR-2002 (first entry)  
XX  
DE Poly h nucleotide sequence.  
XX  
KW ss; fluorochrome; nucleic acid probe; fluorescence.  
XX  
OS Unidentified.  
XX  
PN JP2001286300-A.  
XX  
PD 16-OCT-2001.  
XX  
PF 20-APR-2000; 2000JP-00120097.  
XX  
PR 20-APR-1999; 99JP-00111601.  
PR



PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX  
PA (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
XX  
DR WPI; 2002-134193/18.  
XX  
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of  
PT the obtained data.  
XX  
PS Example 5; Page 17; 34pp; Japanese.  
XX  
CC This invention relates to a method for measuring nucleic acids using a  
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
CC decreases the fluorescence of the fluorochrome when hybridised with a  
CC target nucleic acid, the decrease in the fluorescence is measured. The  
CC method can be used for measuring a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAGAAAAA 12  
RESULT 1941  
ABA97618/c  
ID ABA97618 standard; DNA; 30 BP.  
XX  
AC ABA97618;  
XX  
DT 11-APR-2002 (first entry)  
DE Poly g nucleotide sequence.  
XX  
KW ss; fluorochrome; nucleic acid probe; fluorescence.  
XX  
OS Unidentified.  
XX  
PN JP2001286300-A.  
XX  
PD 16-OCT-2001.  
XX  
PF 20-APR-2000; 2000JP-00120097.  
XX  
PR 20-APR-1999; 99JP-00111601.  
PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX  
PA (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
XX  
DR WPI; 2002-134193/18.  
XX  
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of  
PT the obtained data.  
XX  
PS Example 5; Page 17; 34pp; Japanese.  
XX  
CC This invention relates to a method for measuring nucleic acids using a  
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe  
CC decreases the fluorescence of the fluorochrome when hybridised with a  
CC target nucleic acid, the decrease in the fluorescence is measured. The  
CC method can be used for measuring a target nucleic acid

XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAGAAAAA 12  
RESULT 1942  
ABL95891/c  
ID ABL95891 standard; DNA; 30 BP.  
XX  
AC ABL95891;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly g for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAGAAAAA 12

RESULT 1943  
ABL95892/c  
ID ABL95892 standard; DNA; 30 BP.  
XX  
AC ABL95892;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly h for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
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XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAAGAAAAA 12  
  
RESULT 1944  
ABL56888/c  
ID ABL56888 standard; DNA; 30 BP.  
XX  
AC ABL56888;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Synthetic deoxyribonucleotide poly a.  
XX

KW Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN EP1046717-A2.  
XX  
PD 25-OCT-2000.  
XX  
PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
PT Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.  
XX  
PS Example 5; Page 21; 55pp; English.  
XX  
CC The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC conventional PCR conditions can be used). The specificity of PCR is kept  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAACAAAA 12  
  
RESULT 1945  
ABA97612/c  
ID ABA97612 standard; DNA; 30 BP.  
XX  
AC ABA97612;  
XX  
DT 11-APR-2002 (first entry)  
XX  
DE Poly a nucleotide sequence.  
XX  
KW ss; fluorochrome; nucleic acid probe; fluorescence.  
XX

OS Unidentified.  
XX  
PN JP2001286300-A.  
XX  
PD 16-OCT-2001.  
XX  
PF 20-APR-2000; 2000JP-00120097.  
XX  
PR 20-APR-1999; 99JP-00111601.  
PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX  
PA (BIOT-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
XX  
DR WPI; 2002-134193/18.  
XX  
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of the obtained data.  
PT  
XX  
PS Example 5; Page 17; 34pp; Japanese.  
XX  
CC This invention relates to a method for measuring nucleic acids using a nucleic acid probe labelled with a fluorochrome. The nucleic acid probe decreases the fluorescence of the fluorochrome when hybridised with a target nucleic acid, the decrease in the fluorescence is measured. The method can be used for measuring a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db ||||| ||||| ||||| |||||  
30 AAAAAAAAAAAAAAAAAA 12  
  
RESULT 1946  
ABL95885/c  
ID ABL95885 standard; DNA; 30 BP.  
XX  
AC ABL95885;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly a for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis; microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K; Yokomaku T;  
XX  
DR WPI; 2002-195876/25.

XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification.  
PS Example 12; Page 60; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful for assaying nucleic acids by hybridising with a target nucleic acid, in which a single-stranded oligonucleotide is labelled with a fluorescent substance and a quencher in a manner that the fluorescence intensity of the hybridisation reaction system is increased after completion of the hybridisation but no stem loop structure is formed. The probes are useful for assaying nucleic acids and their polymorphism and mutation, particularly useful for e.g. analytical applications, disease diagnosis and microbial identification. The present sequence was used to illustrate the invention  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db ||||| ||||| ||||| |||||  
30 AAAAAAAAAAAAAAAAAA 12  
  
RESULT 1947  
ABL56892/c  
ID ABL56892 standard; DNA; 30 BP.  
XX  
AC ABL56892;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Synthetic deoxyribonucleotide poly e.  
XX  
KW Concentration; quantification; mutation detection; polymorphic; polymerase chain reaction; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN EP1046717-A2.  
XX  
PD 25-OCT-2000.  
XX  
PF 20-APR-2000; 2000EP-00108643.  
XX  
PR 20-APR-1999; 99JP-00111601.  
XX  
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.  
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI; 2000-657765/64.  
XX  
PT Determining the concentration of a target nucleic acid, useful e.g. for detecting genetic mutations, comprises using a fluorescently labeled probe in which emission is reduced by binding to the target nucleic acid.  
PT  
XX  
PS Example 5; Page 21; 55pp; English.  
XX  
CC The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC conventional PCR conditions can be used). The specificity of PCR is kept  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||||  
Db 30 AAAAAAAAAACAAAAAAAAA 12

RESULT 1948  
ABL56896/C  
ID ABL56896 standard; DNA; 30 BP.

XX ABL56896;

XX 26-JUL-2002 (first entry)

XX Synthetic deoxyribonucleotide poly i.

XX Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.

XX Synthetic.

XX EP1046717-A2.

XX 25-OCT-2000.

XX 20-APR-2000; 2000EP-00108643.

XX 20-APR-1999; 99JP-00111601.

XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.

PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;

XX WPI; 2000-657765/64.

XX Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.

XX Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the  
CC invention allow target nucleic acids to be quantified quickly, easily and  
CC accurately. Particularly there is no need to remove unbound probe, and no  
CC materials are introduced that inhibit amplification by Taq polymerase (so  
CC conventional PCR conditions can be used). The specificity of PCR is kept  
CC high (amplification of primer dimers is delayed), and the limit of  
CC quantitation is reduced. Complex probes are not needed, and amplification  
CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribonucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||||  
Db 30 AAAAAAAAAAGAAAAAAAAA 12

RESULT 1949  
ABL56890/C  
ID ABL56890 standard; DNA; 30 BP.

XX ABL56890;

XX 26-JUL-2002 (first entry)

XX Synthetic deoxyribonucleotide poly c.

XX Concentration; quantification; mutation detection; polymorphic;  
KW polymerase chain reaction; PCR; ss.

XX Synthetic.

XX EP1046717-A2.

XX 25-OCT-2000.

XX 20-APR-2000; 2000EP-00108643.

XX 20-APR-1999; 99JP-00111601.

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PA (KANK-) KANKYO ENG CO LTD.

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PI Koyama O, Furusho K;

XX WPI; 2000-657765/64.

XX Determining the concentration of a target nucleic acid, useful e.g. for  
PT detecting genetic mutations, comprises using a fluorescently labeled  
PT probe in which emission is reduced by binding to the target nucleic acid.

XX Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a  
CC nucleic acid target, using a fluorescently labeled probe which produces  
CC reduced fluorescence emission when hybridised to the target nucleic acid.  
CC The method comprises measuring the reduction in emission caused by  
CC hybridisation. The new method is particularly used to quantify target  
CC nucleic acids by a real-time polymerase chain reaction, e.g. for  
CC quantifying microbial cells in co-cultures or symbiotic systems, for  
CC detecting gene mutations or polymorphisms, and for analysing melting  
CC curves of target nucleic acids to determine a Tm value. Methods of the





high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed, and amplification can be monitored in real time. The working graph for data analysis (automatically generated by a computer) has a higher correlation coefficient than conventional graphs so more accurate quantitation is possible. The current sequence represents a synthetic deoxyribonucleotide that was used for investigating the base selectivity of a target nucleic acid

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAA 12

RESULT 1952  
ABL56889/c  
ID ABL56889 standard; DNA; 30 BP.

DT	26-JUL-2002	(first entry)
XX		
DE		Synthetic deoxyribonucleotide poly b.
XX		
KW		Concentration; quantification; mutation detection; polymorphic;
KW		polymerase chain reaction; PCR; ss.

PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;  
PI Koyama O, Furusho K;  
XX  
DR WPI: 2000-657765/64.

Determining the concentration of a target nucleic acid, useful e.g. for detecting genetic mutations, comprises using a fluorescently labeled probe in which emission is reduced by binding to the target nucleic acid.

Example 5; Page 21; 55pp; English.

The invention relates to the determination of the concentration of a nucleic acid target, using a fluorescently labeled probe which produces reduced fluorescence emission when hybridised to the target nucleic acid. The method comprises measuring the reduction in emission caused by hybridisation. The new method is particularly used to quantify target nucleic acids by a real-time polymerase chain reaction, e.g. for quantifying microbial cells in co-cultures or symbiotic systems, for detecting gene mutations or polymorphisms, and for analysing melting curves of target nucleic acids to determine a  $T_m$  value. Methods of the invention allow target nucleic acids to be quantified quickly, easily and accurately. Particularly there is no need to remove unbound probe, and no materials are introduced that inhibit amplification by Taq polymerase (so conventional PCR conditions can be used). The specificity of PCR is kept high (amplification of primer dimers is delayed), and the limit of quantitation is reduced. Complex probes are not needed and amplification

CC can be monitored in real time. The working graph for data analysis  
CC (automatically generated by a computer) has a higher correlation  
CC coefficient than conventional graphs so more accurate quantitation is  
CC possible. The current sequence represents a synthetic  
CC deoxyribopolynucleotide that was used for investigating the base  
CC selectivity of a target nucleic acid

Query Match 0.6%; Score 17.4; DB 1;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels

Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAAAAAAAAA 12

RESULT 1953  
ABA97613/c  
ID ABA97613 standard: DNA: 30 BP.

11-APR-2002	(first entry)
Poly b	nucleotide sequence.
ss;	fluorochrome; nucleic acid probe; fluorescence.

PA (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

DR WPI; 2002-134193/18.

Measurement of nucleic acids, using a nucleic acid probe and analysis of the obtained data.

PS Example 5; Page 17; 34pp; Japanese.

This invention relates to a method for measuring nucleic acids using a nucleic acid probe labelled with a fluorochrome. The nucleic acid probe decreases the fluorescence of the fluorochrome when hybridised with a target nucleic acid, the decrease in the fluorescence is measured. The method can be used for measuring a target nucleic acid

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels

Qy	2786	AAAAAAAAAAAAAAAAAAAA	2804
D <sub>b</sub>	30	AAAAAAAAAAAAAAAAAAAA	12

RESULT 1954  
ABA97620/c



SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAACAAAAA 12  
RESULT 1957  
ABA97616/c  
ID ABA97616 standard; DNA; 30 BP.  
XX  
AC ABA97616;  
XX  
DT 11-APR-2002 (first entry)  
XX  
DE Poly e nucleotide sequence.  
XX  
KW ss; fluorochrome; nucleic acid probe; fluorescence.  
XX  
OS Unidentified.  
XX  
PN JP2001286300-A.  
XX  
PD 16-OCT-2001.  
XX  
PF 20-APR-2000; 2000JP-00120097.  
XX  
PR 20-APR-1999; 99JP-00111601.  
PR 24-AUG-1999; 99JP-00236666.  
PR 30-AUG-1999; 99JP-00242693.  
PR 01-FEB-2000; 2000JP-00028896.  
XX  
PA (BIOI-) BIOINDUSTRY KYOKAI SH.  
PA (KANK-) KANKYO ENG KK.  
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.  
XX  
DR WPI; 2002-134193/18.  
XX  
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of the obtained data.  
XX  
PS Example 5; Page 17; 34pp; Japanese.  
XX  
CC This invention relates to a method for measuring nucleic acids using a nucleic acid probe labelled with a fluorochrome. The nucleic acid probe decreases the fluorescence of the fluorochrome when hybridised with a target nucleic acid, the decrease in the fluorescence is measured. The method can be used for measuring a target nucleic acid  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAACAAAAA 12  
RESULT 1958  
ABL95886/c  
ID ABL95886 standard; DNA; 30 BP.  
XX  
AC ABL95886;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly b for assaying nucleic acids.

XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis; microbial identification; ss.  
KW  
XX Unidentified.  
OS  
XX WO200208414-A1.  
XX  
XX 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K; Yokomaku T;  
PI  
XX WPI; 2002-195876/25.  
DR  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and their polymorphism and mutation, particularly useful in science and medicine for e.g. analytical applications, disease diagnosis and microbial identification.  
PT  
PT  
PT  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful for assaying nucleic acids by hybridising with a target nucleic acid, in which a single-stranded oligonucleotide is labelled with a fluorescent substance and a quencher in a manner that the fluorescence intensity of the hybridisation reaction system is increased after completion of the hybridisation but no stem loop structure is formed. The probes are useful for assaying nucleic acids and their polymorphism and mutation, particularly useful for e.g. analytical applications, disease diagnosis and microbial identification. The present sequence was used to illustrate the invention  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAACAAAAA 12  
RESULT 1959  
ABL95887/c  
ID ABL95887 standard; DNA; 30 BP.  
XX  
AC ABL95887;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly c for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis; microbial identification; ss.  
KW  
XX Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.



XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAACAAAAA 12  
RESULT 1960  
ABL95894/C  
ID ABL95894 standard; DNA; 30 BP.  
XX  
AC ABL95894;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly j for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
XX WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
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XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
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DR WPI; 2002-195876/25.  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
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PS Example 12; Page 60; 152pp; Japanese.  
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CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
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CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 30 AAAAAAAAAAGAAAAA 12  
RESULT 1961  
ABL95888/C  
ID ABL95888 standard; DNA; 30 BP.  
XX  
AC ABL95888;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly d for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
XX WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
XX 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in

CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 AAAAAAAAAAACAAAAAA 12

RESULT 1962  
ABL95889/c  
ID ABL95889 standard; DNA; 30 BP.  
XX  
AC ABL95889;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly e for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.

XX (NAAD-) NAT INST ADVANCED. IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX

CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX

SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 AAAAAAAAAAACAAAAAA 12

RESULT 1963  
ABL95893/c  
ID ABL95893 standard; DNA; 30 BP.  
XX  
AC ABL95893;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe poly I for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX  
PR 27-JUN-2000; 2000JP-00193133.  
PR 03-AUG-2000; 2000JP-00236115.  
PR 26-SEP-2000; 2000JP-00292483.

XX (NAAD-) NAT INST ADVANCED. IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Example 12; Page 60; 152pp; Japanese.  
XX

CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.4; DB 1; Length 30;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 AAAAAAAAAAGAAAAAA 12

RESULT 1964  
AAT94431

ID AAT94431 standard; mRNA; 19 BP.  
XX  
AC AAT94431;  
XX  
DT 02-MAR-1998 (first entry)  
XX  
DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.  
XX  
KW Primer; detection; characterisation; mRNA; restriction display PCR;  
KW synthesis; cDNA; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9729211-A1.  
XX  
PD 14-AUG-1997.  
XX  
PF 07-FEB-1997; 97WO-US002009.  
XX  
PR 09-FEB-1996; 96US-0011379P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Weinstein JN, Boulamwini J;  
XX  
DR WPI; 1997-415362/38.  
XX  
PT Detection and characterisation of mRNA by restriction display PCR -  
PT comprising synthesis of cDNA, digestion with a restriction endonuclease,  
PT ligation to an adaptor DNA and PCR amplification.  
XX  
PS Disclosure; Page 24; 40pp; English.  
XX  
XX A method has been improved for detecting and characterising mRNA  
CC molecules which includes synthesising a double stranded (ds) cDNA from  
CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to  
CC produce cDNA fragments in which at least one end of the cDNA fragments  
CC has a sequence capable of hybridising to an adaptor DNA sequence. The  
CC improvement comprises: (a) hybridising adaptor DNA sequences to at least  
CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to  
CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated  
CC adaptor DNA sequences by a PCR using primers that hybridise to the ends  
CC of the cDNA fragments, where the primers have at least one nucleotide at  
CC the 3' end that specifically hybridises to a subset of cDNA molecules;  
CC and (d) detecting the presence of the resulting amplified cDNA fragments.  
CC The present sequence represent a template poly-A tail used in the present  
CC specification. The method designate restriction display PCR can be used  
CC for characterising cells based on their mRNA content, for representing  
CC expressed genes, and for discovery of therapeutics that alter cellular  
CC gene expression. The method is also useful for characterising cells of a  
CC variety of types and under a variety of physiological conditions. The  
CC method is also useful for identifying cells or tissue from particular  
CC individuals or species based on the fingerprint obtained from the mRNA  
CC content of isolated cells or tissue and comparing it to cells or tissue  
CC from a known source  
XX  
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.2e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2785 GAAAAA AAAAAAAAAA 2802  
Db :|||||  
2 BAAAAA AAAAAAAAAA 19  
RESULT 1965  
AAT94431/C  
ID AAT94431 standard; mRNA; 19 BP.  
XX  
AC AAT94431;

XX 02-MAR-1998 (first entry)  
DT  
XX  
DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.  
XX  
KW Primer; detection; characterisation; mRNA; restriction display PCR;  
KW synthesis; cDNA; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9729211-A1.  
XX  
PD 14-AUG-1997.  
XX  
PF 07-FEB-1997; 97WO-US002009.  
XX  
PR 09-FEB-1996; 96US-0011379P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Weinstein JN, Boulamwini J;  
XX  
DR WPI; 1997-415362/38.  
XX  
PT Detection and characterisation of mRNA by restriction display PCR -  
PT comprising synthesis of cDNA, digestion with a restriction endonuclease,  
PT ligation to an adaptor DNA and PCR amplification.  
XX  
PS Disclosure; Page 24; 40pp; English.  
XX  
XX A method has been improved for detecting and characterising mRNA  
CC molecules which includes synthesising a double stranded (ds) cDNA from  
CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to  
CC produce cDNA fragments in which at least one end of the cDNA fragments  
CC has a sequence capable of hybridising to an adaptor DNA sequence. The  
CC improvement comprises: (a) hybridising adaptor DNA sequences to at least  
CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to  
CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated  
CC adaptor DNA sequences by a PCR using primers that hybridise to the ends  
CC of the cDNA fragments, where the primers have at least one nucleotide at  
CC the 3' end that specifically hybridises to a subset of cDNA molecules;  
CC and (d) detecting the presence of the resulting amplified cDNA fragments.  
CC The present sequence represent a template poly-A tail used in the present  
CC specification. The method designate restriction display PCR can be used  
CC for characterising cells based on their mRNA content, for representing  
CC expressed genes, and for discovery of therapeutics that alter cellular  
CC gene expression. The method is also useful for characterising cells of a  
CC variety of types and under a variety of physiological conditions. The  
CC method is also useful for identifying cells or tissue from particular  
CC individuals or species based on the fingerprint obtained from the mRNA  
CC content of isolated cells or tissue and comparing it to cells or tissue  
CC from a known source  
XX  
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.2e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2170 TTTTTT TTTTTT TTTT TTA 2187  
Db |||||  
19 TTTTTT TTTTTT TTTT TTV 2  
RESULT 1966  
AAX18390  
ID AAX18390 standard; DNA; 19 BP.  
XX  
AC AAX18390;  
XX  
DT 11-MAY-1999 (first entry)  
XX





CC designed to rapidly array and normalize a complex cDNA library obtained  
CC from a target species. Clones are arrayed into multi-well plates. Each  
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run  
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,  
CC which allows an anchored oligonucleotide in each well to selectively  
CC hybridise only to those cDNA clones with a complementary 5' end. The  
CC unique 3' key sequences are designed to give a comprehensive level of  
CC degeneracy since they are diverse and numerous enough to ensure that  
CC every possible cDNA sequence can be bound by an individual, specific  
CC oligonucleotide in a single well. The cDNA library is heated to denature  
CC the clones into single stranded DNA, and an aliquot is added to every  
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and  
CC the common 5' region present in every cDNA clone serves as the 5' priming  
CC site. Denaturing and washing leave anchored cDNA in each well. The  
CC library is now arrayed and normalised. The method was used to identify  
CC and isolate clones encoding G-protein coupled receptors, especially  
CC odourant receptors, and active effectors involved in the olfactory  
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,  
CC or other olfactory or neuronal proteins. The identified receptors and  
CC proteins are useful for identifying compounds that reduce a target  
CC animal's sensitivity to odours, for manufacturing compounds or devices  
CC that mask odours, or trapping invertebrates with odourants.  
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed  
CC with desirable effects on specific species, for the development of pest  
CC monitoring systems or non-toxic, species-specific pesticide alternatives,  
CC for controlling insect feeding and breeding behaviour, detecting the  
CC presence of small air-borne molecules, etc  
XX  
SQ Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2172 TTTTCTTTTCTTTTAACTTTG 2193  
|||||  
Db 1 TTTTCTTTTCTTTTGAATGG 22

RESULT 1969  
AAT33703  
ID AAT33703 standard; DNA; 23 BP.  
XX  
AC AAT33703;  
XX  
DT 19-MAY-1997 (first entry)  
XX  
DE Primer #3 for tissue or cell derived RNA.  
XX  
KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;  
KW molecular indexing; class IIS restriction enzyme; cancer; causative gene;  
KW viral infection; hereditary disease; agricultural gene; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 1  
FT /\*tag= a  
FT /note= "hydroxylated"  
XX  
PN EP735144-A1.  
XX  
PD 02-OCT-1996.  
XX  
PF 26-MAR-1996; 96EP-00104817.  
XX  
PR 28-MAR-1995; 95JP-00069695.  
PR 20-JUL-1995; 95JP-00184006.  
PR 12-SEP-1995; 95JP-00234122.  
XX  
PA (SHKJ ) RES DEV CORP JAPAN.  
XX  
PI Kato K;

XX WPI; 1996-435619/44.  
DR  
XX Molecular indexing of DNA - using restriction enzymes, PCR amplification  
PT and electrophoresis to analyse DNA fragments.  
XX  
PS Claim 3; Page 14; 20pp; English.  
XX  
CC AAT33701-T33703 represent amplification primers used in the reverse-  
CC transcription of tissue or cell derived mRNA, in the method of the  
CC invention. The method of the invention is a molecular indexing method,  
CC and comprises digesting the cDNA amplified by these sequences with a  
CC class IIS restriction enzyme. Each resultant cDNA fragment is then  
CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors  
CC cohesive to all possible overhangs), and digesting the products with two  
CC further class IIS restriction enzymes. These steps are repeated (but the  
CC enzyme used for the first step is different in each) to produce two  
CC further cDNA samples. The ligation samples are then recovered using  
CC streptavidin-coated paramagnetic beads, removing the strand complementary  
CC to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer  
CC (such as this sequence) are then used to amplify the cDNA samples. The  
CC amplified products are separated, and the sizes of the fragments obtained  
CC is recorded. The method can be used for the analysis and diagnosis or  
CC diseases such as cancers or viral infections, for the search and  
CC isolation of the genes of physiologically active substances that are  
CC potential pharmaceuticals, or causative genes of hereditary diseases, as  
CC well as for the isolation of genes for improving agricultural products.  
CC Using this method, it is possible to classify (index) DNA into groups in  
CC a short period of time without duplication  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2183  
||| |||||  
Db 1 CTCGAGTTTCTTTTCTTTTCTTTT 22

RESULT 1970  
AAV61556  
ID AAV61556 standard; DNA; 23 BP.  
XX  
AC AAV61556;  
XX  
DT 08-DEC-1998 (first entry)  
XX  
DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.  
XX  
KW primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;  
KW kidney; apolipoprotein; ATAC-PCR; Adaptor-tagged Competitive PCR;  
KW gene expression; internal standard; calibration curve; ss.  
XX  
OS Synthetic.  
OS Mus sp.  
XX  
PN BP870842-A2.  
XX  
PD 14-OCT-1998.  
XX  
PF 07-APR-1998; 98EP-00302726.  
XX  
PR 07-APR-1997; 97JP-00088495.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Kato K;  
XX  
DR WPI; 1998-523164/45.  
XX  
PT Determination of gene expression levels - using combinations of different

PT cDNA samples tagged with different PCR adaptors.  
XX  
PS Example 2; Page 9; 22pp; English.  
XX  
CC The present sequence represents a primer which was used to synthesise  
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers  
CC AAV61554 and AAV61555 were added to both mouse liver-derived and mouse  
CC kidney-derived total RNA to generate single-stranded cDNA. These primers  
CC were used in the method of the invention to determine the amount ratio  
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA  
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-  
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to  
CC be quantitatively determined, and because internal standards are not  
CC required to prepare a calibration curve, it is a quicker and less  
CC laborious process  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT 2183  
Db 1 CTCGAGTT TTTT TTTT TTTT TTTT 22

RESULT 1971  
AAA08409  
ID AAA08409 standard; DNA; 23 BP.  
AC AAA08409;  
XX  
DT 13-JUL-2000 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO:3.  
XX  
KW Detection; primer; adapter; probe; hybridisation; gene cluster;  
KW fractionation; ss.  
XX  
OS Synthetic.  
XX JP2000055914-A.  
PN  
XX  
PD 25-FEB-2000.  
XX  
PF 13-AUG-1998; 98JP-00228944.  
XX  
PR 13-AUG-1998; 98JP-00228944.  
XX  
PA (TAIS ) TAISHO PHARM CO LTD.  
XX  
DR WPI; 2000-368733/32.  
XX  
XX  
PT Gene detection method involves hybridizing probe opposite to objective  
PT gene out of fractional gene cluster.  
XX  
PS Example 1; Page 9; 11pp; Japanese.  
XX  
CC The present invention describes a gene detection method which comprises  
CC fractionating using a probe opposite to the objective gene which is  
CC hybridised out of fractioned gene cluster. The objective gene detected  
CC belongs to the group of objective genes contained in the sample. The  
CC method is used for gene detection by fractionation of cDNA by molecular  
CC index method using specific primer. It provides high detection  
CC sensitivity of objective gene. AAA08407 to AAA08414 represent  
CC oligonucleotides used in the exemplification of the present invention  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2162 CTCCTTTT TTTT TTTT TTTT TTTT 2183  
Db 1 CTCGAGTT TTTT TTTT TTTT TTTT 22

RESULT 1972  
AAS04989/c  
ID AAS04989 standard; DNA; 23 BP.  
XX  
AC AAS04989;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Neurofibromatosis (NF1) genomic DNA sequencing primer #41.  
XX  
KW Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;  
KW Epstein-Barr virus; B-lymphoblastoid cell; phytohaemagglutinin; PHA;  
KW frame shift mutation; mis-sense mutation; silent mutation; PCR primer;  
KW sequencing primer.  
XX  
OS Homo sapiens.  
XX  
PN WO200129251-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 18-OCT-2000; 2000WO-EP010255.  
XX  
PR 18-OCT-1999; 99EP-00870216.  
PR 05-JUN-2000; 2000EP-00870122.  
XX  
PA (UYGE-) UNIV GENT.  
XX  
PI Messiaen L, Callens T;  
XX  
DR WPI; 2001-300341/31.  
XX  
PT Mutation analysis of NF1 gene by treating EBV transformed lymphoblastoid  
PT cell lines formed with lymphocytes of patient with protein synthesis  
PT inhibitor, and obtaining peptides by translating amplified RNA from cell  
PT line.  
XX  
PS Claim 9; Page 60; 102pp; English.  
XX  
CC The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and  
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A  
CC method for mutation analysis of the NF1 gene involves isolating  
CC peripheral blood lymphocytes (PBL) of a patient, establishing Epstein-  
CC Barr virus (EBV) transformed B-lymphoblastoid cell line with isolated  
CC PBL, or short-term culturing of PBL by phytohaemagglutinin (PHA)  
CC stimulation, treating the cell line or short-term culture with protein  
CC synthesis inhibitor and immediately extracting RNA from the cultures. The  
CC RNA is then amplified and peptide fragments are obtained by in vitro  
CC transcription/translation of amplified fragments. Mutation analysis of  
CC NF1 is used for detection of frame shift, mis-sense and silent mutations  
CC in various exons of the gene. This is useful in screening for NF1  
CC mutations in young children who are often oligosymptomatic. Efficacy of a  
CC drug or agent can be identified by a screening process in which the  
CC modulation is monitored in vitro using cell systems in which the  
CC defective NF1 gene is expressed. The sequences can be used to design  
CC drugs which modulate NF1 activity, by using knowledge of the structure of  
CC the NF1 protein and of specific defects of the various NF1 mutant  
CC proteins. The method allows for reliable analysis of mutations that are  
CC difficult to detect due to unstable or wrong-spliced transcripts  
XX  
SQ Sequence 23 BP; 7 A; 4 C; 3 G; 9 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2750 GATACGTGTATATAAAGTAT 2771



CC animal's sensitivity to odours, for manufacturing compounds or devices  
CC that mask odours, or trapping invertebrates with odourants.  
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed  
CC with desirable effects on specific species, for the development of pest  
CC monitoring systems or non-toxic, species-specific pesticide alternatives,  
CC for controlling insect feeding and breeding behaviour, detecting the  
CC presence of small air-borne molecules, etc  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 3 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2172 TTTTCTTTTCTTTTAACTTTG 2193  
Db 1 TTTTCTTTTCTTTTGAATGG 22  
  
RESULT 1975  
AAH75510/c  
ID AAH75510 standard; DNA; 24 BP.  
AC AAH75510;  
XX  
DT 18-OCT-2001 (first entry)  
XX  
DE Human CCR4 related protein 31 PCR primer 2.  
XX  
KW Human; CCR4; cancer; HIV; Human immunodeficiency virus; infection;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1296960-A.  
XX  
PD 30-MAY-2001.  
XX  
PF 22-NOV-1999; 99CN-00124049.  
XX  
PR 22-NOV-1999; 99CN-00124049.  
XX  
PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.  
XX  
PI Mao Y, Xie Y;  
XX  
WPI; 2001-489558/54.  
XX  
PT Polypeptide-human CCR4 related protein 31 and polynucleotide for coding  
PT polypeptide, useful for treating e.g. cancer and HIV infection, is  
PT prepared by DNA recombination.  
XX  
PS Example 3; Page 17 (Disclosure); 34pp; Chinese.  
XX  
CC The invention relates to human CCR4 related protein 31, the  
CC polynucleotide encoding it and the use of the protein in treating e.g.  
CC cancer and HIV infection. The present sequence is that of a human CCR4  
CC PCR primer of the invention  
XX  
SQ Sequence 24 BP; 3 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2783 TTGAAAAAAGAAAAA 2804  
Db 23 TTAATAAAAGAAAAA 2  
  
RESULT 1976  
AAV82670  
ID AAV82670 standard; DNA; 24 BP.

XX AAV82670;  
AC  
XX 16-FEB-1999 (first entry)  
DT  
DE Primer used to identify cDNA encoding ST38.2.  
XX  
KW Rat; chemokine; ST38.2; chemotaxis; leucocyte-activating; inflammation;  
KW immune response; brain injury; trauma; ischaemia;  
KW autoimmune inflammation; multiple sclerosis; stroke;  
KW rheumatoid arthritis; meningitis; encephalitis; PCR primer; ss.  
XX  
OS Synthetic.  
OS Rattus sp.  
XX  
PN WO9849309-A1.  
XX  
PD 05-NOV-1998.  
XX  
PF 23-APR-1998; 98WO-EP002405.  
XX  
PR 30-APR-1997; 97EP-00107135.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX  
PI Lesslauer W, Utansschneitz U;  
XX  
DR WPI; 1999-009430/01.  
XX  
PT New chemokine ST38.2 with chemotactic and leucocyte-activating properties  
PT - used to treat inflammation and immune responses and to identify  
PT specific modulators.  
XX  
PS Example 3; Page 28; 64pp; English.  
XX  
CC PCR primers AAV82670-71 were used to amplify cDNA encoding a novel rat  
CC chemokine designated ST38.2. In addition, primer AAV82670 was used to  
CC reverse transcribe rat RNA. The protein has chemotactic and leucocyte-  
CC activating properties. ST38.2 is involved in inflammation and immune  
CC responses, particularly inflammatory response to brain injury (trauma,  
CC ischaemia or autoimmune inflammation) but also in multiple sclerosis,  
CC stroke, rheumatoid arthritis and infections (particularly meningitis and  
CC encephalitis)  
XX  
SQ Sequence 24 BP; 2 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2161 TCTCCTTTTCTTTTCTTTTCTTTT 2182  
Db 3 TCTAGATTTTCTTTTCTTTTCTTTT 24  
  
RESULT 1977  
AAI69702/c  
ID AAI69702 standard; DNA; 24 BP.  
XX  
AC AAI69702;  
XX  
DT 12-DEC-2001 (first entry)  
XX  
DE Human neuropeptide 11 PCR primer #2.  
XX  
KW Human; neuropeptide 11; cytostatic; virucidal; immunomodulatory;  
KW antiinflammatory; haemostatic; anti-HIV; gene therapy; malignant tumour;  
KW haemopathy; HIV infection; immunological disease; inflammation;  
KW vegetative nervous function disturbance; vascular function disturbance;  
KW endocrinosis; developmental disturbance; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX



PN WO200172807-A1.  
XX  
PD 04-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-CN0000466.  
XX  
PR 28-MAR-2000; 2000CN-00115223.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX WPI; 2001-602848/68.  
DR  
XX New human neuropeptide 11 for diagnosing and treating endocrinosis,  
PT malignant tumor, hemopathy, human immunodeficiency virus infection,  
PT immunological diseases and various inflammations.  
XX  
PS Example 2; Page 17; 35pp; Chinese.  
XX  
CC The present invention relates to human neuropeptide 11 (see AAI65200 and  
CC AAG78860). The neuropeptide and its coding sequence are useful in the  
CC diagnosis and treatment of malignant tumours, haemopathy, HIV infection,  
CC immunological diseases, various inflammations, vegetative nervous  
CC function disturbance, vascular function disturbance, endocrinosis and  
CC developmental disturbance. The present sequence is a PCR primer which was  
CC used in an example from the present invention  
XX  
SQ Sequence 24 BP; 4 A; 7 C; 2 G; 11 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1504 GAAACACAGGAAATATAAATTGG 1525  
Db 23 GAAACACAGTAAAGAAAGTTGG 2  
RESULT 1978  
ABV77761/c  
ID ABV77761 standard; DNA; 24 BP.  
XX  
AC ABV77761;  
XX  
DT 03-FEB-2003 (first entry)  
XX  
DE Human DNA-PK interaction protein 9.9 PCR primer #2.  
XX  
KW Human; DNA-PK interaction protein 9.9; cancer; HIV infection; cytostatic;  
KW anti-HIV; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1351066-A.  
XX  
PD 29-MAY-2002.  
XX  
PF 26-OCT-2000; 2000CN-00125835.  
XX  
PR 26-OCT-2000; 2000CN-00125835.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-609430/66.  
XX  
PT New polypeptide-human DNA-PK interaction protein 9.9 for treating  
PT diseases, such as, cancer, and human immunodeficiency virus infection.  
XX  
PS Example 2; Page 16 (Disclosure); 31pp; Chinese.  
XX

CC The present invention relates to human DNA-PK interaction protein 9.9.  
CC The protein can be used for treating diseases such as cancer and HIV  
CC infection. The present sequence is a PCR primer, which was used in an  
CC example from the invention  
XX  
SQ Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2780 GAATTGAAAAAATAAAAAA 2801  
Db 22 GATTTCAAAAAATAAAAAACA 1  
RESULT 1979  
ABQ78896  
ID ABQ78896 standard; DNA; 24 BP.  
XX  
AC ABQ78896;  
XX  
DT 17-OCT-2002 (first entry)  
XX  
DE Human zinc finger protein 27.50 PCR primer 2.  
XX  
KW Human; zinc finger protein 27.50; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1341649-A.  
XX  
PD 27-MAR-2002.  
XX  
PF 07-SEP-2000; 2000CN-00125059.  
XX  
PR 07-SEP-2000; 2000CN-00125059.  
XX  
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-520724/56.  
XX  
PT Novel human zinc finger protein 27.50.  
XX  
PS Example 3; Page 17 (Disclosure); 31pp; Chinese.  
XX  
CC The invention relates to a novel human zinc finger protein 27.50, and the  
CC polynucleotide encoding it. The polypeptide is useful for treating  
CC several diseases, such as solid tumour, nervous system disease, malignant  
CC disease of blood, development disturbance and HIV infection. The sequence  
CC represents a PCR primer used in example 3 of the invention  
XX  
SQ Sequence 24 BP; 5 A; 0 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2166 TTTTATTTTATTTTATTTT 2187  
Db 3 TTTTATTTTATTTTATTTT 24  
RESULT 1980  
AAC96060/c  
ID AAC96060 standard; DNA; 25 BP.  
XX  
AC AAC96060;  
XX  
DT 26-FEB-2001 (first entry)  
XX









CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

XX  
SQ Sequence 25 BP; 8 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 25;  
Best Local Similarity 86.4%; Pred. No. 2.1e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2277 ATGTTTCGAGTAAACTTGAAAA 2298  
|||||  
Db 25 ATGTTTCGAGAAACTCGTAA 4

RESULT 1988  
AAT61049/c  
ID AAT61049 standard; DNA; 26 BP.  
XX  
AC AAT61049;  
XX  
DT 06-OCT-1997 (first entry)  
XX  
DE Primer Mt-2.  
XX  
KW primer; PCR; polymerase chain reaction; origin; test; cytochrome b;  
KW food control; processed meat; ss.  
XX  
OS Synthetic.  
XX DE19629166-A1.  
XX  
PD 27-FEB-1997.  
XX  
PF 19-JUL-1996; 96DE-01029166.  
XX  
PR 22-AUG-1995; 95DE-01031377.  
PR 07-NOV-1995; 95DE-01041368.  
XX  
PA (ZBTB-) ZTB ZENT TECHNOLOGIETRANSFER BIOMEDIZIN.  
XX  
PI Puehler A, Arnold W, Kriete G, Weidner S;  
XX  
DR WPI; 1997-146900/14.  
XX  
PT Amplification primer for animal cytochrome b gene - and determining  
PT origin of biological material, esp. of meat prods. used in foods.  
XX  
PS Claim 7; Col 5; 6pp; German.  
XX  
CC This oligonucleotide is primer Mt-2. It is used in a claimed method, with  
CC primer Mt-11 (AAT61048) to determine the origin of a biological material.  
CC The primers amplify the cytochrome b gene. The method is especially  
CC applied to material derived from chicken, poultry, pigs, cattle, sheep,  
CC game, fish and seafoods, particularly for control of foods. The origin of  
CC the material can be determined reliably and relatively quickly, in an

CC automated procedure capable of examining 100 samples per day. It uses  
CC standard methods of genetic engineering, is highly sensitive and  
CC universally applicable. Since the primers generate a relatively small  
CC amplicon, the method can be used on processed meats where the DNA is  
CC likely to be highly fragmented

XX  
SQ Sequence 26 BP; 9 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 26;  
Best Local Similarity 86.4%; Pred. No. 2.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2678 GTGTGGTGAAATGGAGATTG 2699  
|||||  
Db 24 GTATGGTGGAATGGAATTG 3

RESULT 1989  
AAV07974  
ID AAV07974 standard; DNA; 26 BP.  
XX  
AC AAV07974;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1999 (first entry)  
XX  
DE Helicobacter pylori polypeptide GHPO 711 5' DNA primer.  
XX  
KW GHPO 711; infection; gastritis; ulcer; vaccine; diagnosis; therapy; PCR;  
KW primer; ss.  
XX  
OS Synthetic.  
OS Helicobacter pylori.  
XX  
PN WO9843479-A1.  
XX  
PD 08-OCT-1998.  
XX  
PF 31-MAR-1998; 98WO-US0006421.  
XX  
PR 01-APR-1997; 97US-00831310.  
PR 01-APR-1997; 97US-00834666.  
XX  
PA (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Kleanthous H, Lissolo L, Tomb J, Miller C, Algarawi A;  
XX  
DR WPI; 1998-568251/48.  
XX  
PT New isolated Helicobacter polynucleotides - used to develop products for  
PT the diagnosis, prevention and treatment of Helicobacter infections and  
PT gastroduodenal diseases.  
XX  
PS Example 3.B; Page 64; 184pp; English.  
XX  
CC This 5' primer was used with a 3' primer (see AAV07975) in the PCR  
CC amplification of Helicobacter pylori strain ORV2001 genomic DNA in order  
CC to obtain DNA (see AAV07917) encoding a 76 kDa polypeptide (see AAW73028)  
CC designated GHPO 711. The primer pair includes a 5' clamp and BamHI and  
CC XhoI restriction enzyme recognition sequences for cloning purposes. The  
CC PCR product was ligated into vector pET28a, and recombinant polypeptide  
CC was expressed as a histidine-tagged fusion protein in E. coli host cells.  
CC The polypeptide can be used to develop vaccines for the treatment and  
CC prevention of Helicobacter infections. (Updated on 25-MAR-2003 to correct  
CC PI field.)  
XX  
SQ Sequence 26 BP; 16 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 26;  
Best Local Similarity 86.4%; Pred. No. 2.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAAAAAAAAAAAAAA 2801  
Db 3 GAATTCAAAAAAAAACGAAAAAAAA 24

RESULT 1990  
AAC92118/c  
ID AAC92118 standard; DNA; 26 BP.  
XX  
AC AAC92118;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE Human MLT gene intron-exon boundary #2.  
XX  
KW Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;  
KW mucosa-associated lymphoid tissue lymphoma associated translocation;  
KW chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;  
KW molecular characterisation; chromosome translocation; carcinogenesis;  
KW fusion protein; malignancy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073500-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 26-MAY-2000; 2000WO-EP004796.  
XX  
PR 27-MAY-1999; 99EP-00201683.  
XX  
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
XX  
PI Baens M, Marynen P, Dierlamm J;  
XX  
DR WPI; 2001-061556/07.  
XX

Determining if a tissue sample has a chromosome (11:18) translocation associated with malignancies by amplifying a nucleic acid sample using primers complementary to chromosome 11 region q21-22.3 and chromosome 18 region q21.1-22.

Example 3; Page 22; 47pp; English.

The present invention describes a method for determining if a tissue sample comprises a cell with a chromosome (11:18) translocation associated with malignancies such as mucosa-associated lymphoid tissue (MALT) lymphomas. The method comprises subjecting a sample nucleic acid to amplification using primers complementary to sequences which are on chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The method can be used for determining if a tissue sample or analogue comprises a chromosome (11:18) translocation associated with malignancies such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or the antibody may be used as a probe for detection, for hybridisation to southern blot cell DNAs or for in situ hybridisation of cells, or for determining the presence of complementary DNA. The present sequence represents an intron-exon boundary oligonucleotide from the human MALT-lymphoma associated translocation (MLT) gene, which is used in an example from the present invention

Sequence 26 BP; 6 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 26;  
Best Local Similarity 96.4%; Pred. No. 2.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAAAAAAA 2803  
Db 22 ATTCCTAAAAAAAAAAAAAAAAA 1

RESULT 1991  
AAT13977/c

ID AAT13977 standard; DNA; 28 BP.  
XX  
AC AAT13977;  
XX  
DT 03-OCT-1996 (first entry)  
XX  
DE E. spinifera fumonisin esterase end-blocked polyT primer BamT17V.  
XX  
KW Fumonisin; esterase; transgenic plant; recombinant microorganism;  
KW expression; probiotic; feed inoculant; degradation; detoxification;  
KW maize seed; grain; animal feed; end blocked; polyT primer; nested;  
KW polymerase chain reaction; Exophiala spinifera; ss.  
XX  
OS Synthetic.  
XX  
PN WO9606175-A2.  
XX  
PD 29-FEB-1996.  
XX  
PF 11-AUG-1995; 95WO-US010284.  
XX  
PR 12-AUG-1994; 94US-00289595.  
PR 07-JUN-1995; 95US-00484815.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Duvick J, Rood TA;  
XX  
DR WPI; 1996-151378/15.  
XX

Detoxification of fumonisin and related mycotoxin cpds. in grains - using an enzyme esp. an esterase, from Exophiala spinifera, Rhinocladiella atrovirens or a bacterium.

Example 8; Page 33; 54pp; English.

The present sequence is a primer for the nested PCR amplification of the Exophiala spinifera (ATCC 74269), fumonisin esterase, cDNA, which was isolated from a maize seed. The esterase cDNA can be used to produce transgenic plants and genetically engineered microorganisms, capable of expressing the esterase. The microorganisms can be used as a probiotic or feed inoculant, along with the esterase to degrade fumonisins and related cpds., partic. for the detoxification of maize seed pre- or post-harvest (i.e. during the storage or processing of the harvested grain, or in the processed grain) prior to its use as an animal feed

Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 28;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 28 BAAAAAAAAAAAAAAAAA 11

RESULT 1992  
AAV65735/c  
ID AAV65735 standard; DNA; 28 BP.  
XX  
AC AAV65735;  
XX  
DT 17-DEC-1998 (first entry)  
XX  
DE A. phoenices APOXD DNA amplifying 5' RACE primer Bam T17V.  
XX  
KW APOXD; oxalate decarboxylase; oxalic acid; degradation; plant pathogen;  
KW oxalic acid toxicity; oxalate; plant tissue; diagnosis; treatment;  
KW enzyme; urinary tract disorder; hyperoxaluric syndrome; PCR primer; ss.  
XX  
OS Synthetic.  
OS Aspergillus phoenicis.

XX WO9842827-A2.  
XX  
PD 01-OCT-1998.  
XX  
PF 19-MAR-1998; 98WO-US005432.  
XX  
PR 21-MAR-1997; 97US-00821827.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Scelonge CJ, Bidney DL;  
XX  
DR WPI; 1998-557032/47.  
XX  
PT New isolated oxalate decarboxylase gene - obtained from Aspergillus  
PT phenices, used for e.g. degrading oxalic acid, protecting against oxalic  
PT toxicity or as a selectable marker in plants.  
XX  
PS Example 1; Page 24; 58pp; English;  
XX  
CC Sequences AAV65729 to AAV65740 represent primers used for the PCR  
CC amplification of the genomic DNA encoding an Aspergillus phenices  
CC oxalate decarboxylase (APOXD) enzyme. A vector containing the APOXD  
CC nucleic acid can be used to transform host cells for the recombinant  
CC production of the enzyme. The APOXD can be used for the degradation of  
CC oxalic acid in providing protection against oxalic acid toxicity. It is  
CC useful in combating and providing protection against plant pathogens that  
CC utilise oxalate to gain access to plant tissue or otherwise in the course  
CC of the pathogenesis of the disease. The APOXD gene is also useful as a  
CC selectable marker of transformed cells, for diagnostic assay of oxalate,  
CC and for production of the enzyme in plants. The product can also be used  
CC in diagnostic assays to quantify oxalate, e.g. in the diagnosis and  
CC treatment of patients with urinary tract disorders or hyperoxaluric  
CC syndromes  
XX  
SQ Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 17.2; DB 1; Length 28;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA...AAAAA 2802  
Db 28 BAAAAA...AAAAA 11  
  
RESULT 1993  
AAX05727/c  
ID AAX05727 standard; DNA; 28 BP.  
XX  
AC AAX05727;  
XX  
DT 07-MAY-1999 (first entry)  
XX  
DE E. spinifera fumonisin esterase (ESP26-1) cDNA amplifying polyT primer.  
XX  
KW Fumonisin esterase; enzyme; fumonisin; degrade; harvesting; grain; ss;  
KW animal feed; plant tissue; silage; fruit; vegetable; detoxification;  
KW mycotoxin; phytohormone; tricarballic acid; TCA; bacterium; PCR primer.  
XX  
OS Synthetic.  
OS Exophiala spinifera.  
XX  
PN WO9902703-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 07-JUL-1998; 98WO-US013987.  
XX  
PR 07-JUL-1997; 97US-00888949.  
PR 07-JUL-1997; 97US-00888950.  
XX

PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Duwick J, Maddox JR, Rood TA, Wang X, Bowen BA, Gilliam JT;  
XX  
DR WPI; 1999-120904/10.  
XX  
PT Newly isolated polynucleotides useful for degrading and detoxifying  
PT fumonisins - and methods for identifying transformed plant cells.  
XX  
PS Example 8; Page 37; 88pp; English.  
XX  
CC The invention relates to fumonisin esterases from E. spinifera and Gram-  
CC negative bacteria. This enzyme can degrade fumonisin. The polynucleotides  
CC encoding fumonisin degrading enzymes are useful for degrading fumonisins  
CC during the process of harvesting grain for animal feed, or in plant  
CC tissues, which are used for silage or as a spray on grain, fruit or  
CC vegetables. They are also useful for detoxifying fumonisins, structurally  
CC related mycotoxins, and fumonisin hydrolysis products of both. The  
CC fumonisin esterase genes (contained within an expression cassette,  
CC encoding a fumonisin degradative enzyme) is introduced into plant cells  
CC that are cultured on a medium containing a phytohormone linked to a  
CC tricarballic acid (TCA), which inactivates the phytohormone unless it  
CC is cleaved by an esterase. The polynucleotides are also used in a method  
CC for measuring gene expression, comprising transforming cells with the  
CC esterase genes operably linked to a promoter, adding substrate, and  
CC measuring the level of hydrolysed product. The isolation of the  
CC polynucleotides encoding the fumonisin degrading enzymes permits the  
CC degradation and detoxification of fumonisins, which are toxic and  
CC potentially widespread in food and feed. The present sequence represents  
CC a E. spinifera fumonisin esterase gene specific primer used for the  
CC isolation of a full-length cDNA of ESP26-1  
XX  
SQ Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 17.2; DB 1; Length 28;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA...AAAAA 2802  
Db 28 BAAAAA...AAAAA 11  
  
RESULT 1994  
ABZ70568/c  
ID ABZ70568 standard; DNA; 28 BP.  
XX  
AC ABZ70568;  
XX  
DT 23-MAY-2003 (first entry)  
XX  
DE 5' RACE primer Bam T17V.  
XX  
KW Oxalate decarboxylase; APOXD; enzyme; selectable marker;  
KW transgenic plant; crop protection; oxalic acid; degradation;  
KW Aspergillus phenices; PCR; RACE; primer; ss.  
XX  
OS Synthetic.  
XX  
PN CA2350328-A1.  
XX  
PD 26-DEC-2002.  
XX  
PF 26-JUN-2001; 2001CA-02350328.  
XX  
PR 26-JUN-2001; 2001CA-02350328.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Scelonge C, Bidney D;  
XX  
DR WPI; 2003-248733/25.  
XX

PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus  
PT phenices, for degrading oxalic acid, identifying transformed plant  
PT cells, and preventing pathogenic disease in plants.

XX Example 1; Page 28; 60pp; English.

PS The present sequence is that of a dT-based primer, which was used in a 5'  
XX RACE to obtained a fragment of the Aspergillus phenices oxalate-  
CC decarboxylase (APOXD) gene. Following 3' and 5' RACE, a full-length  
CC nucleic acid (see ABZ70560) encoding APOXD enzyme (see ABP72475) was  
CC obtained. The APOXD gene and its encoded protein are useful for degrading  
CC oxalate, protecting plants from pathogenic disease, in diagnostic assays  
CC of oxalate, and as a selectable marker

XX Sequence 28 BP; 1 A; 4 C; 4 G; 18 T; 0 U; 1 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 28;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802

Db :|||||  
28 BAAAAAAAAAAAAAAAAA 11

RESULT 1995

AAQ52157/c

ID AAQ52157 standard; RNA; 35 BP.

XX AAQ52157;

XX 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

DT 26-MAY-1994 (first entry)

XX Breast cancer specific mRNA ribozyme cleavable nucleotide (4416).

DE Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;  
XX resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;  
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;  
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;  
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;  
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;  
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;  
KW hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.

XX Homo sapiens.

OS WO9323057-A1.

PN 25-NOV-1993.

XX 13-MAY-1993; 93WO-US004573.

XX 14-MAY-1992; 92US-00882822.

XX 14-MAY-1992; 92US-00882885.

PR 26-AUG-1992; 92US-00936110.

PR 26-AUG-1992; 92US-00936421.

PR 26-AUG-1992; 92US-00936422.

PR 26-AUG-1992; 92US-00936531.

PR 26-AUG-1992; 92US-00936532.

PR 07-DEC-1992; 92US-00987131.

PR 19-JAN-1993; 93US-00006122.

PR 19-JAN-1993; 93US-00008910.

XX (RIBO-) RIBOZYME PHARM INC.

PA Thompson JD, Draper KG;

XX WPI; 1993-386203/48.

XX New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated

PT with tumours or mRNA expressed from gene encoding multiple drug

PT resistance.

XX Claim 3; Fig 8; 69pp; English.

CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are  
CC associated with development or maintenance of chronic myelogenous  
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute  
CC lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic  
CC leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.  
CC The full length mRNAs containing these target sequences, encode aberrant  
CC cellular proteins which are able to control cellular proliferation and  
CC are directly linked to a leukemic phenotype. These target sequences are  
CC identified by the ribozyme of the invention. The ribozymes is formed in a  
CC hammerhead motif, but may also be formed in the motif of a hairpin,  
CC hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes  
CC may be used to inhibit the development or expression of a transformed  
CC phenotype in man and other animals by modulating expression of the  
CC corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic  
CC and transformed cells elicits inhibition of the transformed state.  
CC Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the  
CC mechanism of drug resistance used by transformed cells and thus enhances  
CC drug therapies for tumours. The ribozymes may also be used to study  
CC genetic drift and mutations within cells. (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX Sequence 35 BP; 5 A; 1 C; 4 G; 0 T; 25 U; 0 Other;

Query Match 0.6%; Score 17.2; DB 1; Length 35;

Best Local Similarity 86.4%; Pred. No. 3.4e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAAAAAA 2804

Db |||||  
33 TTAAAAAAAAACAAACAAAAAAAA 12

RESULT 1996

AAQ69800

ID AAX69800 standard; RNA; 17 BP.

XX AAX69800;

AC 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.

DT Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

XX KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

XX tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

XX fms-like tyrosine kinase 1; kinase insert domain containing receptor;

XX foetal liver kinase 1; ss.

XX Homo sapiens.

OS WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR ) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.



PS Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the

CC synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the

CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

CC treated by administering the nucleic acid molecule or the expression

CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 5.9%; Pred. No. 9.5e+02;

Matches 1; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTT 2181

Db |:::UUUUUUUUUUUUUUUU 17

1 CUUUUUUUUUUUUUUUUU 17

RESULT 1997

AAX69801/C

ID AAX69801 standard; RNA; 17 BP.

XX

AC AAX69801;

XX

DT 28-JUL-1999 (first entry)

XX

DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.

XX

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

KW foetal liver kinase 1; ss.

XX

OS Homo sapiens.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017480.

XX

PR 26-OCT-1995; 95US-0005974P.

PR 11-JAN-1996; 96US-00584040.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (CHIR ) CHIRON CORP.

XX

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX

DR WPI; 1997-259017/23.

XX

PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

PT rheumatoid arthritis, etc., in a human patient.

XX

PS Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the

CC synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the

CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

CC treated by administering the nucleic acid molecule or the expression

CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention

CC of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAAAAAA 2801

Db |||||

17 GAAAAAATAAAAAAAAAA 1

RESULT 1998

AAX18370

ID AAX18370 standard; DNA; 17 BP.

XX

AC AAX18370;

XX

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 11.

XX

KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX

OS Synthetic.

XX

PN JP11032765-A.

XX

PD 09-FEB-1999.

XX

PF 18-JUL-1997; 97JP-00208312.

XX

PR 18-JUL-1997; 97JP-00208312.

XX

PA (TAKI ) TAKARA SHUZO CO LTD.

XX

DR WPI; 1999-183822/16.

XX

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

XX

PS Disclosure; Page 11; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX

SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTTCTTTTCTTTTCTTTTAA 2188

Db |||||

1 TTTTCTTTTCTTTTCTTTTAA 17

RESULT 1999

AAA25450

ID AAA25450 standard; DNA; 17 BP.

XX

AC AAA25450;

XX 19-JUL-2000 (first entry)  
DT Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.  
XX  
DE  
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO9954459-A2.  
PN  
XX  
XX 28-OCT-1999.  
PD  
XX  
XX 19-APR-1999; 99WO-US008547.  
PF  
XX  
XX 20-APR-1998; 98US-0082404P.  
PR  
XX 23-JUN-1998; 98US-00103636.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
PI Matulic-Adamic J;  
PI  
XX  
XX WPI; 2000-013248/01.  
DR  
XX  
XX New nucleic acids that interact, and optionally cleave, target sequences,  
PT used to treat cancer.  
PT  
XX  
XX Claim 77; Page 79; 148pp; English.  
PS  
XX  
XX The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphoro(di)thioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A') that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium),  
CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
CC for other conditions associated with levels of oestrogen receptor.  
CC Because of the high selectivity for targeted RNA, (A) can also be used to  
CC correlate inhibition of gene expression with alterations in phenotype,  
CC particularly for identification of therapeutic targets, and as research  
CC reagents (for RNA, in the same way that restriction endonucleases are  
CC used with DNA). The combination of modifications in (A) improves  
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
CC AAA24748 to AAA25992 represent their corresponding target sequences.  
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2000  
AAA25450/C  
ID AAA25450 standard; DNA; 17 BP.  
XX  
AC AAA25450;  
XX  
DT 19-JUL-2000 (first entry)

XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1948.  
DE  
XX  
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO9954459-A2.  
PN  
XX  
XX 28-OCT-1999.  
PD  
XX  
XX 19-APR-1999; 99WO-US008547.  
PF  
XX  
XX 20-APR-1998; 98US-0082404P.  
PR  
XX 23-JUN-1998; 98US-00103636.  
PR  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA  
XX  
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
PI Matulic-Adamic J;  
PI  
XX  
XX WPI; 2000-013248/01.  
DR  
XX  
XX New nucleic acids that interact, and optionally cleave, target sequences,  
PT used to treat cancer.  
PT  
XX  
XX Claim 77; Page 79; 148pp; English.  
PS  
XX  
XX The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphoro(di)thioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A') that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium),  
CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
CC for other conditions associated with levels of oestrogen receptor.  
CC Because of the high selectivity for targeted RNA, (A) can also be used to  
CC correlate inhibition of gene expression with alterations in phenotype,  
CC particularly for identification of therapeutic targets, and as research  
CC reagents (for RNA, in the same way that restriction endonucleases are  
CC used with DNA). The combination of modifications in (A) improves  
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
CC AAA24748 to AAA25992 represent their corresponding target sequences.  
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAA AAAA AAAA AAAA AAAA 2802  
Db 17 AAAA AAAA AAAA AAAA AAAA 1  
RESULT 2001  
AAA98232  
ID AAA98232 standard; DNA; 17 BP.  
XX  
AC AAA98232;  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Human retrovirus HERV LTR PCR primer #31.









XX 12-SEP-2001 (first entry)  
DT Human cDNA synthesis and differential display primer, HT11CA.  
XX  
DE Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;  
XX differential display of reverse transcribed mRNAs by PCR;  
KW testicular cancer; breast cancer; prostate cancer; endometrial cancer;  
KW asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;  
KW HRT; endocrine system; HT11GA.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO200134834-A2.  
PN  
XX 17-MAY-2001.  
PD  
XX 10-NOV-2000; 2000WO-DK000628.  
XX  
XX 11-NOV-1999; 99DK-00001626.  
XX  
XX (RIGS-) RIGSHOSPITALET.  
PA  
XX Leffers H, Jorgensen M, Skakkebaek NE;  
PI  
XX WPI; 2001-335941/35.  
DR  
XX  
XX Evaluating a cellular response to an environmental compound, for use in  
PT toxicological analysis, involves determining or comparing the expression  
PT levels of at least one endogenous gene.  
XX  
XX Example 3; Page 27; 77pp; English.  
PS  
XX The sequence represents a downstream PCR primer used in a DDRT-PCR  
CC experiment (and in cDNA synthesis), demonstrating the method of the  
CC invention. The method relates to evaluating a cellular response to an  
CC environmental compound, comprising determining or comparing the  
CC expression levels of at least one endogenous gene e.g by differential  
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be  
CC adapted to identify compounds that act on the level of endogenous gene  
CC expression through activating nuclear receptors. The method is useful in  
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.  
CC testicular, breast, prostate and endometrium), asthma, hypospadia,  
CC cryptorchism and/or allergy, and for evaluating the efficiency of a  
CC treatment for hormonal deficiency or hormonal replacement therapy, in a  
CC human such as a post-menopausal female. The method is also useful for  
CC identifying environmental chemicals or pharmaceutical compositions that  
CC interact with endocrine systems, and for detecting chemicals that pose a  
CC health threat. Expression levels of endogenous genes are determined  
CC rapidly using a sensitive technique, and the expression of any gene can  
CC be monitored. The assays are far more informative than the currently used  
CC assays, and significantly reduces the number of animals required for the  
CC testing, as it is expected that essentially all the animals in a test  
CC group will respond to the compound  
XX  
SQ Sequence 17 BP; 3 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTGTGGA 1783  
Db 1 AAGCTTTTGTGGA 17  
  
RESULT 2006  
ABK13941/C  
ID ABK13941 standard; DNA; 17 BP.  
XX  
XX ABK13941;  
AC  
XX

DT 21-MAY-2002 (first entry)  
XX  
DE 5'-PCR primer used to produce single pattern characteristic by FokI.  
XX  
KW Identification of transcribed gene; mRNA profile; gene expression;  
KW cellular process; fingerprinting; susceptibility to external factor;  
KW development; disease; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200208461-A2.  
XX  
PD 31-JAN-2002.  
XX  
XX 23-JUL-2001; 2001WO-IB001539.  
PF  
XX 21-JUL-2000; 2000GB-00018016.  
PR  
XX 21-JUL-2000; 2000US-0219925P.  
XX  
PA (GLOB-) GLOBAL GENOMICS AB.  
XX  
XX Linnarsson S, Ernfors P, Bauren G;  
PI  
XX WPI; 2002-217065/27.  
DR  
XX Providing mRNA profile, by generating two independent patterns  
PT characteristic of sample mRNA population, analyzing patterns, comparing  
PT gene expression by cell types under varied conditions, and identifying  
PT genes.  
XX  
XX Disclosure; Fig 2; 67pp; English.  
PS  
XX The present invention relates to a method for providing a profile of mRNA  
CC molecules present in a sample. The method comprises generating two  
CC independent patterns characteristic of the population of mRNA molecules  
CC expressed in the sample and analysing the patterns using a combinatorial  
CC algorithm, comparing gene expression by different or same cell types  
CC under different conditions, and identifying genes having a role in  
CC various cellular processes. The method is useful for the analysis and  
CC identification of transcribed genes, and fingerprinting. The method can  
CC be used to identify genes which play a role in determining various  
CC cellular processes, including susceptibility to external factors,  
CC development, and disease. The present sequence for a PCR primer is used  
CC in the production of a single pattern characteristic of a sample,  
CC employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the  
CC present invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2801  
Db 17 GAAAAAAGAAAAA 1  
  
RESULT 2007  
ADB04271  
ID ADB04271 standard; DNA; 17 BP.  
XX  
XX ADB04271;  
AC  
XX 20-NOV-2003 (first entry)  
DT  
XX Human MDZ7 scanning oligonucleotide SEQ ID 5257.  
DE  
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
KW  
XX

OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD  
XX 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
PI WPI; 2003-423107/40.  
DR  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5257; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTT 2181  
Db 1 CTTTTTTTTTTTTTTT 17  
  
RESULT 2008  
AAD56441  
ID AAD56441 standard; DNA; 17 BP.  
XX  
AC AAD56441;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 9..10  
FT /\*tag= a  
FT /note= "Bases 9 and 10 are linked by a butanediol linker  
FT which is represented as B in page 49 and X in page 59,  
FT Fig 9 and 10 of the specification"  
XX  
PN WO2003037909-A1.

XX 08-MAY-2003.  
XX  
XX 29-OCT-2002; 2002WO-CA001628.  
PF  
XX  
XX 29-OCT-2001; 2001US-0330719P.  
PR  
XX  
XX (UYMC-) UNIV MCGILL.  
PA  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI WPI; 2003-421516/39.  
XX  
XX  
PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Page 90; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
  
RESULT 2009  
AAD56441/c  
ID AAD56441 standard; DNA; 17 BP.  
XX  
AC AAD56441;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE Antisense oligo #2, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT misc\_feature 9..10  
FT /\*tag= a  
FT /note= "Bases 9 and 10 are linked by a butanediol linker  
FT which is represented as B in page 49 and X in page 59,  
FT Fig 9 and 10 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
XX 29-OCT-2002; 2002WO-CA001628.  
PF  
XX  
XX 29-OCT-2001; 2001US-0330719P.

XX (UYMC-) UNIV MCGILL.  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI WPI; 2003-421516/39.  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
DR decreasing translation, reverse transcription and/or replication of a  
XX target RNA in a system, comprises a modified deoxyribonucleotide.  
XX Example 2; Page 90; 104pp; English.  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 2010  
AAD56448  
ID AAD56448 standard; DNA; 17 BP.  
XX AAD56448;  
AC AAD56448;  
XX 07-AUG-2003 (first entry)  
DT 2'-F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.  
DE Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
XX antisense; ss.  
KW Unidentified.  
XX Key Location/Qualifiers  
FH modified\_base 1. .17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 9. .10  
FT /\*tag= b  
FT /note= "Bases 9 and 10 are linked by a butanediol linker  
FT which is represented as B in page 49 and Fig 5 and as X  
FT in page 52, 55 and Fig 6 of the specification"  
XX WO2003037909-A1.  
PN 08-MAY-2003.  
XX 29-OCT-2002; 2002WO-CA001628.  
XX 29-OCT-2001; 2001US-0330719P.  
XX (UYMC-) UNIV MCGILL.  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI

XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI WPI; 2003-421516/39.  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
DR decreasing translation, reverse transcription and/or replication of a  
XX target RNA in a system, comprises a modified deoxyribonucleotide.  
XX Example 2; Fig 5; 104pp; English.  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
RESULT 2011  
AAD56448/c  
ID AAD56448 standard; DNA; 17 BP.  
XX AAD56448;  
AC AAD56448;  
XX 07-AUG-2003 (first entry)  
DT 2'-F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.  
DE Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
XX antisense; ss.  
KW Unidentified.  
XX Key Location/Qualifiers  
FH modified\_base 1. .17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 9. .10  
FT /\*tag= b  
FT /note= "Bases 9 and 10 are linked by a butanediol linker  
FT which is represented as B in page 49 and Fig 5 and as X  
FT in page 52, 55 and Fig 6 of the specification"  
XX WO2003037909-A1.  
PN 08-MAY-2003.  
XX 29-OCT-2002; 2002WO-CA001628.  
XX 29-OCT-2001; 2001US-0330719P.  
XX (UYMC-) UNIV MCGILL.  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI

XX WPI; 2003-421516/39.

PT Novel acyclic linker-containing oligonucleotide useful for preventing or

PT decreasing translation, reverse transcription and/or replication of a

PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX

PS Example 2; Fig 5; 104pp; English.

XX

CC The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.

CC They are useful for selectively preventing gene expression in a sequence-

CC specific manner, for hybridising to complementary RNA such as cellular

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments

CC to prevent or treat a disease characterised by the expression of a

CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)

CC H degradation of target RNA. This sequence is used in the exemplification

CC of the invention

XX

SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2012

AAD56449

ID AAD56449 standard; DNA; 17 BP.

XX

AC AAD56449;

XX

DT 07-AUG-2003 (first entry)

XX

DE 2'-F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.

XX

KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

KW antisense; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT modified\_base 1..17

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT 12..13

FT /\*tag= b

FT /note= "Bases 12 and 13 are linked by a butanediol linker

FT which is represented as B in page 49 and Fig 5 and as X

FT in page 55 and Fig 6 of the specification"

XX

PN WO2003037909-A1.

XX

PD 08-MAY-2003.

XX

PF 29-OCT-2002; 2002WO-CA001628.

XX

PR 29-OCT-2001; 2001US-0330719P.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX

DR WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or

PT decreasing translation, reverse transcription and/or replication of a

PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX

PS Example 2; Fig 5; 104pp; English.

XX

CC The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.

CC They are useful for selectively preventing gene expression in a sequence-

CC specific manner, for hybridising to complementary RNA such as cellular

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments

CC to prevent or treat a disease characterised by the expression of a

CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)

CC H degradation of target RNA. This sequence is used in the exemplification

CC of the invention

XX

SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182

Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2013

AAD56449/c

ID AAD56449 standard; DNA; 17 BP.

XX

AC AAD56449;

XX

DT 07-AUG-2003 (first entry)

XX

DE 2'-F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.

XX

KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

KW antisense; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT modified\_base 1..17

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT 12..13

FT /\*tag= b

FT /note= "Bases 12 and 13 are linked by a butanediol linker

FT which is represented as B in page 49 and Fig 5 and as X

FT in page 55 and Fig 6 of the specification"

XX

PN WO2003037909-A1.

XX

PD 08-MAY-2003.

XX

PF 29-OCT-2002; 2002WO-CA001628.

XX

PR 29-OCT-2001; 2001US-0330719P.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX

DR WPI; 2003-421516/39.

XX

PT Novel acyclic linker-containing oligonucleotide useful for preventing or



PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX Example 2; Fig 5; 104pp; English.

XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAA 2802

Db 17 AAAAAAAAAAAAAAAA 1

RESULT 2014

AAD56447

ID AAD56447 standard; DNA; 17 BP.

XX

AC AAD56447;

XX 07-AUG-2003 (first entry)

DT 2'-F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.

XX Unidentified.

XX Key Location/Qualifiers

FH modified\_base 1..17

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT 4..5

FT /tag= b

FT /note= "Bases 4 and 5 are linked by a butanediol linker  
FT which is represented as B in page 49 and Fig 5 and as X  
FT in page 55 and Fig 6 of the specification"

XX WO2003037909-A1.

PN 08-MAY-2003.

XX 29-OCT-2002; 2002WO-CA001628.

XX 29-OCT-2001; 2001US-0330719P.

XX (UYMC-) UNIV MCGILL.

XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX Example 2; Fig 5; 104pp; English.

XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182

Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2015

AAD56447/c

ID AAD56447 standard; DNA; 17 BP.

XX

AC AAD56447;

XX 07-AUG-2003 (first entry)

DT 2'-F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.

XX Unidentified.

XX Key Location/Qualifiers

FH modified\_base 1..17

FT /tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT 4..5

FT /tag= b

FT /note= "Bases 4 and 5 are linked by a butanediol linker  
FT which is represented as B in page 49 and Fig 5 and as X  
FT in page 55 and Fig 6 of the specification"

XX WO2003037909-A1.

PN 08-MAY-2003.

XX 29-OCT-2002; 2002WO-CA001628.

XX 29-OCT-2001; 2001US-0330719P.

XX (UYMC-) UNIV MCGILL.

XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

XX WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX Example 2; Fig 5; 104pp; English.

XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
DB 17 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 2016  
AAD56450  
ID AAD56450 standard; DNA; 17 BP.  
XX  
AC AAD56450;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE 2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 9. .10  
FT /\*tag= b  
FT /note= "Bases 9 and 10 are linked by a secouridine linker  
FT which is represented as S in page 49 and X in page 57 and  
FT Fig 1, 2, 7 and 8 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX  
PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2182  
DB 1 TTTTTTTTTTTTTTTTTT 17  
  
RESULT 2017  
AAD56450/c  
ID AAD56450 standard; DNA; 17 BP.  
XX  
AC AAD56450;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE 2'F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.  
XX  
KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1. .17  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 9. .10  
FT /\*tag= b  
FT /note= "Bases 9 and 10 are linked by a secouridine linker  
FT which is represented as S in page 49 and X in page 57 and  
FT Fig 1, 2, 7 and 8 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
PR 29-OCT-2001; 2001US-0330719P.  
XX  
PA (UYMC-) UNIV MCGILL.  
XX  
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
XX  
DR WPI; 2003-421516/39.  
XX  
PT Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
CC The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAA 1  
  
RESULT 2018  
ACF36345/c  
ID ACF36345 standard; DNA; 17 BP.  
XX  
AC ACF36345;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA fragment.  
XX  
KW Gene variant identification; restriction enzyme; FokI; ds.  
XX  
OS Synthetic.  
XX  
PN WO2003064689-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 28-JAN-2003; 2003WO-IB000255.  
XX  
PR 29-JAN-2002; 2002US-0352245P.  
XX  
PA (GLOB-) GLOBAL GENOMICS AB.  
XX  
PI Lonnerberg P, Oldin M, Linnarsson S, Ernfors P;  
XX  
DR WPI; 2003-627619/59.  
XX  
PT Determining polyadenylation sites within transcribed gene sequences  
PT present in a sample comprises assigning to gene fragments gene candidates  
PT within a database by comparing signals in the dataset with the database.  
XX  
PS Example; Fig 3; 81pp; English.  
XX  
CC The invention relates to determining the presence of and/or identifying a  
CC polyadenylation site within a sequence of a transcribed gene or variants  
CC present in a sample. The method involves assigning to gene fragments gene  
CC candidates within a database by comparing signals in the dataset with the  
CC database, the database comprising data representing mRNAs with known  
CC polyA sites and/or 'virtual genes', representing a possible  
CC polyadenylation site within an actual gene. The method is useful for  
CC determining the presence of and/or identifying a polyadenylation site or  
CC alternative polyadenylation sites within a sequence of a transcribed gene  
CC or sequences of transcribed gene variants present or potentially present  
CC in a sample, in identifying gene features, particularly in identifying  
CC differences between sequence variants that occur in a population of  
CC nucleic acid molecules, especially in identifying or discovering polyA  
CC site usage or determining polyA site usage in a nucleic acid sample, and  
CC gene variants arising from alternative polyA sites. The present sequence  
CC represents a double stranded product DNA fragment  
XX

SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAA 2801  
Db 17 GAAAAAAAAAAAAAA 1  
  
RESULT 2019  
ACF36370/c  
ID ACF36370 standard; DNA; 17 BP.  
XX  
AC ACF36370;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA.  
XX  
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;  
KW electrophoresis; type II restriction enzyme; FokI; ds.  
XX  
OS Synthetic.  
XX  
PN WO2003064691-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 28-JAN-2003; 2003WO-IB000843.  
XX  
PR 29-JAN-2002; 2002US-0352215P.  
XX  
PA (GLOB-) GLOBAL GENOMICS AB.  
XX  
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;  
PI Montelius A;  
XX  
DR WPI; 2003-618365/58.  
XX  
PT Producing a population of double-stranded product DNA molecules, useful  
PT for mRNA profiling, comprises amplification by nested polymerase chain  
PT reaction.  
XX  
PS Example; Fig 2; 105pp; English.  
XX  
CC The invention relates to producing a population of double-stranded  
CC product DNA molecules comprising amplification by a nested PCR method.  
CC The method is useful in profiling mRNA transcribed in a system under  
CC investigation. The oligonucleotides are used as size standards in  
CC electrophoresis, and as internal controls allowing for calculation of  
CC relative amounts of material present. The present sequence represents a  
CC double stranded product DNA, which aids in outlining an approach to  
CC production of a single pattern characteristic of a sample, employing a  
CC type II restriction enzyme (FokI)  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAA 2801  
Db 17 GAAAAAAAAAAAAAA 1  
  
RESULT 2020  
ADB45110  
ID ADB45110 standard; DNA; 17 BP.  
XX  
AC ADB45110;

XX DT 18-DEC-2003 (first entry)  
XX DE Tumour suppression/reversion associated nucleotide #5433.  
XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
KW KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
KW KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
XX KW diagnosis.  
XX OS Homo sapiens.  
XX PN WO2003040369-A2.  
XX PD 15-MAY-2003.  
XX PF 17-SEP-2002; 2002WO-IB004219.  
XX PR 17-SEP-2001; 2001FR-00011981.  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX PI Telerman A, Amson R, Tuijnder M;  
XX DR WPI; 2003-441574/41.  
XX CC New nucleic acid encoding human prostate membrane-specific antigen,  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX PS Disclosure; Page 667; 771pp; French.  
XX CC The invention relates to the isolation of 6327 nucleotide sequences,  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity, after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal  
CC expression of the nucleotides.  
XX SQ Sequence 17 BP; 6 A; 2 C; 1 G; 8 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2460 GATCCAATTTTAAATATT 2476  
Db 1 GATCCAATTTTAAATATT 17  
RESULT 2021  
AAT94667/c  
ID AAT94667 standard; DNA; 18 BP.  
XX AC AAT94667;  
XX DT 27-MAR-1998 (first entry)  
XX DE Anchored poly(T) oligonucleotide polyT-AnchA.

XX KW Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;  
KW KW snapdragon; primer; ss.  
XX OS Synthetic.  
XX PN WO9732023-A1.  
XX PD 04-SEP-1997.  
XX PF 28-FEB-1997; 97WO-AU0000124.  
XX PR 01-MAR-1996; 96AU-00008386.  
XX PA (FLOR-) FLORIGENE LTD.  
XX PI Brugliera F, Holton TA, Michael MZ;  
XX DR WPI; 1997-448691/41.  
XX CC Novel flavonoid 3'-hydroxylase(s) from flowering plants - and  
PT corresponding DNA, used in the manipulation of pigmentation in plants.  
PT Example 15; Page 59; 234pp; English.  
XX CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC  
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream  
CC region of a polyadenylation sequence. They were used to prime cDNA  
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and  
CC were also utilised in the PCR amplification of plant cytochrome P450  
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding  
CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential  
CC display approach. This can be used to manipulate the pigmentation of  
CC transgenic plants  
XX SQ Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 2022  
AAT94668  
ID AAT94668 standard; DNA; 18 BP.  
XX AC AAT94668;  
XX DT 27-MAR-1998 (first entry)  
XX DE Anchored poly(T) oligonucleotide polyT-AnchC.  
XX KW Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;  
KW KW snapdragon; primer; ss.  
XX OS Synthetic.  
XX PN WO9732023-A1.  
XX PD 04-SEP-1997.  
XX PF 28-FEB-1997; 97WO-AU0000124.  
XX PR 01-MAR-1996; 96AU-00008386.  
XX PA (FLOR-) FLORIGENE LTD.  
XX PI Brugliera F, Holton TA, Michael MZ;  
XX DE Anchored poly(T) oligonucleotide polyT-AnchA.



DR WPI; 1997-448691/41.  
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and  
PT corresponding DNA, used in the manipulation of pigmentation in plants.  
PT  
XX  
PS Example 15; Page 59; 234pp; English.  
XX  
CC Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC  
CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream  
CC region of a polyadenylation sequence. They were used to prime cDNA  
CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and  
CC were also utilised in the PCR amplification of plant cytochrome P450  
CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding  
CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential  
CC display approach. This can be used to manipulate the pigmentation of  
CC transgenic plants  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
DB 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2023  
AAV37712/C  
ID AAV37712 standard; cDNA; 18 BP.  
XX  
AC AAV37712;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-SEP-1998 (first entry)  
XX  
DE Human protein AQ2\_1i 3'-portion and polyA tail.  
XX  
KW Human; secreted protein; murine adult spleen; human foetal kidney; ovary;  
KW bone marrow; thymus; AE648\_1i; AK438\_1i; AK609\_1i; AM1060\_1i;  
KW AQ2\_1i; K433\_1i; L256\_1i; prevent; treat; ameliorate; medical; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO9820130-A2.  
XX  
PD 14-MAY-1998.  
XX  
PF 31-OCT-1997; 97WO-US019857.  
XX  
PR 01-NOV-1996; 96US-00742973.  
PR 29-OCT-1997; 97US-00960024.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
PI Spaulding V, Agostino MJ;  
XX  
DR WPI; 1998-286946/25.  
XX  
PT New secreted proteins and associated polynucleotides - obtained from  
PT murine adult spleen, human foetal kidney, human ovary, murine bone marrow  
PT and murine adult thymus.  
XX  
PS Disclosure; Page 58; 75pp; English.  
XX  
CC The present invention describes novel proteins isolated from cDNA clones:  
CC AE648\_1i; AE693\_1i; AK438\_1i; AK609\_1i; AM1060\_1i; AQ2\_1i; K433\_1i; or  
CC L256\_1i, deposited as ATCC 98237. The present sequence represents the 3'-  
CC portion of AQ2\_1i isolated from a human ovary cDNA library. The proteins  
CC from the present invention may be administered in a composition to  
CC prevent, treat or ameliorate a medical condition. The proteins may

CC exhibit biological activities such as nutritional activity, cytokine and  
CC cell proliferation/differentiation activity, immune stimulating or  
CC suppressing activity, haematopoiesis regulating activity, tissue growth  
CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,  
CC haemostatic and thrombotic activity, receptor/ligand activity, anti-  
CC inflammatory activity, cadherin/tumour invasion suppressor activity,  
CC tumour inhibition activity and other activities. (Updated on 25-MAR-2003  
CC to correct PR field.)  
XX  
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
DB 18 TTTT TTTT TTTT TTTT TTTT 2  
  
RESULT 2024  
AAA40563/C  
ID AAA40563 standard; cDNA; 18 BP.  
XX  
AC AAA40563;  
XX  
DT 16-NOV-2000 (first entry)  
XX  
DE Human adult ovary cDNA fragment AQ2\_1i #2.  
XX  
KW Secreted protein; cytostatic; immunostimulatory; antimicrobial;  
KW antiviral; immunosuppressive; antiinflammatory; vulnerrary; cytokine;  
KW cell proliferation; differentiation; regulator; treatment; tumor;  
KW autoimmune disease; inflammatory disorder; wound; microbial infection;  
KW viral disease; graft versus host reaction suppression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200037630-A1.  
XX  
PD 29-JUN-2000.  
XX  
PF 22-DEC-1999; 99WO-US031005.  
XX  
PR 23-DEC-1998; 98US-00220876.  
XX  
PA (GEMY ) GENETICS INST INC.  
XX  
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Bowman MR;  
XX  
DR WPI; 2000-442661/38.  
DR P-PSDB; AAB10274.  
XX  
PT Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors,  
PT autoimmune diseases, inflammatory disorders, wounds, microbial infections  
PT and viral diseases.  
XX  
PS Disclosure; Page 269; 293pp; English.  
XX  
CC This invention describes novel secreted human proteins (I) which have  
CC cytostatic, immunostimulatory, antimicrobial, antiviral,  
CC immunosuppressive, antiinflammatory and vulnerrary activity and which act  
CC as cytokine, cell proliferation or differentiation regulators. (I) is  
CC useful for treating tumors, autoimmune diseases, inflammatory disorders,  
CC wounds, microbial infections and viral diseases. (I) is also useful for  
CC suppressing graft versus host reaction. AAA40490-A40580 represent cDNA  
CC fragments that encode the secreted proteins AAB10226-B10288 described in  
CC the method of the invention  
XX  
SQ Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 18;









RESULT 2034  
AAD20091



CC determining the presence of and/or identifying a polyadenylation site or  
CC alternative polyadenylation sites within a sequence of a transcribed gene  
CC or sequences of transcribed gene variants present or potentially present  
CC in a sample, in identifying gene features, particularly in identifying  
CC differences between sequence variants that occur in a population of  
CC nucleic acid molecules, especially in identifying or discovering polyA  
CC site usage or determining polyA site usage in a nucleic acid sample, and  
CC gene variants arising from alternative polyA sites. The present sequence  
CC represents a double stranded product DNA fragment  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2801  
Db 17 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 2038  
ACF36364/c  
ID ACF36364 standard; DNA; 18 BP.  
XX  
AC ACF36364;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA.  
XX  
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;  
KW electrophoresis; type II restriction enzyme; HaeII; ds.  
XX  
OS Synthetic.  
XX  
PN WO2003064691-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 28-JAN-2003; 2003WO-IB000843.  
XX  
PR 29-JAN-2002; 2002US-0352215P.  
XX  
PA (GLOB-) GLOBAL GENOMICS AB.  
XX  
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;  
PI Montelius A;  
XX  
DR WPI; 2003-618365/58.  
XX  
PT Producing a population of double-stranded product DNA molecules, useful  
PT for mRNA profiling, comprises amplification by nested polymerase chain  
PT reaction.  
XX  
PS Example; Fig 1; 105pp; English.  
XX  
CC The invention relates to producing a population of double-stranded  
CC product DNA molecules comprising amplification by a nested PCR method.  
CC The method is useful in profiling mRNA transcribed in a system under  
CC investigation. The oligonucleotides are used as size standards in  
CC electrophoresis, and as internal controls allowing for calculation of  
CC relative amounts of material present. The present sequence represents a  
CC double stranded product DNA, which aids in outlining an approach to  
CC production of a single pattern characteristic of a sample, employing a  
CC type II restriction enzyme (HaeII)  
XX  
SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2801  
Db 17 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 2039  
AAQ75558  
ID AAQ75558 standard; DNA; 19 BP.  
XX  
AC AAQ75558;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
  
RESULT 2040  
AAQ75551/c  
ID AAQ75551 standard; DNA; 19 BP.  
XX  
AC AAQ75551;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.

XX 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 2041  
AAQ75555  
ID AAQ75555 standard; DNA; 19 BP.  
AC AAQ75555;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2042  
AAQ75550  
ID AAQ75550 standard; DNA; 19 BP.  
XX  
AC AAQ75550;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2043  
AAQ75547  
ID AAQ75547 standard; DNA; 19 BP.  
XX  
AC AAQ75547;  
XX



DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
PS  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2044  
AAQ75547/c  
ID AAQ75547 standard; DNA; 19 BP.  
XX  
AC AAQ75547;  
XX  
XX 04-AUG-1995 (first entry)  
DT  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
DE  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
RESULT 2045  
AAQ49436/c  
ID AAQ49436 standard; cDNA; 20 BP.  
XX  
AC AAQ49436;  
XX  
DT 25-MAR-2003 (revised)  
DT 27-APR-1994 (first entry)  
XX  
DE Cytochrome P450 sequence amplification PCR primer polyT.  
XX  
XX Transgenic plants; altered petal colour; polymerase chain reaction; ss.  
XX  
OS Synthetic.  
XX WO9320206-A1.  
XX  
PD 14-OCT-1993.  
XX  
PF 25-MAR-1993; 93WO-AU000127.  
XX  
PR 27-MAR-1992; 92AU-00001538.  
PR 07-JAN-1993; 93AU-00006698.  
XX  
PA (ITPL-) INT FLOWER DEV PTY LTD.  
XX  
PI Holton TA, Cornish EC, Tanaka Y;  
XX  
DR WPI; 1993-336914/42.  
XX  
PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to  
PT create transgenic plants with altered petal colour.  
XX  
PS Disclosure; Page 25; 86pp; English.  
XX  
CC The sequence is that of a PCR primer which was used in polymerase chain  
CC reactions for the amplification of cloned cytochrome P450 sequences.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1

RESULT 2046  
AAQ75572  
ID AAQ75572 standard; DNA; 20 BP.  
XX  
AC AAQ75572;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
XX  
RESULT 2047  
AAQ75604  
ID AAQ75604 standard; DNA; 20 BP.  
XX  
AC AAQ75604;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
XX

PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
XX  
RESULT 2048  
AAQ75578/c  
ID AAQ75578 standard; DNA; 20 BP.  
XX  
AC AAQ75578;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

```
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2049
AAQ75592
ID AAQ75592 standard; DNA; 20 BP.
XX
AC AAQ75592;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2182
Db 1 TTTTTTTTTTTTTTTTTT 17

RESULT 2050
ABZ88266
ID ABZ88266 standard; DNA; 20 BP.
XX
AC ABZ88266;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
```

```
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antisense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antisense to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.
XX
PS Disclosure; SEQ ID NO 3508; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antisense to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
antiinflammatory steroid and ubiquinone. A composition of the invention
has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytostatic activity. The composition may have a
use in antisense gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
antiinflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
```

```
Query Match 0.6%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 4 AAAAAAAAAAAAAAAAAA 20

RESULT 2051
AAQ75591
ID AAQ75591 standard; DNA; 20 BP.
XX
AC AAQ75591;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
```

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
KW Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 1lpp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
XX  
RESULT 2052  
AAQ75605  
ID AAQ75605 standard; DNA; 20 BP.  
XX  
AC AAQ75605;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX

PS Disclosure; Page 5; 1lpp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
XX  
RESULT 2053  
AAQ75575/c  
ID AAQ75575 standard; DNA; 20 BP.  
XX  
AC AAQ75575;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 1lpp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
XX  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
XX



RESULT 2054  
AAQ75577/C  
ID AAQ75577 standard; DNA; 20 BP.  
XX  
AC AAQ75577;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2056  
AAQ75594  
ID AAQ75594 standard; DNA; 20 BP.  
XX  
AC AAQ75594;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1

RESULT 2055  
AAQ75593  
ID AAQ75593 standard; DNA; 20 BP.  
XX  
AC AAQ75593;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.



XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAAA 1

RESULT 2060  
ABZ89896/c  
ID ABZ89896 standard; DNA; 20 BP.  
XX  
AC ABZ89896;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 5138; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 20 TTTT TTTT TTTT TTTT TTTT 4

RESULT 2061  
ABZ89719  
ID ABZ89719 standard; DNA; 20 BP.  
XX  
AC ABZ89719;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.  
OS  
XX WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX Disclosure; SEQ ID NO 4961; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also





PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2065  
AAQ75559  
ID AAQ75559 standard; DNA; 20 BP.  
XX  
AC AAQ75559;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2066  
AAQ75559/c  
ID AAQ75559 standard; DNA; 20 BP.  
XX  
AC AAQ75559;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2067  
AAQ75560  
ID AAQ75560 standard; DNA; 20 BP.  
XX  
AC AAQ75560;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2066  
AAQ75559/c  
ID AAQ75559 standard; DNA; 20 BP.  
XX  
AC AAQ75559;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
OS JP06303997-A.  
PN  
XX  
XX 01-NOV-1994.  
PD  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2067  
AAQ75560  
ID AAQ75560 standard; DNA; 20 BP.  
XX  
AC AAQ75560;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
KW Query Match 0.6%; Score 17; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
DB 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2068  
AAQ75560/c  
ID AAQ75560 standard; DNA; 20 BP.  
AC AAQ75560;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
KW Query Match 0.6%; Score 17; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2786 AAAAAAAAAAAAAAAA 2802  
DB 17 AAAAAAAAAAAAAAAA 1

RESULT 2069  
AAQ75561  
ID AAQ75561 standard; DNA; 20 BP.  
XX  
AC AAQ75561;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
KW Query Match 0.6%; Score 17; DB 1; Length 20;  
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
DB 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2070

Thu Jun 10 13:10:09 2004

AAQ75561/c  
ID AAQ75561 standard; DNA; 20 BP.  
XX  
AC AAQ75561;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAAAA 1  
  
RESULT 2071  
AAQ75562  
ID AAQ75562 standard; DNA; 20 BP.  
XX  
AC AAQ75562;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.

XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
  
RESULT 2072  
AAQ75562/c  
ID AAQ75562 standard; DNA; 20 BP.  
XX  
AC AAQ75562;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1

RESULT 2073  
ABQ79871  
ID ABQ79871 standard; DNA; 20 BP.  
XX AC ABQ79871;  
XX DT 23-DEC-2002 (first entry)  
XX DE Nucleotide sequence of a PCR primer #1.  
XX KW Polymerase chain reaction; thermal cycle; immobilisation;  
XX KW genetic engineering; PCR; primer; ss.  
XX OS Synthetic.  
XX PN JP2002191369-A.  
XX PD 09-JUL-2002.  
XX PF 27-DEC-2000; 2000JP-00399573.  
XX PR 27-DEC-2000; 2000JP-00399573.  
XX PA (TOJO ) TOYO KOHAN CO LTD.  
XX PA (TAKA/) TAKAHASHI K.  
XX DR WPI; 2002-630904/68.  
XX PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
XX PT a substrate on which a DNA is immobilized used in medical, biochemical,  
XX PT molecular biological and gene engineering fields.  
XX PS Example; Page 9; 13pp; Japanese.  
XX CC The invention relates to performing a thermal cycle of PCR by using a  
XX CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
XX CC method is useful in the medical, biochemical, molecular biological and  
XX CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
XX CC used in the method of the invention  
XX SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 4 TTTTTTTTTTTTTTTT 20

RESULT 2074  
ABQ79871/c  
ID ABQ79871 standard; DNA; 20 BP.  
XX AC ABQ79871;  
XX DT 23-DEC-2002 (first entry)  
XX DE Nucleotide sequence of a PCR primer #1.  
XX KW Polymerase chain reaction; thermal cycle; immobilisation;  
XX KW genetic engineering; PCR; primer; ss.

OS Synthetic.  
XX PN JP2002191369-A.  
XX PD 09-JUL-2002.  
XX PF 27-DEC-2000; 2000JP-00399573.  
XX PR 27-DEC-2000; 2000JP-00399573.  
XX PA (TOJO ) TOYO KOHAN CO LTD.  
XX PA (TAKA/) TAKAHASHI K.  
XX DR WPI; 2002-630904/68.  
XX PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using  
XX PT a substrate on which a DNA is immobilized used in medical, biochemical,  
XX PT molecular biological and gene engineering fields.  
XX PS Example; Page 9; 13pp; Japanese.  
XX CC The invention relates to performing a thermal cycle of PCR by using a  
XX CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The  
XX CC method is useful in the medical, biochemical, molecular biological and  
XX CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers  
XX CC used in the method of the invention  
XX SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
Db 20 AAAAAAAAAAAAAA 4

RESULT 2075  
ABZ91658/c  
ID ABZ91658 standard; DNA; 20 BP.  
XX AC ABZ91658;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human oligonucleotide sequence.  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
XX KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
XX KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
XX KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
XX KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
XX KW lung inflammation; respiratory disease; ds.  
XX OS Homo sapiens.  
XX PN WO200285308-A2.  
XX PD 31-OCT-2002.  
XX PF 23-APR-2002; 2002WO-US013135.  
XX PR 24-APR-2001; 2001US-0286137P.  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;  
XX DR WPI; 2003-229219/22.  
XX PT Pharmaceutical composition for treating ailments associated with impaired





CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2078  
AAQ75717/c  
ID AAQ75717 standard; DNA; 21 BP.  
XX  
AC AAQ75717;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2079  
AAQ75789  
ID AAQ75789 standard; DNA; 21 BP.  
XX

AC AAQ75789;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2080  
AAQ75661  
ID AAQ75661 standard; DNA; 21 BP.  
XX  
AC AAQ75661;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX

DR WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2081  
AAQ75739  
ID AAQ75739 standard; DNA; 21 BP.  
XX AAQ75739;  
XX  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 8; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2082  
AAQ75787  
ID AAQ75787 standard; DNA; 21 BP.  
XX  
XX AAQ75787;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 9; 11pp; Japanese.  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2083  
AAQ75718/c  
ID AAQ75718 standard; DNA; 21 BP.  
XX  
XX AAQ75718;  
XX 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX

PN JP06303997-A.  
XX 01-NOV-1994.  
PD 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA WPI; 1995-018287/03.  
DR Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.  
PT Disclosure; Page 8; 11pp; Japanese.  
PS  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2084  
AAQ75659  
ID AAQ75659 standard; DNA; 21 BP.  
XX  
AC AAQ75659;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA WPI; 1995-018287/03.  
DR Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.  
PT Disclosure; Page 6; 11pp; Japanese.  
PS  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
RESULT 2085  
AAQ75715/c  
ID AAQ75715 standard; DNA; 21 BP.  
XX  
AC AAQ75715;  
XX  
DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
OS  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA WPI; 1995-018287/03.  
DR  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX Disclosure; Page 8; 11pp; Japanese.  
PS  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2086  
AAQ75735  
ID AAQ75735 standard; DNA; 21 BP.  
XX  
AC AAQ75735;



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XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2087
AAQ75738
ID AAQ75738 standard; DNA; 21 BP.
XX
AC AAQ75738;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2088
AAQ75748
ID AAQ75748 standard; DNA; 21 BP.
XX
AC AAQ75748;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 8; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.6%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2089  
AAQ75795  
ID AAQ75795 standard; DNA; 21 BP.  
XX  
AC AAQ75795;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2090  
AAQ75736  
ID AAQ75736 standard; DNA; 21 BP.  
XX  
AC AAQ75736;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.

XX 01-NOV-1994.  
PD  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2091  
AAQ75798  
ID AAQ75798 standard; DNA; 21 BP.  
XX  
AC AAQ75798;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily

CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2092  
AAQ75794  
ID AAQ75794 standard; DNA; 21 BP.  
XX  
AC AAQ75794;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
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XX  
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CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2093  
AAQ75747  
ID AAQ75747 standard; DNA; 21 BP.  
XX  
AC AAQ75747;  
XX

DT 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
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CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in seperate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2094  
AAQ75786  
ID AAQ75786 standard; DNA; 21 BP.  
XX  
AC AAQ75786;  
XX  
DT 04-AUG-1995 (first entry)  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX

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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2095  
AAQ75791  
ID AAQ75791 standard; DNA; 21 BP.  
XX  
AC AAQ75791;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182

Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2096  
AAQ75743  
ID AAQ75743 standard; DNA; 21 BP.  
XX  
AC AAQ75743;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2097  
AAQ75796  
ID AAQ75796 standard; DNA; 21 BP.  
XX  
AC AAQ75796;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX



PD 01-NOV-1994.  
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PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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PT by digestion with restriction enzymes.  
XX  
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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2098  
AAQ75703/c  
ID AAQ75703 standard; DNA; 21 BP.  
XX  
AC AAQ75703;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2099  
AAQ75714/c  
ID AAQ75714 standard; DNA; 21 BP.  
XX  
AC AAQ75714;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
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PF 16-APR-1993; 93JP-00112515.  
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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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PS Disclosure; Page 8; 11pp; Japanese.  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2100  
AAQ75705/c  
ID AAQ75705 standard; DNA; 21 BP.  
XX  
AC AAQ75705;  
XX  
DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX  
XX 16-APR-1993; 93JP-00112515.  
PR  
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XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
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XX  
XX WPI; 1995-018287/03.  
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PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
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PS Disclosure; Page 7; 11pp; Japanese.  
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CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2101  
AAQ75712/c  
ID AAQ75712 standard; DNA; 21 BP.  
XX  
XX  
AC AAQ75712;  
XX  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
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CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2102  
AAQ75737  
ID AAQ75737 standard; DNA; 21 BP.  
XX  
XX  
AC AAQ75737;  
XX  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
OS Synthetic.  
XX  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
XX 16-APR-1993; 93JP-00112515.  
PF  
XX  
XX 16-APR-1993; 93JP-00112515.  
PR  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
XX WPI; 1995-018287/03.  
DR  
XX  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 8; 11pp; Japanese.  
XX  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2166 TTTTTTTTTTTTTTTT 2182  
Db 17 TTTTTTTTTTTTTTTT 1

Db 1 TTTTTTTTTTTTTTTTTT 17

RESULT 2103  
AAQ75706/C  
ID AAQ75706 standard; DNA; 21 BP.  
XX  
AC AAQ75706;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
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PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
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CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1

RESULT 2104  
AAQ75746  
ID AAQ75746 standard; DNA; 21 BP.  
XX  
AC AAQ75746;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX by digestion with restriction enzymes.  
XX Disclosure; Page 8; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
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CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2105  
AAQ75784  
ID AAQ75784 standard; DNA; 21 BP.  
XX  
AC AAQ75784;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
PD 01-NOV-1994.

CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2106  
AAQ75785  
ID AAQ75785 standard; DNA; 21 BP.  
XX  
AC AAQ75785;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2107  
AAQ75704/c  
ID AAQ75704 standard; DNA; 21 BP.  
XX  
AC AAQ75704;  
XX  
DT 04-AUG-1995 (first entry)  
XX

DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2108  
AAQ75707/c  
ID AAQ75707 standard; DNA; 21 BP.  
XX  
AC AAQ75707;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.



XX PS Disclosure; Page 7; 1lpp; Japanese.

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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred.No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2109

AAQ75750

ID AAQ75750 standard; DNA; 21 BP.

XX AC AAQ75750;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 1lpp; Japanese.

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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

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CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred.No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182

Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2110

AAQ75710/c

ID AAQ75710 standard; DNA; 21 BP.

XX AC AAQ75710;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 1lpp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred.No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2111

AAQ75711/c

ID AAQ75711 standard; DNA; 21 BP.

XX AC AAQ75711;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2112  
AAQ75783  
ID AAQ75783 standard; DNA; 21 BP.  
XX  
AC AAQ75783;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 9; 11pp; Japanese.  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
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CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
CC

XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2113  
AAQ75620  
ID AAQ75620 standard; DNA; 21 BP.  
XX  
AC AAQ75620;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2114  
AAQ75668  
ID AAQ75668 standard; DNA; 21 BP.  
XX  
AC AAQ75668;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2115  
AAQ75614/c  
ID AAQ75614 standard; DNA; 21 BP.  
XX  
AC AAQ75614;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
XX  
PN 01-NOV-1994.  
XX  
PD 16-APR-1993; 93JP-00112515.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX

PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
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CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
  
RESULT 2116  
AAQ75621/c  
ID AAQ75621 standard; DNA; 21 BP.  
XX  
AC AAQ75621;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
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XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred.No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1







XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2123  
AAQ75667  
ID AAQ75667 standard; DNA; 21 BP.  
XX  
AC AAQ75667;

DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX aggregate; restriction enzyme; ss.  
XX Synthetic.

XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 7; 11pp; Japanese.

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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX

SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2124  
AAQ75655  
ID AAQ75655 standard; DNA; 21 BP.  
XX  
AC AAQ75655;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.

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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2125  
AAQ75663  
ID AAQ75663 standard; DNA; 21 BP.  
XX  
AC AAQ75663;

DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX JP06303997-A.  
XX 01-NOV-1994.  
XX 16-APR-1993; 93JP-00112515.  
XX

PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
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PT by digestion with restriction enzymes.  
XX  
XX  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2126  
AAQ75666  
ID AAQ75666 standard; DNA; 21 BP.  
XX  
AC AAQ75666;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
XX  
PS Disclosure; Page 7; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2127  
AAQ75658  
ID AAQ75658 standard; DNA; 21 BP.  
XX  
AC AAQ75658;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2128  
AAQ75611  
ID AAQ75611 standard; DNA; 21 BP.  
XX  
AC AAQ75611;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
KW  
XX  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2129  
AAQ75611/c  
ID AAQ75611 standard; DNA; 21 BP.  
XX  
AC AAQ75611;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
KW  
XX  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1  
RESULT 2130  
AAQ75622  
ID AAQ75622 standard; DNA; 21 BP.  
XX  
AC AAQ75622;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
KW  
XX  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2131



XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2133  
AAQ75609/C  
ID AAQ75609 standard; DNA; 21 BP.  
XX  
XX AC AAQ75609;  
XX  
XX DT 04-AUG-1995 (first entry)  
XX  
XX DE Reverse transcription primer used in cDNA analysis technique.  
XX  
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;  
XX KW aggregate; restriction enzyme; ss.  
XX  
XX OS Synthetic.  
XX  
XX PN JP06303997-A.  
XX  
XX PD 01-NOV-1994.  
XX  
XX PF 16-APR-1993; 93JP-00112515.  
XX  
XX PR 16-APR-1993; 93JP-00112515.  
XX  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
XX PA WPI; 1995-018287/03.  
XX  
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed  
XX PT by digestion with restriction enzymes.  
XX  
XX  
XX Disclosure; Page 5; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
XX CC and using the aggregate of mRNAs as the template for each reverse  
XX CC transcription primer; (b) digesting each of the prepared aggregates of  
XX CC the double-stranded cDNAs with restriction enzyme and; (c)  
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
XX CC method can be used to analyse gene expression rapidly and easily  
XX  
XX Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1

RESULT 2134  
AAQ75607  
ID AAQ75607 standard; DNA; 21 BP.  
XX  
AC AAQ75607;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 2135  
AAQ75607/c  
ID AAQ75607 standard; DNA; 21 BP.  
XX  
AC AAQ75607;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.

XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1

RESULT 2136  
AAQ75618  
ID AAQ75618 standard; DNA; 21 BP.  
XX  
AC AAQ75618;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of



PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2140  
AAQ75615  
ID AAQ75615 standard; DNA; 21 BP.  
XX  
AC AAQ75615;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2182  
Db 1 TTTTTTTTTTTTTTTT 17  
RESULT 2141  
AAQ75615/c  
ID AAQ75615 standard; DNA; 21 BP.  
XX  
AC AAQ75615;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 17 AAAAAAAAAAAAAA 1  
RESULT 2142  
AAQ75610  
ID AAQ75610 standard; DNA; 21 BP.  
XX  
AC AAQ75610;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX



OS Synthetic.  
XX JP06303997-A.  
PN  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
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PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 5; 11pp; Japanese.  
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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2143  
AAQ75610/c  
ID AAQ75610 standard; DNA; 21 BP.  
XX  
AC AAQ75610;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
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XX  
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PT by digestion with restriction enzymes.  
XX  
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CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA AAAAAA 1  
RESULT 2144  
AAQ75619  
ID AAQ75619 standard; DNA; 21 BP.  
XX  
AC AAQ75619;  
XX  
DT 04-AUG-1995 (first entry)  
XX  
DE Reverse transcription primer used in cDNA analysis technique.  
XX  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX  
OS Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX  
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
XX  
DR WPI; 1995-018287/03.  
XX  
PT Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
RESULT 2145  
AAQ75619/c  
ID AAQ75619 standard; DNA; 21 BP.

XX AAQ75619;  
AC 04-AUG-1995 (first entry)  
XX Reverse transcription primer used in cDNA analysis technique.  
DE  
XX  
DE  
KW Analysis; gene expression; reverse transcription; primer; cDNA;  
KW aggregate; restriction enzyme; ss.  
XX Synthetic.  
XX  
PN JP06303997-A.  
XX  
PD 01-NOV-1994.  
XX  
PF 16-APR-1993; 93JP-00112515.  
XX  
PR 16-APR-1993; 93JP-00112515.  
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.  
PA WPI; 1995-018287/03.  
XX  
XX Analysis of cDNA and gene expression - by amplification of mRNA followed  
PT by digestion with restriction enzymes.  
PT  
XX  
PS Disclosure; Page 6; 11pp; Japanese.  
XX  
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of  
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of  
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)  
CC and using the aggregate of mRNAs as the template for each reverse  
CC transcription primer; (b) digesting each of the prepared aggregates of  
CC the double-stranded cDNAs with restriction enzyme and; (c)  
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The  
CC method can be used to analyse gene expression rapidly and easily  
XX  
SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
DB 17 AAAAAAAAAAAAAAAAAA 1  
RESULT 2146  
AAZ26584/C  
ID AAZ26584 standard; DNA; 21 BP.  
XX  
AC AAZ26584;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 773.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.

XX 20-MAR-1997; 97US-0041057P.  
XX (VARI-) VARIAGENICS INC.  
PA  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
XX Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2172 TTTTTTTTTTTTTTAA 2188  
DB 21 TTTTTTTTTTTTTTAA 5  
RESULT 2147  
AAT92356/C  
ID AAT92356 standard; DNA; 22 BP.  
XX  
AC AAT92356;  
XX  
DT 26-JAN-1998 (first entry)  
XX  
DE Amino modified oligodeoxyribonucleotide.  
XX  
KW Amino modified oligodeoxyribonucleotide; oligonucleotide;  
KW achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;  
KW N-fluoresceinyl-(5-aminomethyl)-1,3-benzenedimethanol;  
KW hybridisation probe; PCR primer; nucleic acid sequencing;  
KW affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT misc\_difference 11 /tag= a  
FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"  
FT misc\_difference 12 /tag= b  
FT /note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"  
XX  
PN WO9705156-A1.  
XX

PD 13-FEB-1997.  
XX  
PF 26-JUL-1996; 96WO-DK000330.  
XX  
PR 27-JUL-1995; 95DK-00000863.  
XX (BEHR/) BEHRENS C.  
PA (PETE/) PETERSEN K H.  
PA (EGHO/) EGHOLM M.  
PA (NIEL/) NIELSEN J.  
PA (DAHL/) DAHL O.  
XX  
PI Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;  
XX WPI; 1997-145615/13.  
DR  
XX  
XX New achiral linker reagents - useful for incorporation of multiple amino  
PT gps. or reporter gps. into oligo:nucleotide(s).  
XX  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC Achiral linker reagents have been developed for the incorporation of  
CC multiple amino groups into oligonucleotides. The present sequence  
CC represents a modified oligodeoxyribonucleotide. The achiral linker  
CC reagents can be used for incorporation of multiple primary amino groups  
CC or reporter groups into oligonucleotides. They are compatible with  
CC conventional DNA synthesis following the phosphoramidite methodology, and  
CC can be incorporated in good yields. The linker reagents may be used for  
CC labelling of oligonucleotides. They may also be used for preparation of  
CC oligonucleotides, e.g. for use as hybridisation probes, for use as  
CC primers in the polymerase chain reaction or in nucleic acid sequencing  
CC reactions, for production of affinity matrices for purification of DNA  
CC binding proteins or other biomolecules, for production of affinity  
CC matrices for detection of nucleic acid sequences, for cloning recombinant  
CC DNA or for in-vitro mutagenesis  
XX  
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 22 AAAAAAAAAAAAAAAAAA 4  
  
RESULT 2148  
AAA98276/C  
ID AAA98276 standard; DNA; 22 BP.  
XX  
AC AAA98276;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human mismatch repair gene hMSH6 intron 9 DNA fragment.  
XX  
KW Human mismatch repair gene; hMSH6; disease predisposition; genotype;  
KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;  
KW neoplastic disease; drug development; ss.  
XX  
OS Homo sapiens.  
XX  
XX DE19909878-A1.  
PN  
XX  
XX 07-SEP-2000.  
PD  
XX  
PF 06-MAR-1999; 99DE-01009878.  
XX  
XX 06-MAR-1999; 99DE-01009878.  
PR  
XX (UYDR ) UNIV DRESDEN TECH.  
XX

PI Plaschke J, Kruppa C, Schackert H;  
XX WPI; 2000-588378/56.  
DR  
XX  
PT Novel variants of the human mismatch repair gene, MSH6, useful e.g. for  
PT determining predisposition to cancer and for development of drugs.  
XX  
PS Claim 1; Page 4; 14pp; German.  
XX  
CC This invention describes a novel method of determining a predisposition  
CC to disease by genotyping a subject's DNA sequence (A) of the human  
CC mismatch repair gene, MSH6 at specified positions and comparing with  
CC reference DNA sequences, optionally taking into account all possible  
CC combinations of variations of the individual mutations, including any  
CC chosen absolute number of variations. (A), and analysis of their  
CC sequences, are useful for the following: (i) determining a predisposition  
CC to disease, especially colorectal, endometrial and ovarian carcinoma and  
CC leukemia; (ii) determining an increased mutation rate (frequency of base  
CC substitutions, insertions and/or deletions) in eukaryotic cells; (iii)  
CC predicting the progression, severity and survival time of patients with  
CC neoplastic disease; (iv) the development of therapeutic and 'life-style'  
CC drugs; (v) predicting individual differences in response to known  
CC chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);  
CC (vi) optimizing individual treatments and interventions against neoplasia  
CC ; (vii) controlling the mutation rate in eukaryotic cells, in vitro or in  
CC vivo; (viii) constructing genes and vectors, particularly for development  
CC of pharmaceuticals; (ix) developing diagnostic kits and other systems for  
CC genotyping; and (x) developing in vivo and in vitro test systems for  
CC expressing individual forms of the MSH6 gene, e.g. for studying  
CC pathophysiology of disease or processes in which MSH6 is involved, and  
CC for drug development and testing  
XX  
SQ Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 22 AAAAAAAAAAAAAAAAAA 6  
  
RESULT 2149  
AAA29753/C  
ID AAA29753 standard; DNA; 23 BP.  
XX  
AC AAA29753;  
XX  
DT 15-AUG-2000 (first entry)  
XX  
DE Synthetic oligonucleotide #1.  
XX  
KW Primer; destabilise non-specific duplex formation; PCR; detection;  
KW purification; sequencing; genetic marker; RACE; DNA synthesis; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 8 /\*tag= a  
FT /mod\_base= i  
FT /note= "inosine"  
FT modified\_base 18 /\*tag= b  
FT /mod\_base= i  
FT /note= "inosine"  
XX  
PN WO200020630-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 06-OCT-1999; 99WO-CA000933.  
PF

XX 07-OCT-1998; 98CA-02246623.  
PR (UYMC-) UNIV MCGILL.  
XX Pelletier J, Das M;  
PI WPI; 2000-328943/28.  
XX Novel method of stabilizing duplex formation, or destabilizing non-  
PT specific duplex formation using primer containing modified nucleotide  
PT analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis  
PT or sequencing.  
XX Example 1; Page 25; 46pp; English.  
PS The present invention describes a method for destabilising non-specific  
XX duplex formation, between an oligonucleotide and a target nucleic acid  
CC (NA), comprising incubating the target NA with a modified oligonucleotide  
CC (I) comprising a homopolymeric sequence having a modification which  
CC decreases or abrogates H-bonding between the modified oligonucleotide and  
CC the non-specific target NA. The modified oligonucleotide is used to  
CC improve discrimination between the targeted homopolymeric sequence and a  
CC non-homopolymeric target sequence. It is used to increase the proportion  
CC of full length cDNA clones for a library, to reduce mispriming during  
CC sequencing, 5' or 3' RACE (rapid amplification of cDNA ends) or DNA  
CC synthesis or to generate bona fide genetic markers. The present sequence  
CC represents an oligonucleotide which is used in the exemplification of the  
CC present invention  
XX Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 2 Other;  
SQ Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2804  
Db 23 AAAAAAAAAAAAAA 5  
RESULT 2150  
AAQ45360/c  
ID AAQ45360 standard; DNA; 23 BP.  
XX AAQ45360;  
AC AAQ45360;  
XX 25-MAR-2003 (revised)  
DT 09-OCT-1994 (first entry)  
XX Human protein-tyrosine-phosphatase-1D cDNA primer.  
XX Protein-tyrosine-phosphatase; enzyme; disease diagnosis; DNA primer; ss.  
XX Synthetic.  
XX WO9408017-A1.  
PN 14-APR-1994.  
PD 06-OCT-1993; 93WO-EP002728.  
XX 06-OCT-1992; 92US-00956315.  
PR 16-FEB-1993; 93US-00018129.  
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
PA Ullrich A, Vogel W;  
XX WPI; 1994-135583/16.  
DR New protein tyrosine phosphatase (PTP) protein, PTP-ID - are useful for  
XX diagnosis and treatment of diseases associated with abnormal PTP-ID

PT levels.  
XX Disclosure; Page 48; 99pp; English.  
PS This DNA primer is used in the PCR-based amplification of protein-  
XX tyrosine-phosphatase-1B cDNA. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
CC Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 23 AAAAAAAAAAAAAA 7  
RESULT 2151  
AAT37316/c  
ID AAT37316 standard; DNA; 23 BP.  
XX AAT37316;  
AC AAT37316;  
XX 06-FEB-1997 (first entry)  
DT RT-PCR Primer for aromatic acyl transferase sequence.  
XX Aromatic acyl transferase; transformation; anthocyanin pigment; plants;  
KW acylation; colour; tone; colouration; colour change; Gentiana triflora;  
KW Petunia hybrida; Perilla ocimoides; Scenecio cruentus;  
KW Lavandula angustifolia; ss.  
XX Synthetic.  
XX WO9625500-A1.  
PN 22-AUG-1996.  
PD 16-FEB-1996; 96WO-JP000348.  
PF 17-FEB-1995; 95JP-00067159.  
PR 29-JUN-1995; 95JP-00196915.  
PR 30-JAN-1996; 96JP-00046534.  
XX (SUNR ) SUNTORY LTD.  
PA Ashikari T, Tanaka Y, Fujiwara H, Nakao M, Fukui Y, Yonekura K;  
XX Mizutani M, Kusumi T;  
PI WPI; 1996-393401/39.  
DR DNA coding for aromatic acyl transferase - for transforming plants which  
XX produce anthocyanin pigments and thus altering colour tone, e.g. of  
PT flowers.  
PT Example 2; Page 21; 94pp; Japanese.  
XX Vectors containing DNA fragments encoding proteins of plant origin with  
CC aromatic acyl transferase activity may be used to transform plants which  
CC produce anthocyanin pigments. The aromatic acyl transferase acylates the  
CC pigments in the flower resulting in colour tone changes and allowing new  
CC colourations to be produced. Six specific DNA sequences encoding aromatic  
CC acyl transferase from different plants are described in AAT37308-T37313.  
CC This primer was used to reverse transcribe aromatic acyl transferase RNA  
CC to produce a cDNA ready for cloning into expression vectors  
XX Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 2152  
ABA97431/C  
ID ABA97431 standard; DNA; 23 BP.  
XX  
AC ABA97431;  
XX  
DT 21-MAR-2002 (first entry)  
XX  
DE Glycosyltransferase genes PCR primer #2.  
XX  
KW Glycosyltransferase; anthocyanin; flower colour; enzyme; PCR primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200192509-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 01-JUN-2001; 2001WO-JP004675.  
XX  
PR 02-JUN-2000; 2000JP-00170436.  
XX  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
XX  
PI Mizutani M, Sakakibara K, Tanaka Y, Kusumi T, Ono E;  
XX  
DR WPI; 2002-114345/15.  
XX  
PT New gene encoding protein that transfers a sugar to the 3' position of  
PT anthocyanin for changing flower color.  
XX  
PS Example 3; Page 13; 50pp; Japanese.  
XX  
CC The present invention provides the genes and proteins of  
CC glycosyltransferases from Gentiana triflora, Senesio cruentus and  
CC Clitoria ternatea. The protein transfers a sugar to the 3' position of  
CC anthocyanin, and can be used for changing the colour of flowers. The  
CC present sequence is a PCR primer used to isolate glycosyltransferase  
CC coding sequences of the invention  
XX  
SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 2153  
AAF85497/C  
ID AAF85497 standard; DNA; 23 BP.  
XX  
AC AAF85497;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE PCR primer for DNA encoding Kalata B1 polypeptide fragments.  
XX  
KW Kalata B2; transgenic plant; cotton; calcium channel binding; pain;  
KW stroke; C5a binding; antiinflammatory; PCR primer; ss.  
XX  
OS Oldenlandia affinis.  
XX  
PN WO200134829-A2.

XX  
PD 17-MAY-2001.  
XX  
PF 03-NOV-2000; 2000WO-AU001352.  
XX  
PR 05-NOV-1999; 99AU-00003884.  
PR 25-NOV-1999; 99AU-00004235.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
PA (UYLA-) UNIV LATROBE.  
XX  
PI Craik DJ, Anderson MA, Jennings CV;  
XX  
DR WPI; 2001-343607/36.  
XX  
PT Novel nucleic acid molecule encoding amino acid sequence capable of  
PT forming cyclic structure, for generating transgenic plants capable of  
PT producing cyclic knotted protein and resistant to pathogens such as  
PT insects.  
XX  
PS Example 10; Fig 1B; 112pp; English.  
XX  
CC PCR primers AAF85495-97 were used to amplify a DNA fragment encoding  
CC Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological  
CC activities. The Kalata B1 polynucleotide represents a nucleic acid  
CC molecule of the invention. The specification describes a nucleic acid  
CC molecules which encode an amino acid sequence which is capable of being  
CC cyclised within a cell or a membrane of a cell to form a cyclic backbone.  
CC The amino acid sequence comprises sufficient disulfide bonds to confer a  
CC stabilized folded structure on the three-dimensional structure of the  
CC backbone. The nucleic acid molecules of the invention are useful for  
CC producing transgenic genetically modified food or non-food crop plants,  
CC in particular cotton. The peptides or proteins can be manipulated to  
CC introduce modulating activity, for modulating activity of calcium channel  
CC binding is useful in treatment of pain or stroke and C5a binding activity  
CC useful as an antiinflammatory agent. The nucleic acid molecules are  
CC useful in the generation of molecules having animal or plant therapeutic  
CC properties as well as in a range of diagnostic, industrial and  
CC agricultural including horticultural applications and for protecting  
CC plants such as crop plants from pest and/or pathogen infestation  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 23 AAAAAAAAAAAAAAAAAA 7

RESULT 2154  
ABL95973  
ID ABL95973 standard; DNA; 23 BP.  
XX  
AC ABL95973;  
XX  
DT 19-JUN-2002 (first entry)  
XX  
DE Probe #48 for assaying nucleic acids.  
XX  
KW Probe; polymorphism detection; mutation detection; disease diagnosis;  
KW microbial identification; ss.  
XX  
OS Unidentified.  
XX  
PN WO200208414-A1.  
XX  
PD 31-JAN-2002.  
XX  
PF 27-JUN-2001; 2001WO-IB001147.  
XX

PR 27-JUN-2000; 2000JP-001931133.  
PR 03-AUG-2000; 2000JP-002361115.  
PR 26-SEP-2000; 2000JP-00292483.  
XX  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (KANK-) KANKYO ENG CO LTD.  
XX  
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;  
PI Yokomaku T;  
XX  
DR WPI; 2002-195876/25.  
XX  
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and  
PT their polymorphism and mutation, particularly useful in science and  
PT medicine for e.g. analytical applications, disease diagnosis and  
PT microbial identification.  
XX  
PS Disclosure; Fig 3; 152pp; Japanese.  
XX  
CC The present invention relates to nucleic acid probes, which are useful  
CC for assaying nucleic acids by hybridising with a target nucleic acid, in  
CC which a single-stranded oligonucleotide is labelled with a fluorescent  
CC substance and a quencher in a manner that the fluorescence intensity of  
CC the hybridisation reaction system is increased after completion of the  
CC hybridisation but no stem loop structure is formed. The probes are useful  
CC for assaying nucleic acids and their polymorphism and mutation,  
CC particularly useful for e.g. analytical applications, disease diagnosis  
CC and microbial identification. The present sequence was used to illustrate  
CC the invention  
XX  
SQ Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17  
  
RESULT 2155  
ABQ96219  
ID ABQ96219 standard; DNA; 23 BP.  
XX  
AC ABQ96219;  
XX  
DT 28-OCT-2002 (first entry)  
XX  
DE Tumour suppression-related oligonucleotide #1870.  
XX  
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;  
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;  
KW viral infection; cell degeneration disease; neurodegeneration; ds;  
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.  
XX  
OS Homo sapiens.  
XX  
PN FR2819824-A1.  
XX  
PD 26-JUL-2002.  
XX  
PF 23-JAN-2001; 2001FR-00000899.  
XX  
PR 23-JAN-2001; 2001FR-00000899.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB SA.  
XX  
PI Telerman A, Amson R, Tuijnder M, Susini L;  
XX  
DR WPI; 2002-610803/66.  
XX  
PT New nucleic acid implicated e.g. in tumor suppression, useful for

PT diagnosis of tumors, viral infection and cellular degeneration and for  
PT drug screening.  
XX  
PS Claim 1; Page 512; 623pp; French.  
XX  
CC The present invention relates to novel human nucleic acid sequences (I).  
CC The present sequence is one such nucleic acid sequence. Expression of (I)  
CC are implicated in tumour suppression or reversion and apoptosis and viral  
CC resistance. (I) are useful as probes or primers for detecting,  
CC identifying, measuring and/or amplifying nucleic acid sequences, as  
CC antisense reagents and for recombinant production of polypeptides. (I),  
CC polypeptides (II) encoded by (I), vector containing (I), cells containing  
CC these vectors and antibodies (Ab) against (II) are all useful for  
CC treatment/prevention of viral, tumour and cell degeneration diseases  
CC (especially neurodegeneration, such as Alzheimer's disease and  
CC schizophrenia). Analysing the expression of (I) is also useful for  
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying  
CC (I) are used for studying the aetiology of these diseases (also immune  
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1  
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown  
CC in the specification  
XX  
SQ Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2783 TTGAAA AAAAAA AAAAAA AAAAAA 2801  
Db 3 TNGN AAAAAA AAAAAA AAAAAA 21  
  
RESULT 2156  
ABQ96219/c  
ID ABQ96219 standard; DNA; 23 BP.  
XX  
AC ABQ96219;  
XX  
DT 28-OCT-2002 (first entry)  
XX  
DE Tumour suppression-related oligonucleotide #1870.  
XX  
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;  
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;  
KW viral infection; cell degeneration disease; neurodegeneration; ds;  
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.  
XX  
OS Homo sapiens.  
XX  
PN FR2819824-A1.  
XX  
PD 26-JUL-2002.  
XX  
PF 23-JAN-2001; 2001FR-00000899.  
XX  
PR 23-JAN-2001; 2001FR-00000899.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB SA.  
XX  
PI Telerman A, Amson R, Tuijnder M, Susini L;  
XX  
DR WPI; 2002-610803/66.  
XX  
PT New nucleic acid implicated e.g. in tumor suppression, useful for  
PT diagnosis of tumors, viral infection and cellular degeneration and for  
PT drug screening.  
XX  
PS Claim 1; Page 512; 623pp; French.  
XX  
CC The present invention relates to novel human nucleic acid sequences (I).  
CC The present sequence is one such nucleic acid sequence. Expression of (I)  
CC are implicated in tumour suppression or reversion and apoptosis and viral

CC resistance. (I) are useful as probes or primers for detecting,  
CC identifying, measuring and/or amplifying nucleic acid sequences, as  
CC antisense reagents and for recombinant production of polypeptides. (I),  
CC polypeptides (II) encoded by (I), vector containing (I), cells containing  
CC these vectors and antibodies (Ab) against (II) are all useful for  
CC treatment/prevention of viral, tumour and cell degeneration diseases  
CC (especially neurodegeneration, such as Alzheimer's disease and  
CC schizophrenia). Analysing the expression of (I) is also useful for  
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying  
CC (I) are used for studying the aetiology of these diseases (also immune  
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1  
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown  
CC in the specification

XX  
SQ Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;  
Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
Db 23 CCTTTTCTTTTCTTTTCTTTT 7

RESULT 2157  
AAV48089/c  
ID AAV48089 standard; DNA; 24 BP.  
XX  
AC AAV48089;  
XX  
DT 27-OCT-1998 (first entry)  
XX  
DE Oligonucleotide 25-P.  
XX  
KW In situ translation; RNA-protein fusion; binding reagent; antibody;  
KW industrial catalyst; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 24  
FT /\*tag= a  
FT /note= "Puromycin"  
XX  
PN WO9831700-A1.  
XX  
PD 23-JUL-1998.  
XX  
PF 14-JAN-1998; 98WO-US000807.  
XX  
PR 21-JAN-1997; 97US-0035963P.  
PR 06-NOV-1997; 97US-0064491P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Szostak JW, Roberts RW, Liu R;  
XX  
DR WPI; 1998-414032/35.  
XX  
PT Selection of specific protein by screening protein-RNA fusions generated  
PT in vitro or in situ - useful for, e.g. identifying enzymes and antibodies  
PT with altered properties, potentially useful as catalysts or for therapy  
PT or diagnosis.  
XX  
PS Disclosure; Page 39; 94pp; English.  
XX  
CC The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and  
CC variations were used to generate RNA-protein fusions. These were used in  
CC the selection of a specific protein or RNA, by in vitro or in situ  
CC translation of candidate RNA molecules to produce RNA-protein fusions,  
CC then selecting specific RNA protein fusions. The method is used to select  
CC proteins (or DNA encoding them) having altered properties, e.g. for

CC identification of new binding reagents, to identify improved human  
CC antibodies or new enzymes. These proteins are potentially useful in  
CC diagnosis and therapy, or as industrial catalysts. The methods allow many  
CC rounds of selection and amplification to be performed, resulting in  
CC enrichment of even very rare molecules and allowing isolation of proteins  
CC that bind specifically to almost any compound or catalyse almost any  
CC reaction

XX  
SQ Sequence 24 BP; 0 A; 4 C; 3 G; 16 T; 0 U; 1 Other;  
Query Match 0.6%; Score 17; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAA 2801  
Db 22 GAAAAAATAAAAAA 6

RESULT 2158  
AAT76905  
ID AAT76905 standard; DNA; 24 BP.  
XX  
AC AAT76905;  
XX  
DT 02-JUL-1998 (first entry)  
XX  
DE S. glaucescens dTDP-glucose-dehydratase PCR primer #2.  
XX  
KW Acarbose biosynthesis; acbA gene; acbB gene; acbC gene; acbD gene;  
KW acbE gene; acbF gene; enzyme; alpha-amylase inhibitor; treatment;  
KW diabetes; PCR primer; ss.  
XX  
OS Synthetic.  
OS Streptomyces glaucescens.  
XX  
PN DE19622783-A1.  
XX  
PD 11-DEC-1997.  
XX  
PF 07-JUN-1996; 96DE-01022783.  
XX  
PR 07-JUN-1996; 96DE-01022783.  
XX  
PA (FARH ) HOECHST AG.  
XX  
PI Decker H;  
XX  
DR WPI; 1998-033827/04.  
XX  
PT Recombinant DNA molecule comprising genes for biosynthesis of acarbose -  
PT an alpha-amylase inhibitor useful in treatment of diabetes.  
XX  
PS Example 1; Page 6; 35pp; German.  
XX  
CC AAT76905 and AAT76904 are PCR primers used in a method to amplify a PstI  
CC fragment from Streptomyces glaucescens GLA.O which encodes the genes,  
CC acbA, acbB, acbC, acbD, acbE and acbF which are involved in the acarbose  
CC biosynthesis pathway. These genes and encoded enzymes are useful for  
CC producing acarbose, which is an alpha -amylase inhibitor useful in the  
CC treatment of diabetes

XX  
SQ Sequence 24 BP; 1 A; 3 C; 10 G; 4 T; 0 U; 6 Other;  
Query Match 0.6%; Score 17; DB 1; Length 24;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 799 GGAGCTGGTGGGGCGCGTAAT 819  
Db 2 GGWRCTGGYRSGGSCCGTAGT 22





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XX Example 1; Page 10; 50pp; English.
XX
CC The patent discloses a gene cluster for aclacinomycin biosynthesis being
CC included in a 7 kilobases XhoI-NotI fragment and a flanked 8.5 kilobases
CC BglII fragment derived from Streptomyces galilaeus (ATCC 31615). This
CC gene cluster comprises thirteen genes namely sga1, sga2 (activator), sga3
CC (dehydratase), sga4 (oxidoreductase), sga5 (dTDP-glucose 4,6-
CC dehydratase), sga6 (glycosyl transferase; Grp), sga7 (putative
CC isomerase), sga8 (aklaviketone reductase), sga9 (putative polyketide
CC assembler), sga10 (putative cyclase), sga11 (aminomethylase), sga12
CC (glucose-1-phosphate thymidyl transferase) and sga13
CC (aminotransferase). Aclacinomycin gene cluster is useful for producing
CC metabolites, preferably anthracycline metabolites by transferring
CC aclacinomycin gene cluster into Streptomyces peucetius host. It is useful
CC for the production of hybrid antibiotics and for increasing the yield of
CC aclacinomycin. It is also useful for genetic engineering and for
CC producing anthracycline which is useful as an anticancer agent. The
CC present sequence is a degenerate reverse PCR primer which is used to
CC amplify 6345 to 6861 bases of the aclacinomycin biosynthetic gene cluster
CC (AAD03809), which is internal to the 4, 6-dehydratase gene
XX
SQ Sequence 24 BP; 1 A; 3 C; 10 G; 4 T; 0 U; 6 Other;
Query Match 0.6%; Score 17; DB 1; Length 24;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 14; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 799 GGAGCTGTTGGGGCGCGTAAT 819
DB ||::|||:::|::|::|
2 GGNRCTGGYRSGSGCCGTAGT 22
RESULT 2162
ABQ73254
ID ABQ73254 standard; DNA; 24 BP.
XX
AC ABQ73254;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human macro protein 17.49 PCR primer 1 SEQ ID NO:3.
XX
KW Human; macro protein 17.40; nerve system disorder disease;
KW protein metabolic disorder relative disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1339462-A.
XX
PD 13-MAR-2002.
XX
PF 21-AUG-2000; 2000CN-00119647.
XX
PR 21-AUG-2000; 2000CN-00119647.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PI WPI; 2002-455361/49.
XX
DR New polypeptide-human macro protein 17.49 and polynucleotide for encoding
XX such polypeptide.
XX
PT Human; macro protein 17.40; nerve system disorder disease;
KW protein metabolic disorder relative disease; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX CN1339462-A.
XX
PD 13-MAR-2002.
XX
XX 21-AUG-2000; 2000CN-00119647.
XX
XX 21-AUG-2000; 2000CN-00119647.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-455361/49.
XX
XX New polypeptide-human macro protein 17.49 and polynucleotide for encoding
PT such polypeptide.
XX
XX Example 2; Page 18; 32pp; Chinese.
XX
CC The present invention describes human macro protein 17.49 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) and the polynucleotide encoding it can be used for
CC treating various diseases, such as nerve system disorder disease and
CC protein metabolic disorder relative disease. The present sequence
CC represents a PCR primer for (I), which is used in an example from the
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CC present invention
XX
SQ Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;
Query Match 0.6%; Score 17; DB 1; Length 24;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2166 TTTTNTTTTNTTTTNTTTT 2183
DB |||||::|::|::|::|
2 TTTTNTTTTNTTTTNTTTT 19
RESULT 2163
ABQ73254/c
ID ABQ73254 standard; DNA; 24 BP.
XX
AC ABQ73254;
XX
DT 30-SEP-2002 (first entry)
XX
DE Human macro protein 17.49 PCR primer 1 SEQ ID NO:3.
XX
KW Human; macro protein 17.40; nerve system disorder disease;
KW protein metabolic disorder relative disease; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1339462-A.
XX
PD 13-MAR-2002.
XX
PF 21-AUG-2000; 2000CN-00119647.
XX
PR 21-AUG-2000; 2000CN-00119647.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PI WPI; 2002-455361/49.
XX
DR New polypeptide-human macro protein 17.49 and polynucleotide for encoding
XX such polypeptide.
XX
PT Example 2; Page 18; 32pp; Chinese.
XX
CC The present invention describes human macro protein 17.49 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) and the polynucleotide encoding it can be used for
CC treating various diseases, such as nerve system disorder disease and
CC protein metabolic disorder relative disease. The present sequence
CC represents a PCR primer for (I), which is used in an example from the
CC present invention
XX
SQ Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;
Query Match 0.6%; Score 17; DB 1; Length 24;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2803
DB |||||::|::|::|::|
19 AAAAAAAAAAAAAAAAAA 2
RESULT 2164
ABL40114
ID ABL40114 standard; DNA; 24 BP.
XX
AC ABL40114;
XX
DT 17-MAY-2002 (first entry)
```























PI Ulfendahl P, Wong K;  
XX WPI; 2000-679677/66.  
DR  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX Claim 14; Page 46; 66pp; English.  
PS  
XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein the  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 7 A; 3 C; 0 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2774 TTGTTAGAAATGAAAAA 2798  
| | | | |  
Db 25 TGTATGTGTTAAAAA 1  
  
RESULT 2188  
AAC96219/c  
ID AAC96219 standard; DNA; 25 BP.  
XX  
AC AAC96219;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #186.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 47; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in

CC particular  
XX Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;  
SQ  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2779 AGAATTGAAAAA 2803  
| | | | |  
Db 25 ACAATGGGGAAAAA 1  
  
RESULT 2189  
AAC96598/c  
ID AAC96598 standard; DNA; 25 BP.  
XX  
AC AAC96598;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DRB345 gene PCR primer #69.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 54; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 5 A; 3 C; 2 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA 2797  
| | | | |  
Db 17 AATTGAAAAA 1  
  
RESULT 2190  
AAC96121  
ID AAC96121 standard; DNA; 25 BP.  
XX











XX WO200122972-A2.  
 PN  
 XX  
 PD 05-APR-2001.  
 XX  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 DR WPI; 2001-273485/28.  
 XX  
 XX Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 PT  
 XX  
 PS Claim 101; Page 56; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 17; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
 Db 9 TTTT TTTT TTTT TTTT TTTT 25  
 RESULT 2201  
 AAF99738/c  
 ID AAF99738 standard; DNA; 25 BP.  
 XX  
 AC AAF99738;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #854.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000WO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX  
 PI Krieg AM, Schetter C, Vollmer J;  
 XX  
 DR WPI; 2001-273485/28.  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Claim 101; Page 56; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone  
 XX  
 SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
 Query Match 0.6%; Score 17; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2786 AAAAAA AAAAAA AAAAAA 2802  
 Db 25 AAAAAA AAAAAA AAAAAA 9  
 RESULT 2202  
 AAH39959/c  
 ID AAH39959 standard; DNA; 25 BP.  
 XX  
 AC AAH39959;  
 XX  
 DT 14-AUG-2001 (first entry)  
 XX  
 DE SNP specific SNPE primer SEQ ID 2755.  
 XX  
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
 KW Lesh-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
 KW inflammation; forensic investigation; paternity analysis; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200129262-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028436.  
 XX  
 PR 15-OCT-1999; 99US-0160096P.  
 XX  
 PA (ORCH-) ORCHID BIOSCIENCES INC.  
 XX  
 PI Picoult-Newburg L, Pohl M;  
 XX  
 DR WPI; 2001-290930/30.







CC in the specification  
XX  
SQ Sequence 25 BP; 13 A; 3 C; 3 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2774 TTGTTAGAAATTGAAAAA 2798  
Db 1 TTGATCGCAATTGTCAAAAAA 25  
  
RESULT 2207  
ABQ94375  
ID ABQ94375 standard; DNA; 25 BP.  
XX  
AC ABQ94375;  
XX  
DT 28-OCT-2002 (first entry)  
XX  
DE Tumour suppression-related oligonucleotide #26.  
XX  
KW Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;  
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;  
KW viral infection; cell degeneration disease; neurodegeneration; ds;  
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.  
XX  
OS Homo sapiens.  
XX  
PN FR2819824-A1.  
XX  
PD 26-JUL-2002.  
XX  
PF 23-JAN-2001; 2001FR-000000899.  
XX  
PR 23-JAN-2001; 2001FR-000000899.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB SA.  
XX  
PI Telerman A, Amson R, Tuijnder M, Susini L;  
XX  
DR WPI; 2002-610803/66.  
XX  
PT New nucleic acid implicated e.g. in tumor suppression, useful for  
PT diagnosis of tumors, viral infection and cellular degeneration and for  
PT drug screening.  
XX  
PS Claim 1; Page 46; 623pp; French.  
XX  
CC The present invention relates to novel human nucleic acid sequences (I).  
CC The present sequence is one such nucleic acid sequence. Expression of (I)  
CC are implicated in tumour suppression or reversion and apoptosis and viral  
CC resistance. (I) are useful as probes or primers for detecting,  
CC identifying, measuring and/or amplifying nucleic acid sequences, as  
CC antisense reagents and for recombinant production of polypeptides. (I),  
CC polypeptides (II) encoded by (I), vector containing (I), cells containing  
CC these vectors and antibodies (Ab) against (II) are all useful for  
CC treatment/prevention of viral, tumour and cell degeneration diseases  
CC (especially neurodegeneration, such as Alzheimer's disease and  
CC schizophrenia). Analysing the expression of (I) is also useful for  
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying  
CC (I) are used for studying the aetiology of these diseases (also immune  
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1  
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown  
CC in the specification  
XX  
SQ Sequence 25 BP; 13 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2774 TTGTTAGAAATTGAAAAA 2798  
Db 1 TTGATCGCAATTGTCAAAAAA 25  
  
RESULT 2208  
ABS76278  
ID ABS76278 standard; DNA; 25 BP.  
XX  
AC ABS76278;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1804.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX  
DR WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 312; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 1 A; 7 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2312 GCAATTTGTTGCTGTGTGTCACCCC 2336  
Db 1 GCCAGTTGTTGCTGTGTGTTGTTCCC 25

RESULT 2209  
ABS75770/c  
ID ABS75770 standard; DNA; 25 BP.  
XX  
AC ABS75770;  
XX  
DT 27-DEC-2002 (first entry)

XX DE Human PAPP-Ea associated 25-mer SEQ ID 1296.  
XX KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
XX KW dysgenetic pregnancy; primer; ss.  
OS Homo sapiens.  
XX PN US2002102252-A1.  
XX PD 01-AUG-2002.  
XX PF 06-APR-2001; 2001US-00827998.  
XX XX 26-MAY-2000; 2000US-0207456P.  
PR XX (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX PI Gu Y, Shannon ME;  
XX DR WPI; 2002-697817/75.  
XX PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX XX Example 2; Page 245; 353pp; English.  
XX CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX SQ Sequence 25 BP; 16 A; 0 C; 9 G; 0 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1770 CTTTCTTTTGTGACCCCATTTCTT 1794  
Db 25 CTTTCTTTTGTGACCCCATTTCTT 1  
RESULT 2210  
ABS76277  
ID ABS76277 standard; DNA; 25 BP.  
XX AC ABS76277;  
XX XX 27-DEC-2002 (first entry)  
DT Human PAPP-E exon 7 associated 25-mer SEQ ID 1803.  
DE PAPP-E; human; pregnancy associated plasma protein E; abortive;  
XX KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW KW dysgenetic pregnancy; primer; ss.  
XX OS Homo sapiens.  
XX PN US2002102252-A1.  
XX XX 01-AUG-2002.  
PD

XX PF 06-APR-2001; 2001US-00827998.  
XX XX 26-MAY-2000; 2000US-0207456P.  
PR XX (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX PI Gu Y, Shannon ME;  
XX DR WPI; 2002-697817/75.  
XX XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
PT XX Example 2; Page 312; 353pp; English.  
PS This invention describes a novel isolated nucleic acid that encodes one  
XX of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX SQ Sequence 25 BP; 2 A; 6 C; 7 G; 10 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2311 AGCAATTGTTGCTGCTGTTCACCC 2335  
Db 1 AGCCAGTTGTTGCTGCTGTGTTC 25  
RESULT 2211  
ADB04575  
ID ADB04575 standard; DNA; 25 BP.  
XX AC ADB04575;  
XX XX 20-NOV-2003 (first entry)  
DT Human MD27 scanning oligonucleotide SEQ ID 5561.  
DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;  
KW KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW KW developmental disorder; ss.  
XX OS Homo sapiens.  
XX XX EP1281758-A2.  
XX XX 05-FEB-2003.  
PD 30-JUL-2002; 2002EP-00016874.  
PF 02-AUG-2001; 2001US-00922181.  
XX XX (AEOM-) AEOMICA INC.  
XX PA Shannon M, Gu Y, Nguyen C;  
PI WPI; 2003-423107/40.  
XX DR



PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5561; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2165 CTTTCTTTTCTTTTCTTTT 2181  
Db 1 CTTTCTTTTCTTTTCTTTT 17  
  
RESULT 2212  
ADB04574  
ID ADB04574 standard; DNA; 25 BP.  
XX  
AC ADB04574;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5560.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5560; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2165 CTTTCTTTTCTTTTCTTTT 2181  
Db 2 CTTTCTTTTCTTTTCTTTT 18  
  
RESULT 2213  
ABV76902  
ID ABV76902 standard; DNA; 25 BP.  
XX  
AC ABV76902;  
XX  
DT 12-FEB-2003 (first entry)  
XX  
DE Inverse-PCR primer used to identify MudJ-fusion sequences.  
XX  
KW Enterobacteriaceae; Pseudomonad; cellulose; yhjONML operon;  
KW bacterial cellulosebiosynthesis; bcsABZc; bacterial cellulose synthesis;  
KW adra gene; putative transmembrane protein; MudJ; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200264817-A2.  
XX  
PD 22-AUG-2002.  
XX  
PF 08-FEB-2002; 2002WO-EP001360.  
XX  
PR 09-FEB-2001; 2001EP-00102809.  
PR 12-DEC-2001; 2001EP-00129280.  
XX  
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
XX  
PI Roemling U, Zogaj X, Nimtz M;  
XX  
DR WPI; 2003-058290/05.  
XX  
PT Use of a bacteria comprising bcsABZc operon in their chromosome and  
PT expressing the adra gene, for producing cellulose and for screening  
PT inhibitors of bacterial cellulose biosynthesis.  
XX  
PS Disclosure; Page 24; 47pp; English.  
XX  
CC The specification describes the use of a bacteria selected from  
CC Enterobacteriaceae and Pseudomonads for producing cellulose or for  
CC screening inhibitors of bacterial cellulosebiosynthesis. The bacteria  
CC comprise the bcsABZc (bacterial cellulose synthesis) operon (formerly  
CC yhjONML operon) in their chromosome and express the adra gene (encoding  
CC putative transmembrane protein). The bacteria are useful for producing  
CC cellulose and for screening inhibitors of bacterial cellulose  
CC biosynthesis. Inverse PCR primers ABV76901-02 were used to identify MudJ-  
CC fusion sequences, in the course of the invention  
XX

SQ Sequence 25 BP; 5 A; 7 C; 5 G; 8 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2613 AGAAGCAATAACTTTGTCTCGTTC 2637  
|| |||||  
Db 1 AGTGGCAATAACTTGCTCTCGTTC 25  
RESULT 2214  
ACI00609/c  
ID ACI00609 standard; DNA; 25 BP.  
XX  
AC ACI00609;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 600.  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 600; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 2 A; 8 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1269 AAGACCGGACACCCCATGGGACCAG 1293  
|||||  
Db 25 AAGACAGGACACGTC AAGGGACCTG 1  
RESULT 2215  
ACI03338/c  
ID ACI03338 standard; DNA; 25 BP.  
XX  
AC ACI03338;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human microarray DNA oligonucleotide SEQ ID NO 3329.  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 3329; 9pp; English.  
XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 3 A; 9 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1536 GGTAGGAGAGTAGGGAAGAACAG 1560  
||||| ||| ||||| ||||| |||||  
Db 25 GGTACGACAAATAGGACGACCAG 1

RESULT 2216  
ACI61004/c  
ID ACI61004 standard; DNA; 25 BP.  
XX AC ACI61004;  
XX DT 13-OCT-2003 (first entry)  
XX DE Human microarray DNA oligonucleotide SEQ ID NO 60995.  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX Homo sapiens.  
XX OS US2003104410-A1.  
XX PN 05-JUN-2003.  
XX PD 15-MAR-2002; 2002US-00098263.  
XX PF 16-MAR-2001; 2001US-0276759P.  
XX PR (AFFY-) AFFYMETRIX INC.  
XX PA Mittmann MP;  
XX PI WPI; 2003-567953/53.  
XX DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
XX sequence or specific mutations of any gene.  
PS Claim 1; SEQ ID NO 60995; 9pp; English.  
XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridisation to a DNA library,  
XX in analysis of genetic variation or in hybridisation of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridising at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridisation. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying biallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-  
XX blot hybridisation to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at seqdata.uspto.gov/sequence.html  
SQ Sequence 25 BP; 5 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 572 GTGAGCGCCCGCAGGATGCCTACC 596  
||||| ||||| ||||| ||||| |||||  
Db 25 GTGAGCGACCGCTGGGCTACCTTCC 1

RESULT 2217  
ACI89380/c  
ID ACI89380 standard; DNA; 25 BP.  
XX AC ACI89380;  
XX DT 14-OCT-2003 (first entry)  
XX DE Human microarray DNA oligonucleotide SEQ ID NO 89371.  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX Homo sapiens.  
XX OS US2003104410-A1.  
XX PN 05-JUN-2003.  
XX PD 15-MAR-2002; 2002US-00098263.  
XX PF 16-MAR-2001; 2001US-0276759P.  
XX PR (AFFY-) AFFYMETRIX INC.  
XX PA Mittmann MP;  
XX PI WPI; 2003-567953/53.  
XX DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
XX sequence or specific mutations of any gene.  
PS Claim 1; SEQ ID NO 89371; 9pp; English.  
XX The invention discloses a microarray comprising a plurality of nucleic  
XX acid probes including one of 2,018,500 fully defined sequences, or its  
XX perfect match, perfect mismatch, antisense match or antisense mismatch.  
XX Also disclosed is a method of gene expression analysis. The array is used  
XX in monitoring gene expression levels by hybridisation to a DNA library,  
XX in analysis of genetic variation or in hybridisation of tag-labelled  
XX compounds. The nucleic acid probes are specifically designed for analysis  
XX of at least one target sequence. The method of analysis comprises  
XX hybridising at least one or more nucleic acids to at least two or more  
XX nucleic acid probes and detecting the hybridisation. The nucleic acid  
XX probes are attached to a solid support. The analysis comprises monitoring  
XX gene expression levels, identifying biallelic markers or polymorphisms,  
XX or family members of a gene and a cross-species comparison. Each of the  
XX nucleic acids further comprises a tag sequence. The array of nucleic acid  
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-  
XX blot hybridisation to identify or detect the sequence or specific  
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by  
XX primer extensions or in screening cDNA or genomic libraries or subclones  
XX for additional subclones containing segments of DNA that have been  
XX isolated and previously sequenced. The sequence presented is one of the  
XX nucleic acid probes incorporated in the microarray. Note: The sequence  
XX data for this patent can also be obtained in electronic format directly  
XX from USPTO at seqdata.uspto.gov/sequence.html  
SQ Sequence 25 BP; 12 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2425 ACTGGTGCACTTCTTACGACTTTT 2449  
||||| ||||| ||||| ||||| |||||



Db	25	ATTGGTGGATTCTTACCACCTTTAT	1
RESULT 2218			
ACI62001			
ID	ACI62001	standard; DNA; 25 BP.	
XX			
AC	ACI62001;		
XX			
DT	13-OCT-2003	(first entry)	
XX			
DE	Human microarray DNA oligonucleotide SEQ ID NO 61992.		
XX			
KW	EST; ss; probe; expressed sequence tag; microarray; gene expression;		
KW	genetic variation; biallelic marker; polymorphism; human;		
KW	cross-species comparison.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003104410-A1.		
XX			
PD	05-JUN-2003.		
XX			
PF	15-MAR-2002; 2002US-00098263.		
XX			
PR	16-MAR-2001; 2001US-0276759P.		
XX			
PA	(AFFY-) AFFYMETRIX INC.		
XX			
PI	Mittmann MP;		
XX			
DR	WPI; 2003-567953/53.		
XX			
PT	New array of nucleic acid probes, useful for in situ hybridization, in		
PT	Southern, Northern or dot-blot hybridization to identify or detect the		
PT	sequence or specific mutations of any gene.		
XX			
PS	Claim 1; SEQ ID NO 61992; 9pp; English.		
XX			
CC	The invention discloses a microarray comprising a plurality of nucleic		
CC	acid probes including one of 2,018,500 fully defined sequences, or its		
CC	perfect match, perfect mismatch, antisense match or antisense mismatch.		
CC	Also disclosed is a method of gene expression analysis. The array is used		
CC	in monitoring gene expression levels by hybridisation to a DNA library,		
CC	in analysis of genetic variation or in hybridisation of tag-labelled		
CC	compounds. The nucleic acid probes are specifically designed for analysis		
CC	of at least one target sequence. The method of analysis comprises		
CC	hybridising at least one or more nucleic acids to at least two or more		
CC	nucleic acid probes and detecting the hybridisation. The nucleic acid		
CC	probes are attached to a solid support. The analysis comprises monitoring		
CC	gene expression levels, identifying biallelic markers or polymorphisms,		
CC	or family members of a gene and a cross-species comparison. Each of the		
CC	nucleic acids further comprises a tag sequence. The array of nucleic acid		
CC	probes is useful in in situ hybridisation, in Southern, Northern or dot-		
CC	blot hybridisation to identify or detect the sequence or specific		
CC	mutations of any gene, in mapping the 5' termini of mRNA molecules by		
CC	primer extensions or in screening cDNA or genomic libraries or subclones		
CC	for additional subclones containing segments of DNA that have been		
CC	isolated and previously sequenced. The sequence presented is one of the		
CC	nucleic acid probes incorporated in the microarray. Note: The sequence		
CC	data for this patent can also be obtained in electronic format directly		
CC	from USPTO at seqdata.uspto.gov/sequence.html		
XX			
SQ	Sequence 25 BP; 4 A; 4 C; 6 G; 11 T; 0 U; 0 Other;		
Query Match	0.6%;	Score 17; DB 1; Length 25;	
Best Local Similarity	80.0%;	Pred. No. 2.3e+03;	
Matches	20; Conservative	0; Mismatches 5; Indels	0; Gaps 0;
QY	1917 ATACCTTTTTTTTCAGTGTTAAGGT	1941	
Db	1	AGACTTGCTCTTCAGTGTTCAGGT	25

RESULT 2219			
ACI30406/c			
ID	ACI30406	standard; DNA; 25 BP.	
XX			
AC	ACI30406;		
XX			
DT	13-OCT-2003	(first entry)	
XX			
DE	Human microarray DNA oligonucleotide SEQ ID NO 30397.		
XX			
KW	EST; ss; probe; expressed sequence tag; microarray; gene expression;		
KW	genetic variation; biallelic marker; polymorphism; human;		
KW	cross-species comparison.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003104410-A1.		
XX			
PD	05-JUN-2003.		
XX			
PF	15-MAR-2002; 2002US-00098263.		
XX			
PR	16-MAR-2001; 2001US-0276759P.		
XX			
PA	(AFFY-) AFFYMETRIX INC.		
XX			
PI	Mittmann MP;		
XX			
DR	WPI; 2003-567953/53.		
XX			
PT	New array of nucleic acid probes, useful for in situ hybridization, in		
PT	Southern, Northern or dot-blot hybridization to identify or detect the		
PT	sequence or specific mutations of any gene.		
XX			
PS	Claim 1; SEQ ID NO 30397; 9pp; English.		
XX			
CC	The invention discloses a microarray comprising a plurality of nucleic		
CC	acid probes including one of 2,018,500 fully defined sequences, or its		
CC	perfect match, perfect mismatch, antisense match or antisense mismatch.		
CC	Also disclosed is a method of gene expression analysis. The array is used		
CC	in monitoring gene expression levels by hybridisation to a DNA library,		
CC	in analysis of genetic variation or in hybridisation of tag-labelled		
CC	compounds. The nucleic acid probes are specifically designed for analysis		
CC	of at least one target sequence. The method of analysis comprises		
CC	hybridising at least one or more nucleic acids to at least two or more		
CC	nucleic acid probes and detecting the hybridisation. The nucleic acid		
CC	probes are attached to a solid support. The analysis comprises monitoring		
CC	gene expression levels, identifying biallelic markers or polymorphisms,		
CC	or family members of a gene and a cross-species comparison. Each of the		
CC	nucleic acids further comprises a tag sequence. The array of nucleic acid		
CC	probes is useful in in situ hybridisation, in Southern, Northern or dot-		
CC	blot hybridisation to identify or detect the sequence or specific		
CC	mutations of any gene, in mapping the 5' termini of mRNA molecules by		
CC	primer extensions or in screening cDNA or genomic libraries or subclones		
CC	for additional subclones containing segments of DNA that have been		
CC	isolated and previously sequenced. The sequence presented is one of the		
CC	nucleic acid probes incorporated in the microarray. Note: The sequence		
CC	data for this patent can also be obtained in electronic format directly		
CC	from USPTO at seqdata.uspto.gov/sequence.html		
XX			
SQ	Sequence 25 BP; 10 A; 5 C; 4 G; 6 T; 0 U; 0 Other;		
Query Match	0.6%;	Score 17; DB 1; Length 25;	
Best Local Similarity	80.0%;	Pred. No. 2.3e+03;	
Matches	20; Conservative	0; Mismatches 5; Indels	0; Gaps 0;
QY	2234 GTTCCCTTAAGGTACTGAAGCTTTA	2258	
Db	25	GTTAGTTACGGTACTGAACCTTTA	1

RESULT 2220



ACK15478  
ID ACK15478 standard: DNA: 25 BP.

ACK15478;

DT 14-OCT-2003 (first entry)

Human microarray DNA oligonucleotide SEQ ID NO 115459.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; biallelic marker; polymorphism; human;  
 KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Mittmann MP:

DR WPI: 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

PS Claim 1: SEO ID NO 115459: 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

SQ Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match	0.6%;	Score 17;	DB 1;	Length 25;
Best Local Similarity	80.0%;	Pred. No. 2.3e+03;		
Matches 20;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

**Qy** 541 GCCCACCTCTCCGGGCTGGAGCG 565  
| | | | |  
**Dβ** 1 GTCCCGACTCTCCTGGGTGGAGTCG 25

RESULT 2221  
ACI02702/c  
ID ACI02702 standard; DNA; 25 BP.

XX  
AC AC102702;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 2693.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

OS Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

PI Mitmann MP;

DR WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 2693; 9pp; English.

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Sequence 25 BP; 3 A; 8 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy**      1535 AGGTTAGGACAGCTAGCGGAAGGAACA 1559  
          ||||| | | | | | | | | |  
**p6**         25 AGGTTACGCACAATAGGGACGGACCA 1

RESULT 2222  
ACI83696/C  
ID ACI83696 standard; DNA; 25 BP.  
XX  
AC ACI83696;

XX 14-OCT-2003 (first entry)  
DT Human microarray DNA oligonucleotide SEQ ID NO 83687.  
XX  
DE EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 83687; 9pp; English.  
PS  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 8 A; 9 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2343 CCCGTGGAGGTTCTGTATTTAAGA 2367  
| | | | | | | | | | | | | | | | | | | |  
Db 25 CCCGTGGAGCTTCTGTGTTGGAGA 1  
RESULT 2223  
ACK11064/c  
ID ACK11064 standard; DNA; 25 BP.  
XX  
AC ACK11064;  
XX  
DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 111045.  
DE  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX  
OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.  
XX  
XX New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
XX Claim 1; SEQ ID NO 111045; 9pp; English.  
PS  
XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 25 BP; 12 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2341 TCCCGTGGAGGTTCTGTATTTAA 2365  
| | | | | | | | | | | | | | | | | | | |  
Db 25 TTCTCGTTGAGGTTCTGTGTATTAA 1  
RESULT 2224  
ACH03276  
ID ACH03276 standard; DNA; 25 BP.  
XX  
AC ACH03276;  
XX  
DT 25-SEP-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #911.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
XX US2003050268-A1.  
XX 13-MAR-2003.  
XX 29-MAR-2002; 2002US-00112653.  
XX 29-MAR-2001; 2001US-0279642P.  
XX (KRIE//) KRIEG A M.  
XX (BERG//) BERG D J.  
XX Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 33; 229pp; English.  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 9 TTTT TTTT TTTT TTTT TTTT 25  
RESULT 2225  
ACH03276/c  
ID ACH03276 standard; DNA; 25 BP.  
XX ACH03276;  
AC ACH03276;  
XX 25-SEP-2003 (first entry)  
DT Immunostimulatory nucleic acid #911.  
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
DE antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
XX Synthetic.  
OS US2003050268-A1.  
XX 13-MAR-2003.  
XX 29-MAR-2002; 2002US-00112653.  
XX 29-MAR-2001; 2001US-0279642P.  
PR

XX (KRIE//) KRIEG A M.  
PA (BERG//) BERG D J.  
XX Krieg AM, Berg DJ;  
XX WPI; 2003-521815/49.  
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
PT disease by administering an immunostimulatory nucleic acid.  
XX Disclosure; Page 33; 229pp; English.  
XX The invention describes a method of treating non-allergic inflammatory  
CC disease comprising administering to a subject having or at risk of  
CC developing a non-allergic inflammatory disease an immunostimulatory  
CC nucleic acid for prevention or treatment of the disease. The method is  
CC useful for treating non-allergic inflammatory diseases, such as  
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
CC This sequence represents an immunostimulatory nucleic acid  
XX Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 25 AAAAAAAAAAAAAAAAAA 9  
RESULT 2226  
ADB37240  
ID ADB37240 standard; DNA; 25 BP.  
XX ADB37240;  
AC ADB37240;  
XX 04-DEC-2003 (first entry)  
DT Immunostimulatory nucleic acid #854.  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX Synthetic.  
OS US2003087848-A1.  
XX 08-MAY-2003.  
PD 02-FEB-2001; 2001US-00776479.  
XX 03-FEB-2000; 2000US-0179991P.  
PR (BRAT//) BRATZLER R L.  
PA (PETE//) PETERSEN D M.  
XX (FOUR//) FOURON Y.  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI WPI; 2003-657977/62.  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
XX Disclosure; Page 18; 221pp; English.  
PS The invention relates to a method of treating or preventing allergy or  
XX asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC

CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 9 TTTT TTTT TTTT TTTT TTTT 25  
  
RESULT 2227  
ADB37240/c  
ID ADB37240 standard; DNA; 25 BP.  
XX  
AC ADB37240;  
XX  
DT 04-DEC-2003 (first entry)  
XX Immunostimulatory nucleic acid #854.  
DE  
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
KW hypo-responsive subject; immunostimulatory.  
XX  
OS Synthetic.  
XX US2003087848-A1.  
PN  
XX 08-MAY-2003.  
PD  
XX 02-FEB-2001; 2001US-00776479.  
PF  
XX 03-FEB-2000; 2000US-0179991P.  
PR  
XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
PI WPI; 2003-657977/62.  
XX  
XX Treating and/or preventing allergy or asthma using an immunostimulatory  
PT nucleic acid alone or in combination with an asthma/allergy medicament.  
PT  
XX  
PS Disclosure; Page 18; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
CC asthma which comprises administering to a subject a poly-G nucleic acid  
CC in an aerosol formulation. The methods and compositions of the present  
CC invention are useful for diagnosing and/or treating asthma and allergy  
CC especially in a hypo-responsive subject. The present sequence represents  
CC an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 25 AAAAAAAAAAAAAAAAAA 9  
  
RESULT 2228  
AAT99265/c  
ID AAT99265 standard; DNA; 26 BP.  
XX

AC AAT99265;  
XX  
DT 15-APR-1998 (first entry)  
XX  
DE Human PUR-alpha gene primer PDT-01.  
XX  
DE PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;  
KW cancer; PCR; primer; amplification.  
KW  
XX Synthetic.  
OS Homo sapiens.  
XX  
PN US5672479-A.  
XX  
PD 30-SEP-1997.  
XX  
PF 07-JUN-1995; 95US-00486421.  
XX  
PR 28-AUG-1992; 92US-00938189.  
PR 02-FEB-1993; 93US-00014943.  
PR 06-JUN-1995; 95US-00470911.  
XX  
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
XX Bergemann AD, Johnson EM;  
PI WPI; 1997-488859/45.  
XX  
XX Assays for PUR protein ligands or modulators - using immobilised PUR  
PT protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.  
PT  
XX Disclosure; Col 9; 64pp; English.  
XX  
XX The primers AAT99265-T99269 were used to PCR amplify and isolate the  
CC complete sequence of the human PUR-alpha gene (AAT99264). The PUR  
CC sequence can be used to identify chemical or biological compounds that  
CC bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may  
CC be used to treat hyperproliferative diseases such as cancer  
XX  
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 26 AAAAAAAAAAAAAAAAAA 10  
  
RESULT 2229  
AAV31721/c  
ID AAV31721 standard; DNA; 26 BP.  
XX  
AC AAV31721;  
XX  
DT 24-SEP-1998 (first entry)  
XX  
XX Nucleotide sequence of the PUR specific PCR primer.  
DE  
XX PUR-alpha gene; inhibition; viral infection; cancer; PCR; primer;  
KW hyperproliferative disease; amplification; ss.  
KW  
XX Synthetic.  
OS Homo sapiens.  
XX  
PN US5756684-A.  
XX  
PD 26-MAY-1998.  
XX  
PF 06-JUN-1995; 95US-00470911.  
XX  
PR 28-AUG-1992; 92US-00938189.



PR 02-FEB-1993; 93US-00014943.  
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
PA Bergemann AD, Johnson EM;  
XX WPI; 1998-321632/28.  
DR  
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR  
PT element or other proteins.  
XX  
PS Disclosure; Col 9; 63pp; English.  
XX  
CC This is the nucleotide sequence of the PUR pscific PCR primer used for  
CC amplification in the method of the invention, involving the use of the  
CC PUR protein and its fragments, which inhibit PUR protein binding to PUR  
CC element or other proteins. Inhibitors of PUR activity may be useful for  
CC treating viral infections and hyperproliferative diseases such as cancer  
XX  
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 26 AAAAAAAAAAAAAA 10  
RESULT 2230  
AAX04087/c  
ID AAX04087 standard; DNA; 26 BP.  
XX  
AC AAX04087;  
XX  
DT 12-APR-1999 (first entry)  
XX  
DE PUR-alpha RACE reaction primer PDT-01.  
XX  
KW PUR element; PUR-alpha; hyperproliferative disease; cancer; human;  
KW monoclonal antibody; identification; characterisation; RACE primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX US5869622-A.  
XX  
PD 09-FEB-1999.  
XX  
PF 07-JUN-1995; 95US-00486809.  
XX  
PR 28-AUG-1992; 92US-00938189.  
PR 02-FEB-1993; 93US-00014943.  
PR 06-JUN-1995; 95US-00470911.  
XX  
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
XX  
PI Bergemann AD, Johnson EM;  
XX  
DR WPI; 1999-152881/13.  
XX  
PT Monoclonal antibody specific for PUR protein - useful for treating  
PT cancer.  
XX  
PS Example; Col 9; 64pp; English.  
XX  
CC The present invention describes a monoclonal antibody that specifically  
CC binds to an epitope of the PUR protein. Antibodies that bind to the PUR  
CC protein and neutralise PUR activity may be used to treat  
CC hyperproliferative diseases such as cancer. PUR antibodies may be used  
CC diagnostically to detect aberrant expression of the PUR protein and/or  
CC mutations in the PUR gene. The present sequence represents a PUR-alpha

CC RACE primer which is used in an example from the present invention  
XX  
SQ Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 26 AAAAAAAAAAAAAA 10  
RESULT 2231  
AAS01630/c  
ID AAS01630 standard; DNA; 26 BP.  
XX  
AC AAS01630;  
XX  
DT 18-JUL-2001 (first entry)  
XX  
DE Human CACNA1G R6 3'-target sequence for bisulfite PCR.  
XX  
KW Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;  
KW cellular proliferative disorder; colorectal cancer; age related disease;  
KW apolipoprotein B; APOB; caudal type homeobox transcription factor 2;  
KW CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBN1;  
KW G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';  
KW HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;  
KW PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;  
KW patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;  
KW chromosome 17; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119845-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 14-SEP-2000; 2000WO-US025479.  
XX  
PR 15-SEP-1999; 99US-00398522.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Issa J;  
XX  
DR WPI; 2001-244777/25.  
XX  
PT New nucleic acid molecule for use as a marker for screening cancer,  
PT comprises the coding region for a T-type calcium channel and regulatory  
PT sequences associated with the channel.  
PS Claim 20; Page 37; 125pp; English.  
XX  
CC The present sequence for human T-type calcium channel R6 3'-target  
CC sequence (complementary to the 3'-bisulfite PCR primer) is used to study  
CC the methylation state of R6 of CACNA1G which maps to chromosome 17. The  
CC methylation state of specific regions within CpG islands associated with  
CC the CACNA1G gene correlate with several cancerous phenotypes involving  
CC various tissue and cell types. Since aberrant methylation of normally  
CC unmethylated CpG islands is often observed in immortalised and  
CC transformed cells, CACNA1G is implicated in cellular proliferative  
CC disorders e.g. leukaemia, colorectal, lung, breast and other cancers. The  
CC nucleic acid coding for CACNA1G is useful as a marker for screening  
CC cancer and age related diseases. A diagnostic kit containing primers  
CC (AAS01574-AAS01623) for amplification of a CpG-containing nucleic acid,  
CC where the primer hybridises with a target polynucleotide sequence  
CC (AAS01627-AAS01676), can be used for detecting aberrant methylation. The  
CC CpG island sequences (AAS01677-AAS01692) are selected from genes encoding  
CC CACNA1G, apolipoprotein B (APOB), caudal type homeobox transcription  
CC factor 2 (CDX2), epidermal growth factor receptor (EGFR), fibrillin-1  
CC (FBN1), G protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6



KW Cotton fibre; promoter; differential screening; leaf; ovule; root;  
KW flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.  
XX  
OS Synthetic.  
XX  
PN US5521078-A.  
XX  
PD 28-MAY-1996.  
XX  
PF 19-OCT-1994; 94US-00298687.  
XX  
PR 04-OCT-1988; 88US-00253243.  
PR 21-NOV-1990; 90US-00617239.  
PR 18-MAY-1992; 92US-00885970.  
XX  
PA (CETU ) AGRACETUS INC.  
XX  
PI John M;  
XX  
DR WPI; 1996-267794/27.  
XX  
PT Isolation of fibre-specific cotton promoter sequences - using selected  
PT DNA probes to screen genomic DNA fragments, for production of cotton  
PT fibres with improved characteristics.  
XX  
PS Example; Col 23; 46pp; English.  
XX  
CC Cotton fibre cell-specific promoter sequences were isolated by  
CC differential screening of a cotton plant cDNA library. Of 4788 clones  
CC from a 10 day cell library screened with leaf cDNAs, 800 clones not  
CC present in the leaf were isolated. These were screened with cDNAs from  
CC ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR  
CC analysis was then used to remove cross-hybridising clones. This resulted  
CC in the isolation of 18 cDNA clones specifically expressed in cotton fibre  
CC cells (AAT30242-4 and AAT30253-67). These cDNAs were then used to screen  
CC for homologous genomic sequences (AAT30245-53 and AAT30268) in order to  
CC obtain the corresp. promoter sequences. This primer was used to generate  
CC the first cDNA strand from mRNA isolated from the cotton fibre cells. The  
CC promoters isolated from the fibre cell-specific clones can be used to  
CC generate transgenic cotton plants and lines producing fibres having  
CC altered quantity and quality. (Updated on 25-MAR-2003 to correct PF  
CC field.)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTT TTTT TTTT TTTT TTTT 2180  
Db ||||| ||||| ||||| ||||| |||||  
10 CCTTTT TTTT TTTT TTTT TTTT 26  
  
RESULT 2235  
AAT43363  
ID AAT43363 standard; DNA; 26 BP.  
XX  
AC AAT43363;  
XX  
DT 11-MAR-1997 (first entry)  
XX  
DE Cotton fibre first strand cDNA primer.  
XX  
KW FbLate; promoter; fibre; transgenic plant; cotton; Gossypium hirsutum;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9639021-A1.  
XX  
PD 12-DEC-1996.  
XX

PF 06-JUN-1996; 96WO-US009449.  
XX  
PR 06-JUN-1995; 95US-00467504.  
XX  
PA (MONS ) MONSANTO CO.  
XX  
PI John ME;  
XX  
DR WPI; 1997-042726/04.  
XX  
PT Plant fibre-specific, developmentally regulated FbLate promoter - useful  
PT for producing transgenic plants, esp. cotton, with altered fibre  
PT properties.  
XX  
PS Example 2; Page 15; 79pp; English.  
XX  
CC A primer (AAT43363) was used for first strand cDNA synthesis from RNA  
CC obtd. from fibre cells of 23 day-old Coker 312 or 10 day-old Sea Island  
CC cotton bolls. The cDNA was used to construct a cDNA library from which  
CC cDNA clones (see also AAT43361-62) were isolated that corresponded to RNA  
CC prevalent in later fibre development. These clones were used to identify  
CC the FbLate promoter (AAT43360)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTT TTTT TTTT TTTT TTTT 2180  
Db ||||| ||||| ||||| ||||| |||||  
10 CCTTTT TTTT TTTT TTTT TTTT 26  
  
RESULT 2236  
AAT62627  
ID AAT62627 standard; cDNA to mRNA; 26 BP.  
XX  
AC AAT62627;  
XX  
DT 25-MAR-2003 (revised)  
DT 14-MAY-1997 (first entry)  
XX  
DE Primer for cotton fibre-specific cDNA amplification.  
XX  
KW cotton; fibre-specific; strength; transgenic plant; anthesis;  
KW developmentally regulated; E6; H6; antisense; sense; primer; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN US5597718-A.  
XX  
PD 28-JAN-1997.  
XX  
PF 20-SEP-1995; 95US-00530797.  
XX  
PR 04-OCT-1988; 88US-00253243.  
PR 21-NOV-1990; 90US-00617239.  
PR 18-OCT-1993; 93US-00138814.  
XX  
PA (CETU ) AGRACETUS.  
XX  
PI Brill WJ, Umbeck PF, John ME;  
XX  
DR WPI; 1997-108326/10.  
XX  
PT Prodn. of transgenic cotton plants - by transformation with the H6 coding  
PT sequence or E6 anti-sense sequence, produces fibre of altered strength.  
XX  
PS Example 1; Col 6; 33pp; English.  
XX  
CC AAT62627 is a primer used for first strand cDNA synthesis from mRNA  
CC isolated from cotton fibre cells at different stages of development.

CC Cotton fibre-specific cDNA clones (AAT62609-24) can be used to identify  
CC genomic clones by differential cDNA library screenings. Coding sequences  
CC from these isolated genes are used in sense or antisense orientation to  
CC alter the fibre characteristics, e.g. strength, of transgenic fibre-  
CC producing plants. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
Db 10 CCTTTTCTTTTCTTTTCTTTT 26  
  
RESULT 2237  
AAT63663  
ID AAT63663 standard; DNA; 26 BP.  
XX  
AC AAT63663;  
XX  
DT 25-MAR-2003 (revised)  
DT 11-JUN-1997 (first entry)  
XX  
DE Primer for cotton fibre-specific cDNA synthesis.  
XX  
KW primer; PCR; polymerase chain reaction; cotton fibre; seed floss fibre;  
KW promoter; peroxidase; production; fibre strength; Sea Island;  
KW Gossypium sp; Coker; Kapok; G. barbadense; ss.  
XX  
OS Synthetic.  
XX  
PN US5608148-A.  
XX  
PD 04-MAR-1997.  
XX  
PF 25-JAN-1995; 95US-00378588.  
XX  
PR 30-SEP-1993; 93US-00130086.  
XX  
PA (CETU ) AGRACETUS INC.  
XX  
PI John ME;  
XX  
DR WPI; 1997-164559/15.  
XX  
PT Transgenic cotton plants with increased fibre strength - are transformed  
PT with construct containing peroxidase gene.  
XX  
PS Disclosure; Col 31; 43pp; English.  
XX  
CC This primer sequence was used for first strand cDNA synthesis of mRNA  
CC from cotton fibre-specific library. Cotton plants whose genome contains  
CC heterologous genetic construct comprising a seed floss fibre (SPF)-  
CC specific promoter isolated from cotton plants and a coding sequence  
CC encoding a peroxidase are useful for production of cotton with increased  
CC fibre strength. The peroxidase genes are over-expressed in fibre and not  
CC in other plant tissues where it would be harmful to the plant. (Updated  
CC on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
Db 10 CCTTTTCTTTTCTTTTCTTTT 26  
  
RESULT 2237  
AAT63663  
ID AAT63663 standard; DNA; 26 BP.  
XX  
AC AAT63663;  
XX  
DT 25-MAR-2003 (revised)  
DT 11-JUN-1997 (first entry)  
XX  
DE Primer for cotton fibre-specific cDNA synthesis.  
XX  
KW primer; PCR; polymerase chain reaction; cotton fibre; seed floss fibre;  
KW promoter; peroxidase; production; fibre strength; Sea Island;  
KW Gossypium sp; Coker; Kapok; G. barbadense; ss.  
XX  
OS Synthetic.  
XX  
PN US5608148-A.  
XX  
PD 04-MAR-1997.  
XX  
PF 25-JAN-1995; 95US-00378588.  
XX  
PR 30-SEP-1993; 93US-00130086.  
XX  
PA (CETU ) AGRACETUS INC.  
XX  
PI John ME;  
XX  
DR WPI; 1997-164559/15.  
XX  
PT Transgenic cotton plants with increased fibre strength - are transformed  
PT with construct containing peroxidase gene.  
XX  
PS Disclosure; Col 31; 43pp; English.  
XX  
CC This primer sequence was used for first strand cDNA synthesis of mRNA  
CC from cotton fibre-specific library. Cotton plants whose genome contains  
CC heterologous genetic construct comprising a seed floss fibre (SPF)-  
CC specific promoter isolated from cotton plants and a coding sequence  
CC encoding a peroxidase are useful for production of cotton with increased  
CC fibre strength. The peroxidase genes are over-expressed in fibre and not  
CC in other plant tissues where it would be harmful to the plant. (Updated  
CC on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
Db 10 CCTTTTCTTTTCTTTTCTTTT 26  
  
RESULT 2237  
AAT63663  
ID AAT63663 standard; DNA; 26 BP.  
XX  
AC AAT63663;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-AUG-1997 (first entry)  
XX  
DE Primer for cotton fibre specific cDNA amplification.  
XX  
KW cotton; E6; fibre; promoter; transgenic plant; truncated;  
KW heterologous gene expression; primer; PCR; ss.  
XX  
OS Synthetic.  
XX  
PN US5620882-A.  
XX  
PD 15-APR-1997.  
XX  
PF 19-OCT-1994; 94US-00298829.  
XX  
PR 04-OCT-1988; 88US-00253243.  
PR 21-NOV-1990; 90US-00617239.  
PR 18-MAY-1992; 92US-00885970.  
XX  
PA (CETU ) AGRACETUS INC.  
XX  
PI John M;  
XX  
DR WPI; 1997-235185/21.  
XX  
PT DNA constructs contg. truncated promoter sequence - for fibre-specific  
PT gene expression in cotton plants.  
XX  
PS Example 1; Col 8; 48pp; English.  
XX  
CC AAT70058 is a primer used to synthesize first strand cDNA from mRNA  
CC isolated from cotton fibre cells at different stages of development.  
CC Claimed DNA constructs comprise a truncated promoter sequence (from one  
CC of AAT70031-38) that promotes preferential gene expression in plant fibre  
CC cells, a protein coding sequence not naturally associated with the  
CC promoter sequence and a 3' termination sequence. The DNA constructs are  
CC useful for expressing foreign genes in fibre-producing plants, esp. to  
CC produce transgenic cotton plants with varied cotton fibre characteristics  
CC and quality. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
Db 10 CCTTTTCTTTTCTTTTCTTTT 26  
  
RESULT 2239  
AAZ59153/C  
ID AAZ59153 standard; DNA; 26 BP.  
XX  
AC AAZ59153;  
XX  
DT 17-APR-2000 (first entry)  
XX  
DE Oligonucleotide #10 for DNA determination method.  
XX  
KW Oligonucleotide; restriction enzyme; PCR primer; amplification; template;  
KW vector; ss.  
XX  
OS Synthetic.  
XX







CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 2 A; 4 C; 4 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 27 AAAAAAAAAAAAAAAAAA 11  
RESULT 2244  
AAT70107/C  
ID AAT70107 standard; DNA; 28 BP.  
XX  
AC AAT70107;  
XX  
DT 24-SEP-1997 (first entry)  
XX  
DE PolyTV primer 2.  
XX  
KW primer; polymerase chain reaction; cDNA library; anchored end; PCSUB;  
KW lock-docking; screening; PCR-based cDNA subtractive cloning; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640998-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US008582.  
XX  
PR 07-JUN-1995; 95US-00481687.  
XX  
PA (PION-) PIONEER HI-BRED INT INC.  
XX  
PI Wang X, Duvick JP, Briggs SP;  
XX  
DR WPI; 1997-087067/08.  
XX  
PT Method for prodn. of cDNA libraries with anchored ends - useful for  
PT subtractive cloning of sequences of interest.  
XX  
PS Claim 1; Page 27; 56pp; English.  
XX  
CC The invention provides a PCR-based method for generating a full-length  
CC cDNA library with anchored ends. The method uses lock-docking primers  
CC (AAT70106-11), where one primer, poly TV (V = G,C or A) locks over the  
CC polyA tail of eukaryotic mRNA producing first strand synthesis and a  
CC second primer, polyGH (H = A, C or T) locks onto the polyC tail added by  
CC terminal deoxynucleotidyl transferase (Tdt). In the final step, AAT70112-  
CC 17 (polyAB and polyCD primers; B = G, T or C; D = G, A or T) are used to  
CC amplify the first strand and produce a cDNA library with anchored ends.  
CC cDNA libraries produced may be used to identify new (unique) nucleotide  
CC sequences from PCSUB (PCR-based cDNA subtractive) libraries. The new  
CC method produces discreet sized PCR products which would not necessarily  
CC require further subcloning/screening. The method also produces full-  
CC length cDNA's obtainable from the libraries as opposed to specific cDNA  
CC clones, as produced by previously known methods. Other methods such as  
CC PCR and RACE require a knowledge of the target sequence to be amplified,  
CC by using the PCSUB method no previous knowledge is necessary  
XX  
SQ Sequence 28 BP; 1 A; 4 C; 5 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 27 AAAAAAAAAAAAAAAAAA 11  
RESULT 2245  
ABK52626/C  
ID ABK52626 standard; DNA; 28 BP.  
XX  
AC ABK52626;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Minority genome method VIH-MUT-12 DNA sequence.  
XX  
KW Minority genome method; viral quasi-species; majority genome;  
KW genetic diagnosis; viral infection; human immune deficiency virus;  
KW hepatitis B; hepatitis C; antiviral therapy; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT misc\_difference 1 /\*tag= a  
FT /label= unknown  
FT /note= "C6 aminolinker sequence"  
XX  
PN WO200183815-A1.  
XX  
PD 08-NOV-2001.  
XX  
PF 27-APR-2001; 2001WO-ES000165.  
XX  
PR 27-APR-2000; 2000ES-00001068.  
XX  
PA (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.  
XX  
PI Arias Esteban A, Baranowski E, Briones Llorente C;  
PI Domingo Solans E, Escarmis Homs C, Gomez Castilla J;  
PI Martin Ruiz- Jarabo C, Parro Garcia V;  
XX  
DR WPI; 2002-147445/19.  
XX  
PT Detecting minority genomes in viral quasi-species, useful for identifying  
PT mutants responsible for drug resistance and to individualize therapy.  
XX  
PS Example 2; Page 55; 107pp; Spanish.  
XX  
CC The present invention relates to a new method for detecting minority  
CC genomes, present at less than 50%, in a population of nucleic acids of a  
CC viral quasi-species and having at least one mutation with respect to the  
CC majority genome. The invention can be used for genetic diagnosis of viral  
CC infections, especially human immune deficiency virus and hepatitis B or  
CC C, particularly to detect memory minority genomes that are implicated in  
CC failure of antiviral therapy, so the method may make possible design of  
CC therapies customised for individual patients. The present nucleic acid  
CC sequence represents the VIH-MUT-12 DNA sequence that was used in the  
CC methods of the invention  
XX  
SQ Sequence 28 BP; 3 A; 1 C; 4 G; 19 T; 0 U; 1 Other;  
Query Match 0.6%; Score 17; DB 1; Length 28;  
Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
OY 2780 GAATTGAAAAAAAAAAAAAAAAA 2804  
Db 28 GACTTTACACACAAAAAAAAAAAA 4  
RESULT 2246  
AAQ49467/c  
ID AAQ49467 standard; DNA; 29 BP.

XX AAQ49467;  
AC  
XX 14-APR-1994 (first entry)  
DT  
XX Oligo-dT primer "notldt" to amplify human NK3R C-terminal clone.  
DE  
XX human; neurokinin-3 receptor; NK3R; eledoisin; neurokinin B; tachykinin;  
KW enkephalin release; ss.  
KW  
XX Synthetic.  
OS  
XX GB2265375-A.  
PN  
XX 29-SEP-1993.  
PD  
XX 08-MAR-1993; 93GB-00004708.  
XX  
PR 16-MAR-1992; 92US-00851974.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
XX Fong TM, Huang RRC, Strader CD;  
PI  
XX WPI; 1993-305585/39.  
DR  
XX New recombinant human neurokinin-receptor - used to identify binding  
PT ligands, antagonists and agonists of the receptor.  
PT  
XX Example 1; Page 17; 46pp; English.  
PS  
XX Degenerate PCR primers were designed based on the known sequence of rat  
CC NK3R central transmembrane core. The corresponding human cDNA sequence  
CC was obtained by amplification of human brain cDNA. New primers corresp.  
CC to the human sequence were designed and anchored PCR was performed using  
CC the human primer in the core region. A primary PCR was carried out using  
CC primers "notldt" and "sl068" (AAQ49467 and AAQ49468, respectively) on  
CC template cDNA whose synthesis was initiated by "notldt". After two  
CC further rounds of PCR using "notldt", first with "sl106" (AAQ49469) and  
CC then with "sl137" (AAQ49470), a 600bp cDNA fragment which encodes the C-  
CC terminal region of human NK3R and the 3'-UTR was obtained and sequenced.  
CC The N-terminal coding region was similarly obtained. Finally a full-  
CC length cDNA (AAQ49461) was obtained in a single step using primers from  
CC the 5' and 3' untranslated regions. The human NK3R sequence will be  
CC useful for developing novel NK3 agonists and antagonists  
XX  
SQ Sequence 29 BP; 0 A; 4 C; 4 G; 21 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 29 AAAAAAAAAAAAAAAAAA 13  
RESULT 2247  
AAF74917  
ID AAF74917 standard; DNA; 29 BP.  
XX  
AC AAF74917;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:14.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX

PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
XX Crow MK, Li Y;  
PI  
XX WPI; 2001-244776/25.  
DR  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.  
PT  
XX Example 1; Fig 3; 90pp; English.  
PS  
XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention  
XX  
SQ Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 17; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 1 AAAAAAAAAAAAAAAAAA 17  
RESULT 2248  
AAF74929  
ID AAF74929 standard; DNA; 29 BP.  
XX  
AC AAF74929;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE CD40L poly-A tract sequence SEQ ID NO:26.  
XX  
KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
KW antiinflammatory; inflammatory disease; autoimmune disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200119844-A1.  
XX  
PD 22-MAR-2001.  
XX  
PF 13-SEP-2000; 2000WO-US024966.  
XX  
PR 13-SEP-1999; 99US-0153625P.  
XX  
PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX  
XX Crow MK, Li Y;  
PI  
XX WPI; 2001-244776/25.  
DR  
XX



PT New altered CD40L promoter for use in the study, diagnosis and treatment  
PT of a variety of inflammatory disorders and autoimmune diseases, such as  
PT rheumatoid arthritis.

XX Example 1; Fig 3; 90pp; English.

XX The present invention describes an isolated, purified nucleic acid, which  
CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
CC residues 331-455 of the sequence comprising 455 nucleotides given in  
CC AAF74905 where A in the wild type sequence at position 331 (corresponding  
CC to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
CC be used in gene therapy. (I) is useful in the study, diagnosis and  
CC treatment of inflammatory and autoimmune diseases, as well as diseases in  
CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention

XX

SQ Sequence 29 BP; 22 A; 4 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 17; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 2249  
ABZ92865.

ID ABZ92865 standard; DNA; 20 BP.

XX

AC ABZ92865;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX

PS Disclosure; SEQ ID NO 8107; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAA 2800  
Db 1 AAGTAAAAAAAAAAAAAAAAA 20

RESULT 2250  
ABZ85669

ID ABZ85669 standard; DNA; 20 BP.

XX

AC ABZ85669;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human oligonucleotide sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.

XX

PS Claim 15; SEQ ID NO 911; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTTTCTT 2185  
Db 1 TTTTCTTTTCTTTTCTTTTCTT 20

RESULT 2251  
AAV12302/c  
ID AAV12302 standard; DNA; 20 BP.

XX AC AAV12302;

XX DT 17-JUN-1998 (first entry)

XX DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.

XX KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;  
XX housekeeping gene; identification; modulator; metastasis; neoplastic;  
XX papilloma; atherosclerosis; angiogenesis; viral infection; ss.

XX OS Homo sapiens.

XX PN WO9800532-A2.

XX PD 08-JAN-1998.

XX PF 30-JUN-1997; 97WO-CA000454.

XX PR 01-JUL-1996; 96US-0021152P.

XX PA (WRIG/) WRIGHT J A.

XX PA (YOUN/) YOUNG A H.

XX PI Wright JA, Young AH;

XX DR WPI; 1998-086958/08.

XX PT New oligo-nucleotide(s) complementary to untranslated regions of  
XX housekeeping genes - are useful in, e.g. identifying modulators of tumour  
XX growth/metastasis and inhibiting growth of neoplastic cells.

XX PS Claim 4; Page 29; 64pp; English.

XX CC The present sequence represents a 3'-untranslated region (3'UTR) fragment  
XX of ribonucleotide reductase R1. The present invention describes: (1)  
XX oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)  
XX or their analogues of a UTR of a housekeeping gene; (2) antisense ON  
XX (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous  
XX to ON, and able to cleave it; (4) DNA sequence encoding ON, AON and Rb;  
XX (5) an antibody (Ab) that binds to ON, AON and Rb; (6) a nt probe ntp

CC that hybridise to ON, OAN and Rb. ON, AON, Rb and Ab are used to modulate  
CC (especially inhibit) growth of tumour cells (especially neoplastic cells)  
CC and to reduce their capacity for metastasis. The above may also be used  
CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,  
CC angiogenesis and viral infections, e.g. human immunodeficiency virus,  
CC hepatitis or herpes. ON may further be used: (i) to identify modulators  
CC of tumour growth/metastasis; (ii) to identify compounds (especially  
CC potential antitumour agents) that inhibit or enhance interaction between  
CC ON and its binding substances; (iii) as probes for detecting related  
CC sequences, and (iv) to generate Ab, used for detection and quantification  
CC of UTR especially for monitoring progress of cancer therapy. SON inhibit  
CC tumorigenicity of neoplastic cells, particularly where these are  
CC resistant to hydroxyurea

XX SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2183  
Db 20 CGTTTCTTTTCTTTTCTTTT 1

RESULT 2252  
AAV22586

ID AAV22586 standard; DNA; 20 BP.

XX AC AAV22586;

XX DT 08-JUL-1998 (first entry)

XX DE Antisense oligonucleotide designed to target the R1 message.

XX KW R1 subunit; ribonucleotide reductase; cell proliferation; tumour cell;  
XX antisense; growth; inhibition; sensitivity; hydroxyurea;  
XX chemotherapeutic drug; methotrexate; PALA; treatment; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9805769-A2.

XX PD 12-FEB-1998.

XX PF 01-AUG-1997; 97WO-CA000540.

XX PR 02-AUG-1996; 96US-0023040P.

XX PR 07-MAR-1997; 97US-0039959P.

XX PA (GENE-) GENESENSE TECHNOLOGIES INC.

XX PI Wright JA, Young AH;

XX DR WPI; 1998-145609/13.

XX PT Antisense oligonucleotides to ribonucleotide reductase genes - used to  
XX modulate tumour growth and inhibit tumour cell proliferation.

XX PS Claim 8; Page 49; 79pp; English.

XX CC AAV22531-89 represent antisense oligonucleotides which are targeted  
XX against the mRNA of the R1 subunit sequence of ribonucleotide reductase.  
XX Aberrant expression of the R2 gene, which encodes the second subunit of  
XX the ribonucleotide reductase gene, can determine the malignant  
XX characteristics of cells. Suppression of R2 and R1 gene expression was  
XX found to reduce transformed properties of tumour cells. The antisense  
XX oligonucleotides can be used for modulating tumour cell growth, or for  
XX inhibiting tumour cell proliferation. They can also be used for  
XX increasing the sensitivity of neoplastic cells to chemotherapeutic drugs  
XX (especially to hydroxyurea, methotrexate (MTX), and PALA). The antisense  
XX oligonucleotides may be used to treat proliferative disorders including



CC treating humans prone to a disease or condition associated with  
CC expression of G-alpha-S1. The present sequence an antisense  
CC oligonucleotide targeted to the 3' untranslated region of human G-alpha-  
CC S1  
XX  
SQ Sequence 20 BP; 4 A; 2 C; 1 G; 13 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2264 ATATTATTTCAGATGTTTC 2283  
Db 1 ATATTATTTCATTGTTTC 20  
RESULT 2255  
AAA90815  
ID AAA90815 standard; DNA; 20 BP.  
XX  
AC AAA90815;  
XX  
DT 20-DEC-2000 (first entry)  
XX  
DE Ribonucleotide reductase R1 message antisense oligo AS-I-2769-20.  
XX  
KW Antisense oligonucleotide; ribonucleotide reductase; R1 protein;  
KW R2 protein; tumour cell proliferation inhibition; cancer; cytostatic; ss.  
XX  
OS Synthetic.  
XX  
PN WO200047733-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 09-FEB-2000; 2000WO-CA000120.  
XX  
PR 11-FEB-1999; 99US-00249730.  
XX  
PA (GENE-) GENESENSE TECHNOLOGIES INC.  
XX  
PI Wright JA, Young AH;  
XX  
PS WPI; 2000-558216/51.  
XX  
DR New antisense oligonucleotide, AS-I-618-20, is useful for inhibiting  
XX tumor cell growth.  
PT  
PS Example 3; Page 32; 137pp; English.  
XX  
CC The present sequence is an antisense oligonucleotide directed against the  
CC mRNA encoding the R1 component of mammalian ribonucleotide reductase.  
CC Ribonucleotide reductase catalyses the conversion of ribonucleotides to  
CC their corresponding deoxyribonucleotides and thus plays an important role  
CC in DNA synthesis and cell proliferation. Regulation of ribonucleotide  
CC reductase is altered in cultured malignant cells and increased levels of  
CC R2 protein and R2 mRNA have been found in pre-malignant and malignant  
CC tissues as compared to normal control tissue samples. The present  
CC antisense sequence is therefore useful for inhibiting tumourigenicity of  
CC neoplastic cells and inhibiting metastasis of tumour cells. It is also  
CC useful for increasing sensitivity of neoplastic cells to chemotherapeutic  
CC drugs, thus allowing chemotherapeutic treatments to be used in patients  
CC who have become resistant or less sensitive to chemotherapy. The sequence  
CC may be RNA or DNA and may comprise a modified backbone and/or nucleotide  
CC analogues  
XX  
SQ Sequence 20 BP; 0 A; 3 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2163 TCCTTTTTTTTTTTTTTTT 2182

Db 1 TCCGTTTTTTTTTCTTTT 20  
RESULT 2256  
AAS05713  
ID AAS05713 standard; DNA; 20 BP.  
XX  
AC AAS05713;  
XX  
DT 07-SEP-2001 (first entry)  
XX  
DE Polypyrimidine Crick strand oligonucleotide.  
XX  
KW reverse phase triplex forming oligonucleotide; RP-TFO;  
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;  
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.  
XX  
OS Synthetic.  
XX  
PN WO200132929-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 03-NOV-2000; 2000WO-US030534.  
XX  
PR 03-NOV-1999; 99US-0163356P.  
PR 03-NOV-1999; 99US-0163416P.  
PR 21-DEC-1999; 99US-0171348P.  
PR 07-JUL-2000; 2000US-0216579P.  
XX  
PA (CYGE-) CYGENE INC.  
PA (OSTE/) OSTE C C.  
XX  
PI Oste CC, Ramberg ER;  
XX  
DR WPI; 2001-343488/36.  
XX  
PT Analyzing target nucleic acid sequences, useful for population genetics,  
PT drug development and diagnosing cancer, comprises hybridizing triple  
PT forming oligonucleotide and probe to target sequence.  
XX  
PS Example 2; Page 66; 141pp; English.  
XX  
CC The sequence is a polypyrimidine oligonucleotide for binding a second  
CC reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to  
CC the target SNP used to analyse Factor V Leiden SNP using the method of  
CC the invention. The invention relates to analysing target nucleic acid  
CC sequences comprising restricting isolated DNA, hybridising at least one  
CC triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to  
CC form a protected nucleic acid sequence (PNAS) tail structure, hybridising  
CC the captured structure with a single nucleotide polymorphisms (SNP)  
CC identification probe and determining the SNP score. The methods can be  
CC used for analysing target nucleic acid sequences, especially genomic DNA  
CC sequences, to determine if they contain SNPs or short tandem repeats  
CC (STRs). The methods can be used to detect SNPs for use in population  
CC genetics, drug development, forensics, cancer, genetic disease research,  
CC genomic analysis, diagnostics and therapeutics in humans, plants and  
CC animals  
XX  
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTTT 2185  
Db 1 TTTTTTTTTTTTCTTTT 20  
RESULT 2257  
AAF83959





XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT modified\_base 1..20  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "Phosphorothioate linkages"  
FT modified\_base 1..5  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
FT cytosines are 5-methylcytosine"  
FT modified\_base 16..20  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE  
FT cytosines are 5-methylcytosine"  
XX PN US6271030-B1.  
XX XX  
XX PD 07-AUG-2001.  
XX XX  
XX PF 14-JUN-2000; 2000US-00593711.  
XX XX  
XX PR 14-JUN-2000; 2000US-00593711.  
XX XX  
XX PA (ISIS-) ISIS PHARM INC.  
XX XX  
XX PI Monia BP, Butler MM, Wyatt J;  
XX XX  
XX DR WPI; 2002-214451/27.  
XX XX  
XX PT Novel antisense compound targeted to nucleic acids encoding human or  
XX PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for  
XX PT inhibiting expression of human or mouse C/EBP beta in cells/tissues.  
XX XX  
XX PS Example 15; Col 42; 69pp; English.  
XX XX  
XX CC Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted  
XX CC to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)  
XX CC gene, which inhibit its expression. The antisense oligonucleotides were  
XX CC designed to target different regions of the human and/or mouse C/EBP  
XX CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels  
XX CC by quantitative real-time PCR. The C/EBP family of proteins are a family  
XX CC of transcription factors which regulate the expression of a wide range of  
XX CC genes that control normal tissue development, cellular function, cellular  
XX CC proliferation and functional differentiation. C/EBP beta (also known as  
XX CC C/EPB2, LAP, TCF5, CRP2, NFIL6, IL6DBP, NF-M, AGP/EBP and Apc/EBP)  
XX CC primarily regulates hormone responsiveness and oxidative stress responses  
XX CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is  
XX CC thought to be involved in carbohydrate metabolism, immunity, the Th1  
XX CC response, female fertility and gluconeogenic pathways. C/EBP beta is  
XX CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the  
XX CC highest expression found in the lung. It is also expressed at a higher  
XX CC level in malignant ovarian tissue compared with normal ovarian tissue,  
XX CC and its expression in pancreas is upregulated in response to chronically  
XX CC elevated levels of glucose, indicating that it is involved in the  
XX CC impairment of insulin secretion in type II diabetes. The oligonucleotides  
XX CC of the invention are useful for diagnosis, prevention and treatment of  
XX CC conditions associated with C/EBP beta expression, such as cancer  
XX CC (particularly ovarian cancer), tumour formation, diabetes (particularly  
XX CC type II diabetes), infection, or inflammation  
XX XX  
XX SQ Sequence 20 BP; 0 A; 6 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 47 GCGCGCGCGCGCGCGCGG 66  
Db 1 GCGGCGCGCGCGCGCGCGG 20

RESULT 2260  
ABZ89487/c  
ID ABZ89487 standard; DNA; 20 BP.  
XX AC ABZ89487;  
XX DT 17-OCT-2003 (first entry)  
XX DE Human oligonucleotide sequence.  
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX OS Homo sapiens.  
XX XX  
XX PN WO200285308-A2.  
XX XX  
XX PD 31-OCT-2002.  
XX XX  
XX PF 23-APR-2002; 2002WO-US013135.  
XX XX  
XX PR 24-APR-2001; 2001US-0286137P.  
XX XX  
XX PA (EPIG-) EPIGENESIS PHARM INC.  
XX XX  
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
XX PI Miller S, Tang L, Shahabuddin S;  
XX XX  
XX DR WPI; 2003-229219/22.  
XX XX  
XX PT Pharmaceutical composition for treating ailments associated with impaired  
XX PT respiration, has oligo(s) antisense to specific gene(s) or its  
XX PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
XX PT ubiquinone.  
XX XX  
XX PS Disclosure; SEQ ID NO 4729; 872pp; English.  
XX XX  
XX CC The invention relates to a novel pharmaceutical composition, which has a  
XX CC first active agent comprising an oligonucleotide antisense to the  
XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
XX CC junctions of genes encoding a polypeptide associated with lung and/or  
XX CC nasal airway dysfunction and a second active agent comprising an  
XX CC antiinflammatory steroid and ubiquinone. A composition of the invention  
XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
XX CC immunosuppressive, and cytostatic activity. The composition may have a  
XX CC use in antisense gene therapy. The composition is useful for treating or  
XX CC preventing a respiratory, lung or malignant disease or condition, also  
XX CC for enhancing the prophylactic or therapeutic respiratory effect of an  
XX CC antiinflammatory steroid in a subject, for reducing or depleting levels  
XX CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
XX CC lung inflammation, lung allergies, or a respiratory disease or condition.  
XX CC Note: The sequence data for this patent is not represented in the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
XX SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2185  
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1





RESULT 2263  
ABZ85535/c  
ID ABZ85535 standard; DNA; 20 BP.  
XX  
AC ABZ85535;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Claim 15; SEQ ID NO 777; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, increasing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2166 TTTTCTTTTCTTTTCTTTT 2185  
Db 20 TTTTCTTTTCTTTTCTTTT 1  
  
RESULT 2265  
AAX09559  
ID AAX09559 standard; DNA; 21 BP.  
XX  
AC AAX09559;  
XX  
DT 24-MAR-1999 (first entry)

RESULT 2264  
AAT76021/c  
ID AAT76021 standard; DNA; 21 BP.  
XX  
AC AAT76021;  
XX  
DT 16-SEP-1997 (first entry)  
XX  
DE DEN-2 cloning/sequencing antisense primer, CD2-10261.  
XX  
KW Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;  
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;  
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;  
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;  
KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9640933-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US009209.  
XX  
PR 07-JUN-1995; 95US-00483292.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (UYMA-) UNIV MAHIDOL AT SALAYA.  
XX  
PI Bhamarapravati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;  
PI Kinney R, Trent DW;  
XX  
DR WPI; 1997-052330/05.  
XX  
PT PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -  
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a  
PT quadravalent vaccine for protecting against Dengue virus infection.  
XX  
PS Example; Page 104; 261pp; English.  
XX  
CC The sequences given in AAT75909-T76029 are primers which were used in the  
CC amplification, cloning and sequencing of the Dengue-2 viral CDNA's of the  
CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises  
CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.  
CC The quadravalent vaccine of the invention comprises an attenuated Dengue  
CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3  
CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are  
CC used to protect against infection by all four serotypes of dengue virus,  
CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal  
CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are  
CC used to produce the recombinant protein products of the DNA constructs  
CC which are used in the vaccines  
XX  
SQ Sequence 21 BP; 4 A; 7 C; 3 G; 7 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2019 GTCCTCTGCTAGGAGGCAAA 2038  
Db 21 GTCCTGTGCTAGGAGGCAAA 2  
  
RESULT 2265  
AAX09559  
ID AAX09559 standard; DNA; 21 BP.  
XX  
AC AAX09559;  
XX  
DT 24-MAR-1999 (first entry)



XX DE Human biallelic polymorphic marker upstream primer #439.  
XX KW Polymorphism; biallelic; human; forensic; paternity testing; disease;  
KW detection; phenotypic typing; characteristic; infection; hereditary;  
KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;  
KW treatment; marker; primer; ss.  
XX OS Synthetic.  
OS Homo sapiens.  
XX PN WO9820165-A2.  
XX PD 14-MAY-1998.  
XX PF 05-NOV-1997; 97WO-US020313.  
XX PR 06-NOV-1996; 96US-0030455P.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX PI Lander ES, Wang D, Hudson T;  
XX WPI; 1998-286974/25.  
XX New isolated nucleic acid segments from the human genome - used for  
PT determining polymorphic forms for use in e.g. forensics, paternity  
PT testing or phenotypic typing for disease.  
XX PS Claim 15; Page 204; 310pp; English.  
XX CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the  
CC isolation of various biallelic polymorphic markers found in the human  
CC genome (represented in AAX10269-X12937). These primers can be used in a  
CC method for determining polymorphic forms in an individual for use in e.g.  
CC forensics, paternity testing or for phenotypic typing for diseases such  
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial  
CC hypercholesterolemia, polycystic kidney disease, hereditary  
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary  
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos  
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,  
CC autoimmune diseases, inflammation, cancer, diseases of the nervous  
CC system, infection by pathogenic microorganisms, and characteristics such  
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,  
CC endurance, fertility, and susceptibility or receptivity to particular  
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid  
CC segments can also be used to produce medicaments for the treatment or  
CC prophylaxis of such diseases  
XX SQ Sequence 21 BP; 5 A; 8 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1249 ATTCACAGAACTTCTCAGCC 1268  
||| ||||||||||||  
Db 1 ATCCTCAGAACTTCTCAGCC 20

RESULT 2266  
AAZ26235  
ID AAZ26235 standard; DNA; 21 BP.  
XX AC AAZ26235;  
XX 30-NOV-1999 (first entry)  
DT XX Human polymorphic region 424.  
DE XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;

KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX Homo sapiens.  
OS WO9841648-A2.  
XX PN 24-SEP-1998.  
XX PD 19-MAR-1998; 98WO-US005419.  
XX PF 20-MAR-1997; 97US-0041057P.  
XX PR (VARI-) VARIAGENICS INC.  
XX PA Housman D, Ledley FD, Stanton VP;  
XX PI WPI; 1998-521232/44.  
XX DR Identifying target genes for allele-specific drugs - used for diagnosis,  
XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
PT  
XX Disclosure; Fig 7; 605pp; English.  
PS This invention describes a novel method for identifying an inhibitor  
XX potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX Sequence 21 BP; 17 A; 0 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2798  
||| ||||||||||||  
Db 2 AGAGATGAAAAA 21

RESULT 2267  
AAH91826  
ID AAH91826 standard; DNA; 21 BP.  
XX AC AAH91826;  
XX 09-OCT-2001 (first entry)  
DT XX Human inflammatory bowel disease associated polymorphic site #901.  
DE XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
KW chromosome 5q31-33; forensic test; gene therapy; ds.  
XX Homo sapiens.  
OS  
XX

FH Key Location/Qualifiers  
FT misc\_feature 9 /\*tag= a  
FT /note= "SNP, optionally T or A at this position"  
XX  
PN WO200142511-A2.  
XX  
PD 14-JUN-2001.  
XX  
XX 11-DEC-2000; 2000WO-US033632.  
PF  
XX 10-DEC-1999; 99US-0170257P.  
PR  
XX 10-APR-2000; 2000US-0196046P.  
XX  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
XX  
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
XX  
DR WPI; 2001-367874/38.  
PS  
XX Testing for the presence of polymorphisms associated with inflammatory  
PT bowel disease, using a hybridization assay.  
PT  
XX  
PS Claim 1; Page 76; 463pp; English.  
XX  
CC The present invention describes a method for detecting the presence of  
CC polymorphisms associated with inflammatory bowel diseases such as  
CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
CC the presence of genetic polymorphisms associated with inflammatory bowel  
CC disease and correlating their occurrence with disease states. They may be  
CC used in this way for phenotypic correlations, forensics, paternity  
CC testing, medicine and genetic analysis. The present sequence is a  
CC polymorphic site described in the exemplification of the invention  
XX  
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 16 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2157 TTTTTCCTCTTTTCTTTTCTTTT 2177  
Db 1 TTCATCTCCTTTTCTTTTCTTTT 21  
  
RESULT 2268  
AAT78996  
ID AAT78996 standard; DNA; 22 BP.  
XX  
AC AAT78996;  
XX  
DT 13-JAN-1998 (first entry)  
XX  
DE Human Huntington's disease gene intron 1 3' acceptor site.  
XX  
KW Huntington's disease; animal model; transgenic animal; human; therapy;  
KW drug screening; Hdh gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN CA2178022-A.  
XX  
PD 02-DEC-1996.  
XX  
PF 03-JUN-1996; 96CA-02178022.  
XX  
PR 01-JUN-1995; 95US-00457273.  
XX  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
XX  
PI Hayden M, Lin B, Nasir J;  
XX

DR WPI; 1997-298677/28.  
XX  
PT Mouse Huntington's Disease gene - useful for generating transgenic mice  
PT as a model of Huntington's Disease.  
XX  
PS Disclosure; Page 60; 69pp; English.  
XX  
CC This oligonucleotide comprises the 5' acceptor site of intron 1 of the  
CC human Huntington's disease (HD) gene. The splice site sequences for the  
CC first 5 exons of the mouse HD gene (see AAT78974) and the human HD gene  
CC were compared (see AAT78985-T79002). Targeted disruption of the murine HD  
CC gene, e.g. at exon 5, can be used to examine the function of the HD gene  
CC and its role in development. Transgenic mice can be used as models of HD  
XX  
SQ Sequence 22 BP; 2 A; 3 C; 1 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2163 TCCTTTCTTTTCTTTTCTTTTCTTTT 2182  
Db 1 TCCTTCTTTTCTTTTCTTTTCTTTT 20  
  
RESULT 2269  
AAH37805  
ID AAH37805 standard; DNA; 23 BP.  
XX  
AC AAH37805;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific upper PCR primer SEQ ID 601.  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
PS Claim 1; Page 53; 83pp; English.  
XX  
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The  
CC oligonucleotides are useful for determining the presence, absence or

CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence

XX  
SQ Sequence 23 BP; 16 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 23;  
Best Local Similarity 90.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAAGGAAAAAAAAAAAAA 2803  
Db 1 TGAAGGAAAAAAAAAAAAA 20

RESULT 2270  
AAH37805/c  
ID AAH37805 standard; DNA; 23 BP.  
XX  
AC AAH37805;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE SNP specific upper PCR primer SEQ ID 601.  
XX  
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;  
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;  
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;  
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;  
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;  
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200129262-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 13-OCT-2000; 2000WO-US028436.  
XX  
PR 15-OCT-1999; 99US-0160096P.  
XX  
PA (ORCH-) ORCHID BIOSCIENCES INC.  
XX  
PI Picoult-Newburg L, Pohl M;  
XX  
DR WPI; 2001-290930/30.  
XX  
PT New genotyping oligonucleotide, useful for detecting the presence,  
PT absence or identity of single polynucleotide polymorphism in a nucleic  
PT acid sample.  
XX  
PS Claim 1; Page 53; 83pp; English.  
XX  
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide  
CC primer extension (SNPE) primers, and the sequences of regions flanking  
CC sites of single nucleotide polymorphisms SNPs. The present invention  
CC includes kits for determining the presence or absence of a SNP, using the  
CC oligonucleotides of the invention. The PCR primers are used to amplify a  
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.  
CC The oligonucleotides are useful for genotyping a nucleic acid sample by  
CC performing a single-nucleotide primer extension reaction. The

CC oligonucleotides are useful for determining the presence, absence or  
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to  
CC assess by association analysis the genotype of an individual or group of  
CC individuals, having a pathological phenotypic trait suspected of being  
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.  
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular  
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,  
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic  
CC traits also include symptoms of or susceptibility to multifactorial  
CC disease of which a component is or may be genetic such as autoimmune  
CC diseases, including, rheumatoid arthritis, multiple sclerosis,  
CC inflammation, cancer, nervous system diseases and infection by pathogenic  
CC microorganism. The method is also useful in forensic investigations and  
CC paternity analysis. The present sequence represents a PCR primer specific  
CC for a human SNP containing DNA sequence

XX  
SQ Sequence 23 BP; 16 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 23;  
Best Local Similarity 90.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2164 CCTTTTCTTTTCTTTTCTTTT 2183  
Db 22 CCTTTTCTTTTCTTTTCTTTT 3

RESULT 2271  
ABN86902/c  
ID ABN86902 standard; DNA; 24 BP.  
XX  
AC ABN86902;  
XX  
DT 23-JUL-2002 (first entry)  
XX  
DE Human macroprotein 21.78 PCR primer 2 SEQ ID NO:4.  
XX  
KW Human; macroprotein 21.78; embryo development teratogenesis; tumour;  
KW PCR primer; ss.  
OS Homo sapiens.  
XX  
PN CN1331245-A.  
XX  
PD 16-JAN-2002.  
XX  
PF 30-JUN-2000; 2000CN-00116981.  
XX  
PR 30-JUN-2000; 2000CN-00116981.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-292882/34.  
XX  
PT New polypeptide-human macroprotein 21.78 and polynucleotide encoding it,  
PT for treating diseases such as embryo development teratogenesis and tumor.  
XX  
PS Example 2; Page 19 (Disclosure); 35pp; Chinese.  
XX  
CC The present invention describes human macroprotein 21.78 (I). Also  
CC described is a process for preparing (I) using DNA recombination  
CC techniques. (I) and the polynucleotide sequence encoding it (II) can be  
CC used in the treatment of diseases such as embryo development  
CC teratogenesis and tumours. The present sequence represents a PCR primer  
CC for (I), which is used in an example from the present invention  
XX  
SQ Sequence 24 BP; 0 A; 1 C; 2 G; 21 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804  
Db 24 GAAAAAAAAACAAACAA 5  
RESULT 2272  
ABQ79564  
ID ABQ79564 standard; DNA; 24 BP.  
XX  
AC ABQ79564;  
XX  
DT 25-NOV-2002 (first entry)  
XX  
DE Forward primer for detecting T7 phage gene 10 inserts.  
XX  
KW Protein identification; phage; intercellular; fibroblast; stem cell; PCR;  
KW primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200262965-A2.  
XX  
PD 15-AUG-2002.  
XX  
PF 06-FEB-2002; 2002WO-US005051.  
XX  
PR 06-FEB-2001; 2001US-0266662P.  
XX  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
PI Thomson JA, Xu R;  
XX  
DR WPI; 2002-657535/70.  
XX  
PT Identifying intercellular protein factors, e.g. intercellular factors  
PT expressed by fibroblasts that inhibit stem cell differentiation in  
PT culture, by employing a phage display technique using cDNA from the  
PT signaling cells.  
XX  
PS Example; Page 9; 19pp; English.  
XX  
CC The invention relates to identifying proteins, which function as  
CC intercellular signals between a signaling cell and affected cells. The  
CC method involves (a) inserting a cDNA library from the signaling cell into  
CC a phage; (b) incubating the phage with the affected cells; (c) washing  
CC a phage that does not bind to the affected cells; (d) eluting the phage  
CC that does bind to the affected cells; and (e) sequencing the cDNA inserts  
CC in the bound phage to identify sequence information useful for  
CC characterizing a protein made by the signaling cell and recognized by a  
CC receptor in the affected cells. The method is useful for identifying  
CC intercellular protein factors, e.g. intercellular factors expressed by  
CC fibroblasts that act to inhibit the differentiation of stem cells in  
CC culture. The present sequence represents a PCR primer used for detecting  
CC T7 phage gene 10 inserts  
XX  
SQ Sequence 24 BP; 7 A; 3 C; 10 G; 4 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1186 AGGACGAAATGAGATGGCAG 1205  
Db 2 AGGACGAGATGAGATGGCTG 21  
RESULT 2273  
ABN85224/c  
ID ABN85224 standard; DNA; 24 BP.  
XX  
AC ABN85224;  
XX

DT 24-SEP-2002 (first entry)  
XX  
DE Human translation initiation factor eIF4E binding protein 17.27 primer#2.  
XX  
KW Human; translation initiation factor subunit eIF4E binding protein 17.27;  
KW embryo development malformation; tumour; diabetes; menoxenia;  
KW peptic ulcer; translation initiation factor; eIF4E; binding protein; PCR;  
KW primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1339492-A.  
XX  
PD 13-MAR-2002.  
XX  
PF 23-AUG-2000; 2000CN-00119722.  
XX  
PR 23-AUG-2000; 2000CN-00119722.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-464075/50.  
XX  
PT New polypeptide-human translation initiation factor subunit eIF4E binding  
PT protein 17.27 for treating embryo development malformation, tumors,  
PT diabetes, menoxenia, and peptic ulcer.  
XX  
PS Example 3; Page 20 (Disclosure); 33pp; Chinese.  
XX  
CC The present invention relates to human translation initiation factor  
CC subunit eIF4E binding protein 17.27 (see ABB83427). The protein and its  
CC coding sequence are useful for treating various diseases, such as embryo  
CC development malformation; tumours, diabetes, menoxenia, peptic ulcer,  
CC etc. The present sequence is a PCR primer, which was used in an example  
CC from the invention  
XX  
SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2782 ATTGAAAAAAAAAAAAAAAAA 2801  
Db 21 ATTCAAAAAAAAAAAAAAAAAA 2  
RESULT 2274  
ABL56666  
ID ABL56666 standard; DNA; 24 BP.  
XX  
AC ABL56666;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE PCR primer #1 for human prollyl oligomeric peptidase 13.2 cDNA.  
XX  
KW Human; prollyl oligomeric peptidase 13.2; enzyme; angiocardioopathy;  
KW nervous system retrograde disease; gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200226990-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 29-JUN-2001; 2001WO-CN001090.  
XX  
PR 30-JUN-2000; 2000CN-00116964.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.



XX PI Mao Y, Xie Y;  
XX WPI; 2002-269651/31.  
DR  
XX Prolyl oligomeric peptidase 13.2 polypeptide for diagnosing and treating  
PT angiocardioopathy and nervous system retrograde disease.  
XX  
XX Example 2; Page 17; 35pp; Chinese.  
PS  
XX PCR primers ABL56666-67 were used to amplify cDNA encoding human prolyl  
CC oligomeric peptidase 13.2. The polypeptide and polynucleotide are used in  
CC diagnosis and treatment of angiocardioopathy and nervous system retrograde  
CC disease. The polynucleotide may also be used for gene therapy  
XX  
SQ Sequence 24 BP; 18 A; 3 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2784 TGAAGAAAAAAGAAAAA 2803  
DB 5 TCAGAAAAAAGAAAAA 24  
  
RESULT 2275  
ABL56666/c  
ID ABL56666 standard; DNA; 24 BP.  
XX  
AC ABL56666;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE PCR primer #1 for human prolyl oligomeric peptidase 13.2 cDNA.  
XX  
XX Human; prolyl oligomeric peptidase 13.2; enzyme; angiocardioopathy;  
KW nervous system retrograde disease; gene therapy; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200226990-A1.  
XX  
PD 04-APR-2002.  
XX  
XX 29-JUN-2001; 2001WO-CN001090.  
PF  
XX 30-JUN-2000; 2000CN-00116964.  
PR  
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
PA  
XX Mao Y, Xie Y;  
PI  
XX WPI; 2002-269651/31.  
DR  
XX Prolyl oligomeric peptidase 13.2 polypeptide for diagnosing and treating  
PT angiocardioopathy and nervous system retrograde disease.  
PT  
XX Example 2; Page 17; 35pp; Chinese.  
PS  
XX PCR primers ABL56666-67 were used to amplify cDNA encoding human prolyl  
CC oligomeric peptidase 13.2. The polypeptide and polynucleotide are used in  
CC diagnosis and treatment of angiocardioopathy and nervous system retrograde  
CC disease. The polynucleotide may also be used for gene therapy  
XX  
SQ Sequence 24 BP; 18 A; 3 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2168 TTTTCTTTTCTTTTCTTTTGA 5  
DB 24 TTTTCTTTTCTTTTCTTTTGA 5  
  
RESULT 2276  
ADD19369  
ID ADD19369 standard; DNA; 24 BP.  
XX  
AC ADD19369;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
XX Salmo salar SNP OLA primer SEQ ID NO:4.  
DE  
XX single nucleotide polymorphism; SNP; fish; Salmo salar;  
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;  
KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;  
KW detection; primer; ss.  
XX  
OS Synthetic.  
OS Salmo salar.  
XX  
PN WO2003060160-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 17-JAN-2003; 2003WO-IB000112.  
XX  
PR 18-JAN-2002; 2002US-0349950P.  
PR 16-AUG-2002; 2002US-0404200P.  
XX  
PA (GENO-) GENOMAR ASA.  
XX  
PI Lie O, Slettan A, Hoyum M, Lingaas F;  
XX  
XX WPI; 2003-627388/59.  
XX  
PT Novel isolated nucleic acid molecule comprising single nucleotide  
PT polymorphism associated with fish, useful for forming PCR primers which  
PT are used for detecting single nucleotide polymorphisms in fish nucleic  
PT acids.  
XX  
PS Claim 1; SEQ ID NO 4; 233pp; English.  
XX  
CC The present invention describes an isolated nucleic acid (I) comprising a  
CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of  
CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;  
CC and (ii) a nucleic acid having nucleotide sequence that hybridises to  
CC (i), or its complement under highly stringent hybridisation conditions.  
CC Also described: (1) an isolated oligonucleotide (II) comprising at least  
CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.  
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod  
CC polymorphic sites and seabass polymorphic sites, or their complement; (2)  
CC a primer pair (III) suitable for use in PCR, comprising two (II) capable  
CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.  
CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod  
CC polymorphic sites and seabass polymorphic sites; and determining (M1) the  
CC origin of fish sample comprising providing a parentage genotype database  
CC comprising a collection of candidate parent genotypes, where each of the  
CC candidate parent genotype represents a distinct origin, and comparing a  
CC sample genotype to the parentage genotype database, where a match between  
CC the sample genotype and one of the candidate parent genotype identifies  
CC to the origin of the sample. (M1) is useful for determining the origin of  
CC a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus,  
CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for  
CC detecting nucleic acid molecule comprising SNP in a sample, which  
CC involves contacting the sample containing nucleic acids with one or more  
CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus  
CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is  
CC useful for detecting nucleic acid molecule comprising a polymorphic  
CC sequence in a sample, comprising contacting the sample containing nucleic  
CC acids with one or more (II) which is derived from O. niloticus  
CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic  
CC sites or seabass polymorphic sites, and identifying a nucleic acid that

CC hybridises to (III). (III) is useful for detecting nucleic acid molecule  
CC comprising a microsatellite sequence in sample. The present sequence is  
CC used in the exemplification of the present invention.

XX SQ Sequence 24 BP; 16 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAA 2800  
DB 2 AATTGAAAAAAAAAAAAAAA 21

RESULT 2277  
ADB04574/c

ID ADB04574 standard; DNA; 25 BP.

XX AC ADB04574;

XX AC ADB04574;

DT 20-NOV-2003 (first entry)

XX XX Human MDZ7 scanning oligonucleotide SEQ ID 5560.

DE Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.

XX OS Homo sapiens.

XX PN EPI281758-A2.

XX XX 05-FEB-2003.

XX PF 30-JUL-2002; 2002EP-00016874.

XX PR 02-AUG-2001; 2001US-00922181.

XX XX (AEOM-) AEOMICA INC.

XX PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 5560; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC acids can also be used as probes to detect and characterize gross  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX SQ Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2803  
DB 20 TCAATAAAAAAAAAAAAAA 1

RESULT 2278  
AAQ98161

ID AAQ98161 standard; DNA; 25 BP.

XX AC AAQ98161;

XX DT 05-FEB-1996 (first entry)

XX DE Hind III primer/adaptor.

XX KW Hind III primer/adaptor; random oligonucleotide identification;  
KW beta-galactosidase gene; E. coli; infectious diseases;  
KW herpes simplex virus; ss.

XX OS Synthetic.

XX PN WO9516054-A1.

XX PD 15-JUN-1995.

XX PF 02-DEC-1994; 94WO-US013884.

XX PR 02-DEC-1993; 93US-00161281.

XX PA (MIRA/) MIRABELLI C K.  
PA (ECKE/) ECKER D J.  
PA (VICK/) VICKERS T A.  
PA (ROBE/) ROBERTSON D L.

XX PI Mirabelli CK, Ecker DJ, Vickers TA, Robertson DL;  
XX WPI; 1995-224334/29.

XX PT Identification of oligo:nucleotide(s) with a desired activity, e.g.  
PT activity against an infectious agent - by cloning vectors contg. randomly  
PT sequenced oligo:nucleotide(s) into cells and assaying for the desired  
PT phenotype.

XX PS Claim 25; Page 25; 53pp; English.

XX CC AAQ98161 is a random oligonucleotide Hind III primer/adaptor used in a  
CC new method for the identification of random oligonucleotides which  
CC inhibit the expression of a target gene, e.g. the beta-galactosidase gene  
CC in E. coli. Such random oligonucleotides may be used in the treatment of  
CC infectious diseases, pref. herpes simplex virus infection

XX SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTTCTTTT 2184  
DB 6 CTGGTCTTTTCTTTTCTTTTCTTTT 25

RESULT 2279  
AAC66194

ID AAC66194 standard; DNA; 25 BP.

XX AC AAC66194;

XX DT 14-FEB-2001 (first entry)

XX DE PCR primer EcoRI-dt used in trypsin hL identification.

PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 44; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1771 TTTT TTTT TTTT TGAACCCCAT 1790  
Db 4 TTTT TTTT TTTT TGCACCCCTT 23  
RESULT 2281  
AAC95680  
ID AAC95680 standard; DNA; 25 BP.  
XX  
AC AAC95680;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPB1 gene PCR primer #15.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 38; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

XX Human; trypsin hL; serine protease; lung disease model animal;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP2000253887-A.  
XX  
PD 19-SEP-2000.  
XX  
PF 11-MAR-1999; 99JP-00065337.  
XX  
PR 11-MAR-1999; 99JP-00065337.  
XX  
PA (TTPH-) TT PHARMA KK.  
XX  
DR WPI; 2000-658814/64.  
XX  
PT Novel gene encoding a serine protease and its protein used to screen for  
PT serine protease inhibitors and to prepare lung disease animal models.  
XX  
PS Disclosure; Page 7-8; 17pp; Japanese.  
XX  
CC Nucleotide sequence AAC66182 encodes human trypsin hL AAB35701, a serine  
CC protease. The invention relates to the human hL gene and protein  
CC sequences, to a recombinant vector containing the nucleotide sequence,  
CC and a host cell containing the vector. Human trypsin hL can be used for  
CC screening for serine protease inhibitors, in the preparation of a lung  
CC disease model animal, and for the development of an index marker of lung  
CC diseases caused by an anti-trypsin hL antibody. The present sequence  
CC represents a PCR primer used in the identification of trypsin hL  
XX  
SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2160 TTCTCCTTTT TTTT TTTT TTTT 2179  
Db 6 TTCGCTTT TTTT TTTT TTTT 25  
RESULT 2280  
AAC96039  
ID AAC96039 standard; DNA; 25 BP.  
XX  
AC AAC96039;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #6.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX





XX Ulfendahl P, Wong K;  
PI WPI; 2000-679677/66.  
XX  
DR  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 48; 66pp; English.  
XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in  
CC particular  
XX Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;  
SQ

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. NO. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2172 TTTT TTTT TTTT TTTT TTAACCTT 2191  
|||||  
Db 1 TTTT TTTT TTTT TGTCACCTT 20

RESULT 2285  
AAC95664  
ID AAC95664 standard; DNA; 25 BP.  
XX  
AC AAC95664;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPA1 gene PCR primer #9.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
XX WPI; 2000-679677/66.  
DR  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 37; 66pp; English.  
XX The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to

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CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2172 TTTTTTTTTTTTTTTAACTT 2191
Db      1 TTTTTTTTTTTGTCAACTT 20

RESULT 2286
AAC96455
ID AAC96455 standard; DNA; 25 BP.
XX
AC AAC96455;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #7.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 2 C; 5 G; 14 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2175 TTTTTTTTTTTTAACTTTGA 2194
Db      1 TTTTTTTTTTTTAACTACGA 20

RESULT 2287
AAC96434
ID AAC96434 standard; DNA; 25 BP.

```



CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAATAAAAAAAAAAAAAA 2803  
Db 20 TGTACAAAAAAAAAAAAA 1

RESULT 2290  
AAC96448  
ID AAC96448 standard; DNA; 25 BP.  
XX  
AC AAC96448;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DQA1 gene PCR primer #50.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 51; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1922 TTTTTCAGTCTAAGGT 1941  
Db 5 TTTTTCAGTCTTATGGT 24

RESULT 2291  
AAC95706/c  
ID AAC95706 standard; DNA; 25 BP.  
XX  
AC AAC95706;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DQA1 gene PCR primer #3.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 38; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 5 A; 4 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAA 2797  
Db 20 TAAACTTGAAAAAAAAAAAAA 1

RESULT 2292  
AAC95968/c  
ID AAC95968 standard; DNA; 25 BP.  
XX  
AC AAC95968;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA HLA-B gene PCR primer #79.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.





DNA sequence analysis; sequencing; protein sequence; protein structure;  
gene typing; organ donation; bacteria identification; 16S rRNA; HLA;  
human leukocyte antigen; PCR primer; ss.

Homo sapiens.  
WO200065088-A2.  
02-NOV-2000.  
20-APR-2000; 2000WO-EP003636.  
26-APR-1999; 99EP-00303215.  
(AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
Ulfendahl P, Wong K;  
WPI; 2000-679677/66.  
Identifying extendible primers for use in identification, or  
classification of a nucleic acid of an organism, allele or gene such as  
class 1/2 HLA comprises identifying all possible nucleotide sequences of  
specific length.  
Claim 14; Page 48; 66pp; English.  
The present invention provides a method for identifying a set of  
extendible primers which can be used in the identification, typing and  
classification of genes. This can then be used to predict protein  
sequence and structure, in organ donation to match the organ with the  
receiver, and to identify bacteria in a sample. The method can be used to  
type the human leukocyte antigen genes (HLA) and 16S rRNA genes in  
particular

Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

Query Match            0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY         2168 TTTTTTTTTTTTTTTTAA 2187  
Db          1 TTTTTTTTTTTTGTTGTA 20

RESULT 2297  
ABS76271  
ID ABS76271 standard; DNA; 25 BP.  
XX  
AC ABS76271;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-E exon 7 associated 25-mer SEQ ID 1797.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUYY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX

PI Gu Y, Shannon ME;  
XX WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
PS Example 2; Page 311; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2310 AAGCAATTGTTGCTGCTTG 2329  
Db ||||| ||||| ||||| |||||  
6 AAGCCAGTTGTTGCTGCTTG 25  
  
RESULT 2298  
ACD00129  
ID ACD00129 standard; DNA; 25 BP.  
XX  
AC ACD00129;  
XX  
DT 28-JUL-2003 (first entry)  
XX  
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #602.  
XX  
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031621-A2.  
XX  
AC ACD00129;  
XX  
DT 28-JUL-2003 (first entry)  
XX  
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #602.  
XX  
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031621-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032599.  
XX  
PR 12-OCT-2001; 2001US-0329000P.  
XX  
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
PI Zhang J;  
XX  
DR WPI; 2003-381720/36.  
XX  
PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
PT investigating and/or treating disorders associated with aberrant  
PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX  
PS Example 2; SEQ ID NO 626; 156pp; English.  
XX  
CC The invention describes an isolated nucleic acid encoding a G protein  
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
CC 409 residue amino acid sequence, all given in the specification, with or  
XX  
QY 2106 GGGGCCTTCTGGTTTAGGA 2125

CC without conservative amino acid substitutions, or complements of the  
CC sequence of them. The encoding nucleic acid is not more than 100 kbases in  
CC length. The methods and compositions of the present invention are useful  
CC for diagnosing, investigating and/or treating disorders associated with  
CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.  
CC This sequence represents an oligonucleotide used to analyse the gene  
CC encoding human G-protein coupled receptor GPCR-A-1  
XX  
SQ Sequence 25 BP; 3 A; 4 C; 10 G; 8 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2105 GGGGCCTTCTGGTTTAGG 2124  
Db ||||| ||||| ||||| |||||  
6 GGGGACCTTCTGGTCTTAGG 25  
  
RESULT 2299  
ACD00135  
ID ACD00135 standard; DNA; 25 BP.  
XX  
AC ACD00135;  
XX  
DT 28-JUL-2003 (first entry)  
XX  
DE G-protein coupled receptor GPCR-A-1 analysis oligonucleotide #608.  
XX  
KW Human; G-protein coupled receptor; GPCR-A-1; cancer; tumour;  
KW G-Protein-Agonist; G-Protein-Antagonist; gene therapy; cytostatic; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003031621-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 11-OCT-2002; 2002WO-US032599.  
XX  
PR 12-OCT-2001; 2001US-0329000P.  
XX  
PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.  
XX  
PI Zhang J;  
XX  
DR WPI; 2003-381720/36.  
XX  
PT New GPCR-A-1 nucleic acid and polypeptide, useful for diagnosing,  
PT investigating and/or treating disorders associated with aberrant  
PT expression or activity of GPCR-A-1, such as tumors and cancers.  
XX  
PS Example 2; SEQ ID NO 632; 156pp; English.  
XX  
CC The invention describes an isolated nucleic acid encoding a G protein  
CC coupled receptor (GPCR), mutations of which cause cancer, comprising a  
CC 2225 or 1921 base pair sequence, or their degenerate variants, encoding a  
CC 409 residue amino acid sequence, all given in the specification, with or  
CC without conservative amino acid substitutions, or complements of the  
CC sequence of them. The encoding nucleic acid is not more than 100 kbases in  
CC length. The methods and compositions of the present invention are useful  
CC for diagnosing, investigating and/or treating disorders associated with  
CC aberrant expression or activity of GPCR-A-1, such as tumors and cancers.  
CC This sequence represents an oligonucleotide used to analyse the gene  
CC encoding human G-protein coupled receptor GPCR-A-1  
XX  
SQ Sequence 25 BP; 4 A; 5 C; 10 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2106 GGGGCCTTCTGGTTTAGGA 2125

RESULT 2301  
AAA07786/c  
ID AAA07786 standard; DNA; 23 BP.  
XX  
AC AAA07786;  
XX  
DT 23-JUN-2000 (first entry)  
XX  
DE Structure of a fragment of duplex A target strand.  
XX  
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;  
KW viral infection; inflammatory response; cellular proliferation;  
KW psoriasis; duplex; ss.  
XX  
OS Synthetic.  
XX  
PN WO200011013-A1.  
XX  
PD 02-MAR-2000.  
XX  
PF 20-AUG-1999; 99WO-US019029.  
XX  
PR 22-AUG-1998; 98US-0097712P.  
XX  
PA (UYNE-) UNIV NEBRASKA.  
XX  
PI Gold B;  
XX  
DR WPI; 2000-246530/21.  
XX  
PT Modified nucleomonomers, used in physiologically stable, non-toxic  
PT oligomers used to inhibit expression of nucleic acids and in gene  
PT regulation, antisense technology and diagnostics.  
XX  
PS Disclosure; Page 20; 42pp; English.  
XX  
CC The invention provides modified nucleomonomers of specified formula and  
CC their pharmaceutically acceptable salts. The nucleomonomers are used as  
CC monomers in oligomers, which are used in pharmaceutical compositions to  
CC inhibit expression of nucleic acid molecules including DNA and RNA in  
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-  
CC infected cells. They are used in oligomers for gene regulation, antisense  
CC technology, diagnostic applications to detect target sequences in  
CC biological samples such as those containing pathogenic bacteria, fungi  
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or  
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion  
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and  
CC interleukins associated with pathological conditions such as inflammatory  
CC conditions, cardiovascular disorders, immune reactions, cancer, viral  
CC infections and bacterial infections. The oligomers are suitable for use  
CC in both in vivo and ex vivo therapeutic applications including treatment  
CC of cells such as bone marrow or peripheral blood in conditions such as  
CC leukemia or viral infections, genes as target for cancer treatments  
CC including oncogenes such as ras, k-ras, bcl-2, c-myc, bcr, c-myc, c-abl  
CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6  
CC (Kaposi's sarcoma), HER-2 and translocations such as bcr/abl or RNAs  
CC encoded by such genes, as well as viral gene sequences such as polymerase  
CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1  
CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,  
CC human papilloma virus, varicella zoster virus, influenza virus or  
CC rhinovirus. They can also be used to modulate inflammatory responses by  
CC modulating expression of genes such as IL-1 receptor, IL-1, ICAM-1 or E-  
CC selectin in mediating inflammation and modulation of cellular  
CC proliferation in conditions such as arterial occlusion (restenosis) after  
CC angioplasty by modulating the expression of growth or mitogenic factors  
CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor  
CC or fibroblast growth factor or their receptors or cell proliferation  
CC factor such as c-myc, other extracellular proliferation factors such as  
CC transforming growth factor alpha, IL-6, approx.g-interferon, protein  
CC kinase C for treatment of psoriasis or other conditions, and epithelial  
CC growth factor, transforming growth factor or MHC alleles in autoimmune  
CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex  
CC DNA stability when hybridizing to target nucleic acid sequences, are

compositions that are useful for modulating cellular adhesion or proliferation, and being active against a eukaryotic pathogen, a human retrovirus, a human immunodeficiency virus (HIV), or a non-human retrovirus, including influenza virus, Epstein-Barr virus, Respiratory Syncytial Virus or cytomegalovirus (CMV). The compositions enable characterization of deletion sequence oligonucleotides having related, but different nucleobase sequences, and quantification of different species of deletion sequence ("target") oligonucleotides in a mixture. Also, if the specificity of the oligonucleotide's nucleobase sequence for its reverse complement is not modified, the method may be performed using

AC AAT03687;





XX 03-SEP-1999; 99FR-00011097.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Weissenbach J, Hazan J;  
XX WPI; 2001-283966/30.  
XX  
PT New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of  
PT autosomal dominant familial spastic paraplegia and in drug screening.  
XX  
PS Claim 6; Page 30; 145pp; French.  
XX  
CC AAF84871-AAF84902 represent the acceptor and donor sites of the  
CC intron/exon and exon/intron borders of the human SPG4 gene. The SPG4 gene  
CC encodes a spastin polypeptide. The sequences may be used as PCR primers  
CC and probes. Mutations in the SPG4 gene are responsible for autosomal  
CC dominant familial spastic paraplegia. SPG4 polynucleotides, and their  
CC fragments, are used to screen DNA banks for sequences that encode spastin  
CC (particularly sequences in other mammals, specifically mice); to identify  
CC SPG4 mutations, or other genetic anomalies, particularly for diagnosis of  
CC autosomal dominant familial spastic paraplegia (PSF-AD); to identify  
CC promoters and other regulatory elements of the SPG4 gene; for detection  
CC and amplification; for recombinant production of spastin; and for  
CC diagnostic genotyping of PSF-AD  
XX  
SQ Sequence 24 BP; 6 A; 4 C; 5 G; 9 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1789 ATTCTTTCTCTTCTCTGAAAGTGG 1811  
Db 1 ACTTTTCTCTTGTCAGAAAGTGG 23  
  
RESULT 2307  
ABA95669/c  
ID ABA95669 standard; DNA; 24 BP.  
XX  
AC ABA95669;  
XX  
DT 25-MAR-2002 (first entry)  
XX  
DE Human zinc finger protein 13 PCR primer #1.  
XX  
KW Human; zinc finger protein 13; cytostatic; haemostatic; virucide;  
KW immunomodulatory; antiinflammatory; gene therapy; tumour; haemopathy;  
KW HIV infection; immunological disease; inflammation; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192325-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 21-MAY-2001; 2001WO-CN000832.  
XX  
PR 24-MAY-2000; 2000CN-00115827.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-090035/12.  
XX  
PT Human zinc-finger protein 13 and encoding polynucleotide, used in  
PT diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX

PS Example 2; Page 16; 34pp; Chinese.  
XX  
CC The present invention relates to human zinc finger protein 13 (see  
CC AAM48275). The zinc finger protein and its coding sequence are useful in  
CC the diagnosis and treatment of malignant tumours, haemopathy, HIV  
CC infection, immunological diseases and various inflammations. The present  
CC sequence is a PCR primer, which was used in an example from the present  
CC invention  
XX  
SQ Sequence 24 BP; 6 A; 5 C; 12 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 246 CGCGGGTCCGCCACCTCTCTCTCC 268  
Db 23 CGCGGGTCCACCTCTCTCTCTCC 1  
  
RESULT 2308  
AAL42406  
ID AAL42406 standard; DNA; 24 BP.  
XX  
AC AAL42406;  
XX  
DT 28-JUN-2002 (first entry)  
XX  
DE Human ORC413-64 PCR primer 2.  
XX  
KW Human; ss; replication initiation recognition complex subunit; ORC413.64;  
KW cancer; HIV; PCR; primer.  
XX  
OS Homo sapiens.  
XX  
PN CN1327995-A.  
XX  
PD 26-DEC-2001.  
XX  
PF 12-JUN-2000; 2000CN-00116447.  
XX  
PR 12-JUN-2000; 2000CN-00116447.  
XX  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-270050/32.  
XX  
PT New polypeptide-replication initiation recognition complex subunit  
PT ORC413.64 for treating diseases such as cancer, and human  
PT immunodeficiency virus infection.  
XX  
PS Example 2; Page 18 (Disclosure); 34pp; Chinese.  
XX  
CC The invention comprises the amino acid and nucleotide sequences of the  
CC human replication initiation recognition complex subunit ORC413.64. The  
CC ORC413.64 nucleotide and protein sequences of the invention are useful  
CC for treating diseases such as cancer and HIV. The present DNA sequence  
CC represents a PCR primer specific for the gene sequence of the human  
CC replication initiation recognition complex subunit ORC413.64  
XX  
SQ Sequence 24 BP; 1 A; 4 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2158 TTTTCTCTTTTCTTTTCTTTTCTTTT 2180  
Db 1 TTTCTCTCTTTTCTTTTCTTTTCTTTT 23

RESULT 2309  
ABV76657  
ID ABV76657 standard; DNA; 24 BP.  
XX  
AC ABV76657;  
XX  
DT 21-FEB-2003 (first entry)  
XX  
DE Human EGF receptor protein 10.12 RT-PCR primer, SEQ ID NO:3.  
XX  
KW Human; epidermal growth factor receptor protein 10.12;  
KW EGF receptor protein 10.12; recombinant production; gene therapy;  
KW malignant tumour; cancer; blood disease; human immunodeficiency virus;  
KW HIV infection; immune disorder; inflammatory condition; cytostatic;  
KW antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;  
KW primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1358749-A.  
XX  
PD 17-JUL-2002.  
XX  
PF 13-DEC-2000; 2000CN-00127861.  
XX  
PR 13-DEC-2000; 2000CN-00127861.  
XX  
PA (SHAN-) SHANGHAI BLOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
WPI; 2002-733538/80.  
XX  
Novel polypeptide-human epidermal growth factor 10.12 the polynucleotide  
for encoding the polypeptide.  
XX  
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.  
XX  
The invention relates to human epidermal growth factor (EGF) receptor  
protein 10.12 (ABB99979) and nucleic acids encoding it (ABV76656). The  
protein has a molecular weight of 10.12 kD. The invention also relates to  
a method for the recombinant production of the protein, an antagonist of  
the protein, and the use of the protein, gene and antagonist in  
therapeutic applications. EGF receptor protein 10.12 can be used in the  
treatment of a variety of diseases such as malignant tumours, blood  
diseases, HIV (human immunodeficiency virus) infection, immune disorders  
and inflammatory conditions. Sequences ABV76657-ABV76658 represent  
reverse transcription-PCR (RT-PCR) primers used in an exemplification of  
the invention to isolate human EGF receptor protein 10.12 cDNA  
XX  
SQ Sequence 24 BP; 4 A; 4 C; 12 G; 4 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 111 GGGGCTGGGGGATCCTGGATT 133  
Db 1 GGGGACGAGGAGGCTGGACTT 23  
RESULT 2310  
AAS18179/c  
ID AAS18179 standard; DNA; 24 BP.  
XX  
AC AAS18179;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human proliferating cell nuclear antigen (PCNA) 13 RT-PCR primer #2.  
XX  
KW Human; proliferating cell nuclear antigen 13; PCNA 13; malignant tumour;  
KW cancer; haemopathy; HIV infection; human immunodeficiency virus; ss;

inflammation; transfusion reaction; graft immune rejection; gene chip;  
development disease; microarray; nucleic acid hybridisation; haemostatic;  
cytostatic; virucide; immunomodulatory; antiinflammatory; RT-PCR; primer;  
hereditary disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200190169-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-CN0000787.  
XX  
PR 19-MAY-2000; 2000CN-00115755.  
XX  
PA (BIOW-) BLOWINDOW GENE DEV INC SHANGHAI.  
XX  
PI Mao Y, Xie Y;  
XX  
WPI; 2002-106182/14.  
XX  
Human proliferating cell nuclear antigen 13 and encoded polynucleotide,  
used in diagnosis and treatment of malignant tumors, hemopathy, human  
immunodeficiency virus infection, immunological diseases and  
inflammation.  
XX  
PS Example 3; Page 12; 35pp; Chinese.  
XX  
The invention relates to an isolated polypeptide of human proliferating  
cell nuclear antigen (PCNA) 13. This polypeptide and its related  
polynucleotide are applicable in diagnosis and treatment of tumours,  
transfusion reaction, haemopathy, graft immune rejection, development  
disease, hereditary disease, HIV infection and inflammation. Regulators  
of the polypeptide activity or expression that can mimic, promote,  
antagonise or inhibit human PCNA 13 can be used for this purpose, and  
also an antibody that binds specifically to the polypeptide. A method for  
detecting diseases or disease susceptibility relating to the polypeptide  
involves measuring the expression dose of the polypeptide, determining  
the polypeptide activity, or detecting the polypeptide expression dose  
caused by the polynucleotide that has abnormal activity due to a  
polynucleotide mutation. The polynucleotide can be used to supply primers  
for nucleic acid amplification and probes for hybridisation reactions, or  
in producing gene chips or microarrays. This sequence represents a  
reverse-transcription PCR (RT-PCR) primer used for isolation of cDNA  
encoding human PCNA 13  
XX  
SQ Sequence 24 BP; 4 A; 2 C; 0 G; 18 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2782 ATTGAAAAAATAAAATATAAA 2804  
Db 24 ATGGAAAAAATAAAATATAAA 2  
RESULT 2311  
ABN86867  
ID ABN86867 standard; DNA; 24 BP.  
XX  
AC ABN86867;  
XX  
DT 23-JUL-2002 (first entry)  
XX  
DE Human macroprotein 11.88 PCR primer 2 SEQ ID NO:4.  
XX  
KW Human; macroprotein 11.88; embryo development disorder; tumour;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN CN1331201-A.





XX ABQ79142 standard; DNA; 24 BP.  
XX AC ABQ79142;  
XX DT 15-NOV-2002 (first entry)  
XX DE Primer #2 related to human eukaryotic initial factor -2 protein.  
XX KW Human; eukaryotic initial factor -2; (elf-2); tumour; virus infection;  
XX KW development disorder; PCR; primer; ss.  
XX OS Homo sapiens.  
XX EN CN1340547-A.  
XX XX 20-MAR-2002.  
XX PF 31-AUG-2000; 2000CN-00119830.  
XX PR 31-AUG-2000; 2000CN-00119830.  
XX XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX PA Mao Y, Xie Y;  
XX PI WPI; 2002-436441/47.  
XX DR polypeptide-human eukaryotic initiation factor-2 (elf-2)-associated  
XX PT protein 74.14 and polynucleotide encoding it.  
XX XX Example 2; Page 18 (Disclosure); 36pp; Chinese.  
XX CC This invention relates to a novel polypeptide-human eukaryotic initial  
XX CC factor -2 (elf-2)-associated protein 74.14 and the application of the  
XX CC polypeptide in treating diseases such as tumours, virus infection  
XX CC abnormalities and development disorders. The present sequence represents  
XX CC a primer related to the novel human eukaryotic initial factor -2 (elf-2)-  
XX CC associated protein  
XX SQ Sequence 24 BP; 4 A; 1 C; 0 G; 19 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2782 ATTGAAAAAATAAAAAAAAAA 2804  
Db 24 AATGAATAATAATAATAATAA 2  
RESULT 2315  
ABS56172/c  
ID ABS56172 standard; DNA; 24 BP.  
XX AC ABS56172;  
XX DT 30-JAN-2003 (first entry)  
XX DE PCR primer #4 for DNA encoding human CIS3.  
XX KW Human; effectiveness of interferon treatment; hepatitis C patient;  
XX KW JAK-combined protein; CIS3; hepatocyte sample; hepatotropic;  
XX KW antiinflammatory; virucide; PCR; primer; ss.  
XX OS Homo sapiens.  
XX XX JP2002125683-A.  
XX PN 08-MAY-2002.  
XX PD 27-OCT-2000; 2000JP-00329615.  
XX PF 27-OCT-2000; 2000JP-00329615.  
XX PR 27-OCT-2000; 2000JP-00329615.

XX (TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO KENKYUSHO.  
XX PA (YABA/) YABASHI H.  
XX PA (CHUS ) CHUGAI PHARM CO LTD.  
XX PA (SRLS-) SRL KK.  
XX WPI; 2003-049086/05.  
XX DR Estimation of effectiveness of interferon.  
XX PT Claim 14; Page 7; 17pp; Japanese.  
XX PS The present invention relates to a method for estimating the  
XX CC effectiveness of interferon treatment. The method comprises administering  
XX CC interferon to a hepatitis C patient in which the expression amount of at  
XX CC least one of the JAK-combined protein gene or the CIS3 gene in the  
XX CC hepatocyte sample is measured. The method employs primers and probes  
XX CC which are disclosed in the specification. The method is useful for  
XX CC estimating the effectiveness of interferon treatment in a hepatitis C  
XX CC patient. The present sequence represents a PCR primer used in the method  
XX CC of the present invention  
XX SQ Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 24;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 656 AACCTGGGGTCCACGACATGCC 678  
Db 24 AAGCTGGTGCACCACTACATGCC 2  
RESULT 2316  
AAC96201  
ID AAC96201 standard; DNA; 25 BP.  
XX AC AAC96201;  
XX DT 26-FEB-2001 (first entry)  
XX DE 16S rRNA gene PCR primer #168.  
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;  
XX KW human leukocyte antigen; PCR primer; ss.  
XX OS Homo sapiens.  
XX PN WO200065088-A2.  
XX PD 02-NOV-2000.  
XX PF 20-APR-2000; 2000WO-EP003636.  
XX PR 26-APR-1999; 99EP-00303215.  
XX XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX PA Ulfendahl P, Wong K;  
XX PI WPI; 2000-679677/66.  
XX DR Identifying extendible primers for use in identification, or  
XX XX classification of a nucleic acid of an organism, allele or gene such as  
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
XX PT specific length.  
XX PT Claim 14; Page 47; 66pp; English.  
XX PS The present invention provides a method for identifying a set of  
XX CC extendible primers which can be used in the identification, typing and  
XX CC classification of genes. This can then be used to predict protein

```
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2171 TTTTTTTTTTTTTTTTAACTTTG 2193
Db 1 TTTTTTTTTTTTTTCAGTCTTG 23

RESULT 2317
AAC96219
ID AAC96219 standard; DNA; 25 BP.
XX
AC AAC96219;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #186.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 47; 66pp; English.
XX
SQ Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1771 TTTTTTTTTTGAACCCCTTCT 1793
Db 3 TTTTTTTTTTTTCCCCCATTTG 25

RESULT 2318
```

```
AAC95968
ID AAC95968 standard; DNA; 25 BP.
XX
AC AAC95968;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-B gene PCR primer #79.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 43; 66pp; English.
XX
SQ The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 5 C; 1 G; 17 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTAACT 2190
Db 1 TTTTTTTTTTTCTTTCCACCT 23

RESULT 2319
AAQ55856
ID AAQ55856 standard; DNA; 25 BP.
XX
AC AAQ55856;
XX
DT 25-MAR-2003 (revised)
DT 25-JUL-1994 (first entry)
XX
DE Fragile X probe.
XX
KW FC; foetal cells; marker; probe; hybridise; denature; dye; label;
KW fluorescent; kit; detection; haemoglobin; rhesus; gamma globulin; NR;
KW nitrogen reductase; ss.
XX
OS Homo sapiens.
XX
PN WO9402646-A1.
```



CC the expression of undesirable proteins. The present sequence represents  
CC an antisense fragment inserted into a msDNA  
XX  
SQ Sequence 25 BP; 7 A; 5 C; 1 G; 12 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2531 ATATACAGGGTATTAAAGAAJTAA 2553  
Db 24 ATCTAGAGGGTATTAAATGA 2  
RESULT 2322  
AAX07505  
ID AAX07505 standard; DNA; 25 BP.  
XX  
AC AAX07505;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Synthetic IDDMK1.2-22 PCR primer.  
XX  
KW IDDM; insulin-dependent diabetes mellitus; endogenous retrovirus; SAG;  
KW superantigen; provirus; autoimmune disease; type 1 diabetes; diagnosis;  
KW PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN EP893691-A1.  
XX  
PD 27-JAN-1999.  
XX  
PF 23-JUL-1997; 97EP-00401773.  
XX  
PR 23-JUL-1997; 97EP-00401773.  
XX  
PA (MACH/) MACH B F.  
XX  
PI Conrad B, Mach B;  
XX  
DR WPI; 1999-097928/09.  
XX  
PT Diagnosing human autoimmune disease by detecting retrovirus with  
PT superantigen activity - new retrovirus associated with type 1 diabetes,  
PT its proviral DNA, and related vectors, transformed cells, proteins,  
PT antibodies and specific binding agents, used for treating or preventing  
PT autoimmune disease.  
XX  
PS Example; Page 34; 92pp; English.  
XX  
CC The sequence is that of an insulin-dependent diabetes mellitus associated  
CC human endogenous retrovirus (IDDMK1.2-22) PCR primer. The retrovirus has  
CC Superantigen (SAG) activity. It can be used as part of a method is  
CC specifically used to diagnose type 1 diabetes mellitus. Modified proteins  
CC expressed by the retroviral sequence (without SAG activity but still able  
CC to induce an immune response) are useful in vaccines to treat or prevent  
CC SAG-related autoimmune disease; nucleic acid sequences encoding  
CC (modified) SAG can be used similarly to treat such diseases. Retroviral-  
CC encoded SAG are important in pathogenesis of autoimmune disease, probably  
CC by activating autoreactive T cells. The method is very specific (it can  
CC differentiate between expressed and non-expressed viral nucleic acids)  
CC and can be used even where the pathogen is an ubiquitous endogenous  
CC retrovirus. Blood or plasma samples can be tested without extensive  
CC preparation and diagnosis can be made before clinical signs are apparent,  
CC allowing early intervention before severe tissue damage has occurred  
XX  
SQ Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1951 TTTTGTGTCGCTAAATATTTA 1973  
Db 1 TTTTGTGTCGCTTAGTATTTA 23  
RESULT 2323  
AAX07482  
ID AAX07482 standard; DNA; 25 BP.  
XX  
AC AAX07482;  
XX  
DT 08-JUN-1999 (first entry)  
XX  
DE Synthetic IDDMK1.2-22 poly(A) specific primer.  
XX  
KW IDDM; insulin-dependent diabetes mellitus; endogenous retrovirus; SAG;  
KW superantigen; provirus; autoimmune disease; type 1 diabetes; diagnosis;  
KW primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN EP893691-A1.  
XX  
PD 27-JAN-1999.  
XX  
PF 23-JUL-1997; 97EP-00401773.  
XX  
PR 23-JUL-1997; 97EP-00401773.  
XX  
PA (MACH/) MACH B F.  
XX  
PI Conrad B, Mach B;  
XX  
DR WPI; 1999-097928/09.  
XX  
PT Diagnosing human autoimmune disease by detecting retrovirus with  
PT superantigen activity - new retrovirus associated with type 1 diabetes,  
PT its proviral DNA, and related vectors, transformed cells, proteins,  
PT antibodies and specific binding agents, used for treating or preventing  
PT autoimmune disease.  
XX  
PS Claim 9; Page 52; 92pp; English.  
XX  
CC The sequence is that of an insulin-dependent diabetes mellitus associated  
CC human endogenous retrovirus (IDDMK1.2-22) poly(A) specific primer. The  
CC retrovirus has Superantigen (SAG) activity. It can be used as part of a  
CC method is specifically used to diagnose type 1 diabetes mellitus.  
CC Modified proteins expressed by the retroviral sequence (without SAG  
CC activity but still able to induce an immune response) are useful in  
CC vaccines to treat or prevent SAG-related autoimmune disease; nucleic acid  
CC sequences encoding (modified) SAG can be used similarly to treat such  
CC diseases. Retroviral-encoded SAG are important in pathogenesis of  
CC autoimmune disease, probably by activating autoreactive T cells. The  
CC method is very specific (it can differentiate between expressed and non-  
CC expressed viral nucleic acids) and can be used even where the pathogen is  
CC an ubiquitous endogenous retrovirus. Blood or plasma samples can be  
CC tested without extensive preparation and diagnosis can be made before  
CC clinical signs are apparent, allowing early intervention before severe  
CC tissue damage has occurred  
XX  
SQ Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1951 TTTTGTGTCGCTAAATATTTA 1973  
Db 1 TTTTGTGTCGCTTAGTATTTA 23



RESULT 2324  
AAX05267  
ID AAX05267 standard; DNA; 25 BP.  
XX  
AC AAX05267;  
XX  
DT 14-APR-1999 (first entry)  
XX  
DE Fragile X chromosome detecting probe.  
XX  
DE Genetic testing; foetal cell; maternal; blood; pregnant; hybridisation;  
KW detection; HIV, hepatitis virus; herpes virus; chromosomal abnormality;  
KW probe; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN US5858649-A.  
XX  
PD 12-JAN-1999.  
XX  
XX 31-DEC-1996; 96US-00775609.  
PF  
XX 17-JUL-1992; 92US-00915765.  
PR  
PR 19-JUL-1993; 93US-00094710.  
PR  
PR 19-JUL-1994; 94WO-US008342.  
PR  
PR 17-JAN-1995; 95US-00374144.  
XX  
PA (APRO-) APROGENEX INC.  
XX  
XX Blick M, Cubbage ML, Bresser J, Prashad N, Asgari M;  
PI  
XX WPI; 1999-152096/13.  
DR  
XX Method for distinguishing foetal cells from adult cells in blood - based  
PT on amplification and detection of mRNA selectively expressed in foetal  
PT cells.  
XX  
XX Example 4, 14; Col 49; 49pp; English.  
PS  
XX The invention relates to a method of enriching foetal cells from maternal  
CC blood and for identifying such foetal cells. Foetal cells can be  
CC distinguished from adult cells in a blood specimen by (a) treating a  
CC blood specimen from a pregnant female to yield a mixture of cells  
CC comprising foetal cells and adult cells; (b) amplifying one or more mRNAs  
CC within the cells, the mRNAs being selectively expressed in target foetal  
CC cells to be distinguished but not expressed in adult blood cells; (c)  
CC performing in situ hybridisation on the cells under hybridising  
CC conditions suitable to maintain cell membranes in a substantially intact  
CC state and with a hybridisation medium comprising a detectably labelled  
CC probe complementary to the amplified mRNA that is selectively expressed  
CC in the target foetal cells but not expressed in adult blood cells; (d)  
CC removing the hybridisation medium and unhybridised probe from the mixture  
CC of cells to yield hybridised cells, and (e) detecting the labelled probe  
CC remaining in the hybridised cells; whereby cells in which the labelled  
CC probe is detected are identified as the target foetal cells; A second  
CC method for determining the presence of a target nucleotide sequence in  
CC individual foetal cells present in a cellular specimen is also provided.  
CC The methods (especially the second) is useful for detecting HIV,  
CC hepatitis viruses or herpes viruses in foetal cells, or for detecting  
CC chromosomal abnormalities in foetal cells. The present sequence  
CC represents a probe used for the detection of the Fragile X chromosome in  
CC amniocytes and in peripheral blood mononuclear cells  
XX  
SQ Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 51 GCGGGGGGGCGGGCGGACGACGC 73  
|||||

Db 3 GCGGGGGGGCGGGCGGCGGC 25

RESULT 2325  
AAX07199  
ID AAX07199 standard; DNA; 25 BP.  
XX  
AC AAX07199;  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE IDDM-associated retrovirus polyA specific probe.  
XX  
DE HERV; IDDKK1.2-22; superantigen; SAg; antigen; IDDM;  
KW insulin-dependent diabetes mellitus; autoimmune disease; diagnosis;  
KW therapy; vaccine; probe; PCR; primer; ss.  
XX  
XX Synthetic.  
OS Human endogenous retrovirus.  
OS  
XX WO9905527-A2.  
PN  
XX 04-FEB-1999.  
PD  
XX 22-JUL-1998; 98WO-EP004926.  
PF  
XX 22-JUL-1997; 97EP-00112482.  
PR  
PR 23-JUL-1997; 97EP-00401773.  
PR  
XX (MEDI-) MEDIGEN SA.  
PA  
XX Conrad B, Mach B;  
PI  
XX WPI; 1999-143118/12.  
DR  
XX New isolated human endogenous retrovirus - used to develop products for  
PT the diagnosis, prevention and treatment of autoimmune disease,  
PT particularly insulin dependent diabetes mellitus.  
XX  
XX Claim 8; Page 90; 165pp; English.  
PS  
XX This oligonucleotide is specific to the polyA signal present in the 3' R-  
CC poly(A) sequences at the 3' extremity of IDDMK1.2-22, a newly identified  
CC human endogenous retrovirus (HERV) that is the source of superantigen  
CC (SAG) activity in insulin-dependent diabetes mellitus (IDDM) patients. It  
CC can be used as a probe or primer (claimed) in a method for the diagnosis  
CC of a human autoimmune disease. IDDMK1.2-22 is ubiquitous in the human  
CC genome but is only expressed in diabetic individuals. The invention  
CC provides IDDMK1.2-22 nucleic acids (see AAX07186-91) and encoded  
CC polypeptides (see AAW97745-48). These can be used in methods for the  
CC diagnosis, treatment and prevention of IDDM  
XX  
SQ Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1951 TTTTGTGTCGCTAAATATTTA 1973  
|||||  
Db 1 TTTTGAGTCCCTTAGTATTTA 23  
|||||

RESULT 2326  
AAX07220  
ID AAX07220 standard; DNA; 25 BP.  
XX  
AC AAX07220;  
XX  
DT 27-AUG-2003 (revised)  
DT 21-MAY-1999 (first entry)  
XX  
DE Retroviral R-poly(A) primer.

XX Human endogenous retrovirus; HERV; IDDKK1.2-22; superantigen; SAg;  
KW antigen; IDDM; insulin-dependent diabetes mellitus; autoimmune disease;  
KW diagnosis; therapy; vaccine; PCR; primer; ss.  
XX  
OS Synthetic.  
OS Retroviridae.  
XX  
PN WO9905527-A2.  
XX  
PD 04-FEB-1999.  
XX  
PF 22-JUL-1998; 98WO-EP004926.  
XX  
PR 22-JUL-1997; 97EP-00112482.  
PR 23-JUL-1997; 97EP-00401773.  
XX  
PA (MEDI-) MEDIGEN SA.  
XX  
XX Conrad B, Mach B;  
PI  
XX  
DR WPI; 1999-143118/12.  
XX  
PT New isolated human endogenous retrovirus - used to develop products for  
PT the diagnosis, prevention and treatment of autoimmune disease,  
PT particularly insulin dependent diabetes mellitus.  
XX  
PS Disclosure; Page 75; 165pp; English.  
XX  
CC This is the nucleotide sequence of primer R-poly(A), which was used with  
CC a U3 primer (see AAX07221) in epidemiological studies of IDDMK1.2-22, a  
CC newly identified human endogenous retrovirus that is the source of  
CC superantigen activity in insulin-dependent diabetes mellitus (IDDM)  
CC patients. IDDMK1.2-22 is found in the plasma of IDDM patients at disease  
CC onset but not in the plasma of healthy controls. The invention provides  
CC nucleic acids (see AAX07186-91) and encoded polypeptides (see AAW97745-  
CC 48) of IDDMK1.2-22. These can be used in methods for the diagnosis,  
CC treatment and prevention of IDDM. (Updated on 27-AUG-2003 to correct OS  
CC field.)  
XX  
SQ Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1951 TTTTGTGTCGCTAAATATTTA 1973  
Db ||||| ||||| ||||| |||||  
1 TTTTGAGTCCCTTAGTATTTA 23  
  
RESULT 2327  
AAZ49618  
ID AAZ49618 standard; DNA; 25 BP.  
XX  
AC AAZ49618;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE PCR primer-2 for synthesis of carrot CR16.1 fragment for plant promoter.  
XX  
KW PCR primer; synthetic DNA; plant promoter; CR16 fragment; carrot;  
KW transgenic plant; soybean glycinin; stearyl-ACP-desaturase gene;  
KW male sterility-related gene; ss.  
XX  
OS Daucus carota.  
XX  
XX  
PN EP976832-A2.  
XX  
PD 02-FEB-2000.  
XX  
PF 13-JUL-1999; 99EP-00113732.  
XX

PR 15-JUL-1998; 98JP-00200372.  
XX  
PA (SUMO ) SUMITOMO CHEM CO LTD.  
XX  
PI Ishige F, Nishikawa S, Oeda K;  
XX WPI; 2000-128374/12.  
DR  
XX  
PT Novel promoter used to produce transgenic plants with higher expression  
PT of a desired gene.  
XX  
PS Example 1; Page 14; 24pp; English.  
XX  
CC The present sequence is a PCR primer used to synthesise carrot CR16.1  
CC fragment. This fragment along with a 10 bp synthetic DNA is used in the  
CC construction of a plant promoter. The promoter is used for controlling  
CC the expression of a desired gene e.g. soybean glycinin, stearyl-ACP-  
CC desaturase and S-locus type specific RNase gene (male sterility-related  
CC gene) in a host cell especially a microorganism or a plant cell. The  
CC transformed plant cells can be used to produce transgenic plants. The  
CC promoter is compact and therefore suitable for higher expression of a  
CC desired gene in a particular tissue compared to other host tissues  
XX  
SQ Sequence 25 BP; 8 A; 9 C; 1 G; 7 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1896 CCCTAGATCAACAGATCAACAAT 1918  
Db ||||| ||||| ||||| |||||  
2 CTCTAGATCAACACCTCAACATT 24  
  
RESULT 2328  
AAC96779/c  
ID AAC96779 standard; DNA; 25 BP.  
XX  
AC AAC96779;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA HLA-A gene PCR primer #156.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 57; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and







QY 1771 TTTTGTGAAACCCCATCT 1793  
Db 2 TTTTGTGAAAGGACATCCT 24

RESULT 2334  
AAC96353/c  
ID AAC96353 standard; DNA; 25 BP.  
XX  
AC AAC96353;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPB1 gene PCR primer #85.  
XX  
KW DNA sequence analysis; sequencing; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 49; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 49; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 5 C; 2 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2801  
Db 23 ACTACTGGAACAAAAA 1

RESULT 2335  
AAC96041  
ID AAC96041 standard; DNA; 25 BP.  
XX  
AC AAC96041;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #8.  
XX  
KW DNA sequence analysis; sequencing; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.  
XX Homo sapiens.  
OS  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 44; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 6 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1771 TTTTGTGAAACCCCATCT 1793  
Db 3 TTTTGTGATACCCCATGT 25

RESULT 2336  
AAC96099  
ID AAC96099 standard; DNA; 25 BP.  
XX  
AC AAC96099;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE 16s rRNA gene PCR primer #66.  
XX  
KW DNA sequence analysis; sequencing; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
OS  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 45; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2176 TTTT TTTT TTTT TTAAC TTTGAAAGT 2198  
Db | | | | | | | | | | | | | | | | |  
1 TTTT TTTT TTTT TTTT CCTTGATACT 23

RESULT 2337  
AAC96245/c  
ID AAC96245 standard; DNA; 25 BP.  
XX  
AC AAC96245;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPAL gene PCR primer #2.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX

Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 48; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 1 A; 2 C; 3 G; 19 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2780 GAATGAAAAA AAAAAA AAAAAA 2802  
Db | | | | | | | | | | | | | | | | |  
23 GTACTGGAACAAAAA AAAAAA 1

RESULT 2339  
AAC96089/c  
ID AAC96089 standard; DNA; 25 BP.  
XX  
AC AAC96089;  
XX  
DT 26-FEB-2001 (first entry)

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2782 ATTGAAAAA AAAAAA AAAAAA 2804  
Db | | | | | | | | | | | | | | | | |  
24 ATAGAACACAGAAAAA AAAAAA 2

RESULT 2338  
AAC96396/c  
ID AAC96396 standard; DNA; 25 BP.  
XX  
AC AAC96396;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DPB1 gene PCR primer #128.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX

Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 50; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2780 GAATGAAAAA AAAAAA AAAAAA 2802  
Db | | | | | | | | | | | | | | | | |  
23 GTACTGGAACAAAAA AAAAAA 1

RESULT 2339  
AAC96089/c  
ID AAC96089 standard; DNA; 25 BP.  
XX  
AC AAC96089;  
XX  
DT 26-FEB-2001 (first entry)



The present sequence is a PCR primer used for cloning the human inhibitor of apoptosis (IAP)-like protein-2 (ILP-2) DNA. The ILP-2 interacts with transforming growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2 is used in the area of genetic testing for predisposition to diseases, such as cone-rod retinal dystrophy-2, retinitis pigmentosa, glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer and hyperferritinaemia-cataract syndrome owing to an ILP-2 deletion or mutation. The ILP is also used in the treatment of diseases associated with abnormal apoptosis such as cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and neurodegenerative diseases including retinal degeneration. The ILP-2 gene is also used in gene therapy for treating patients suffering from ILP-2 gene deletions or mutations

SQ Sequence 25 BP; 7 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels

QY           996 CCTGCGGGAGAAGTTGGACAAG 1018  
               ||| ||| ||| ||| ||| |||  
Db           1 CCTGGCCGCGAAGAAGGTGGACAAG 23

RESULT 2342

ID AAH28308 standard; RNA; 25 BP.

AC AAH28308;

DT 05-SEP-2001 (first entry)

DE 3' untranslated region sequence from CTCF gene.

KW mRNA protein complex; tumour development; cell aging; death;  
KW ribonucleic acid; RNA-binding protein; ss.

OS Unidentified.

PN WO200148480-A1.

05-JUL-2001.

28-DEC-2000; 2000WO-US035583.

PR 28-DEC-1999; 99US-0173338P.

PA (KEEN/) KEENE J D.

PI Keene JD, Tenenbaum SA, Carson C:

DR WPI; 2001-425706/45.

Partitioning endogenous mRNA-protein complexes in vivo, by contacting sample comprising the complex with ligand that binds to a component of the complex and separating complex by binding ligand with a binding molecule.

PS Example 6; Page 31: 49pp; English.

The specification describes a method for partitioning endogenous cellular mRNA-protein (mRNP) complexes. The method comprises contacting a biological sample comprising mRNP complex with ligand that specifically binds a component of mRNP complex, separating mRNP complex by binding the ligand with a molecule specific for ligand, which is attached to the solid support and then collecting the mRNP complex by removing the complex from the support. The method is useful for in vivo partitioning of cellular mRNA protein complexes in a biological sample. The method is useful for determining the ribonomic profile of a cell which has numerous uses including monitoring of tumour development, state of growth or state



CC related to it, where the sequences of pre-mRNA of gene B and genes  
CC related to it are situated upstream to an exon in pre-mRNA of gene B or  
CC genes related to it selected to be spliced to the selected exon of gene  
CC A. The DNA construct is useful for constructing a mouse or human antibody  
CC library. A transgenic non-human animal harbouring the construct is useful  
CC for generating a variegated population of cDNA and double-stranded DNA  
CC molecules suitable for preparation of gene libraries encoding scFv  
CC molecules of antibodies or human T-cell receptors (TCRs) of interest. The  
CC construct is useful for generating a human TCR library, preferably a  
CC phage-display library, comprising a variegated population of scFv  
CC molecules of human TCRs of interest expressed and displayed on the  
CC surface of a cell or viral particle. The transgenic animal is useful for  
CC generating an antibody library comprising a variegated population of scFv  
CC molecules of antibodies of interest expressed and displayed on the  
CC surface of a cell or viral particle. The construct is useful for  
CC intracellular functional joining of antibody heavy and light chain genes  
CC in antibody-producing cells, and for the production of invaluable  
CC reagents in medicine, diagnostic research and industry. The construct  
CC allows the faithful reconstruction of entire antibody immune repertoires  
CC in-vitro as libraries of scFvs displayed on phage or other display units,  
CC and such a capacity combines the extraordinary ability of the immune  
CC system to produce specific, high affinity antibodies in response to  
CC antigen, with the fast and easy protocols of in-vitro display  
CC technologies. The present sequence amplifies a fragment from the human  
CC Cgamma gene being a region of the Cgamma1-hinge intron predicted to  
CC contain the branch point and peptide linker sequence

XX Sequence 25 BP; 5 A; 7 C; 13 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 478 CGGCCGCCAGCAGCGGGAG 500  
Db 2 CGGCCGCCAGCAGCGGGAG 24

RESULT 2344  
ABN15565  
ID ABN15565 standard; DNA; 25 BP.  
XX  
AC ABN15565;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15557.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 15557; 214pp; English.

XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence

XX Sequence 25 BP; 5 A; 11 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 443 CCGCGCCCCACAGCCAGCCAGCA 465  
Db 3 CCGGTGGCCAGAGCCAGCCAGCA 25

RESULT 2345  
ABN15567  
ID ABN15567 standard; DNA; 25 BP.  
XX  
AC ABN15567;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15559.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 15559; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 25 BP; 5 A; 9 C; 9 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 443 CCGGCGCCACAGCCAGCCAGCA 465  
Db 1 CCGGTGGCCAGAGCCAGCCAGCA 23  
RESULT 2346  
ABN15566  
ID ABN15566 standard; DNA; 25 BP.  
XX  
AC ABN15566;  
XX  
DT 29-MAY-2002 (first entry)  
XX  
DE Human GDMPLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:15558.  
XX  
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.

XX  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
PF 25-MAY-2001; 2001WO-US016981.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
DR WPI; 2002-179446/23.  
XX  
PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
PS Disclosure; SEQ ID NO 15558; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC protein variants having desired phenotypic improvements, and for  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 25 BP; 5 A; 10 C; 8 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 443 CCGGCGCCACAGCCAGCCAGCA 465  
Db 2 CCGGTGGCCAGAGCCAGCCAGCA 24  
RESULT 2347  
ABL43221/c

ID ABL43221 standard; DNA; 25 BP.  
XX ABL43221;  
AC ABL43221;  
XX 11-APR-2002 (first entry)  
DT Human chromosome 1p36-35 PCR primer SEQ ID NO:265.  
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;  
DE PCR primer; ss.  
KW Homo sapiens.  
XX JP2001321190-A.  
PN 20-NOV-2001.  
XX 12-MAR-2001; 2001JP-00068285.  
PF 10-MAR-2000; 2000JP-00066716.  
XX (RIKA ) RIKAGAKU KENKYUSHO.  
PA (GENO-) GENOTEX YG.  
XX WPI; 2002-144136/19.  
DR Arraying genome clones.  
XX Claim 4; Page 10; 528pp; Japanese.  
PS The present invention describes a method of arraying genome clones. The  
XX method comprises: (a) clones of the genomic libraries contained in  
CC multiwell plates numbered for discrimination are mixed in each of the  
CC multiwell plates; (b) a primer designed based on the chromosome marker  
CC sequence is added to the mixture to carry out an amplification reaction;  
CC (c) a signal corresponding to the marker is detected from the resultant  
CC amplified product to specify the discrimination Nos. of the multiwell  
CC plates containing the clones having said marker sequence; (d) the order  
CC of the markers is changed so that the same discrimination Nos. succeed to  
CC the maximum in the specified discrimination Nos. to array the multiwell  
CC plates; (e) the clones in the multiwell plates of the specified  
CC discrimination Nos. are mixed respectively in each wells of longitudinal  
CC and lateral directions; (f) the mixed clones are cultured and the  
CC resultant cultures are amplified by using the above primer; (g) signals  
CC are detected from the amplified products; (h) the clones in the multiwell  
CC plates are specified from the detected result; and (i) the clones are  
CC reconstituted as the positions on the chromosome and arrayed. The  
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent  
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634  
CC represent PCR primers for human chromosome 21q22.1, which are  
CC specifically claimed for use in the present invention  
XX  
SQ Sequence 25 BP; 13 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2589 CTATTTAATTGAAACTCTCTGTT 2611  
DB 25 CGATTTTATTGAAACCTCTGTT 3  
RESULT 2348  
ABS75946  
ID ABS75946 standard; DNA; 25 BP.  
XX ABS75946;  
AC ABS75946;  
XX 27-DEC-2002 (first entry)  
DT Human PAPP-Ea associated 25-mer SEQ ID 1472.  
XX

KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX Homo sapiens.  
OS US2002102252-A1.  
XX 01-AUG-2002.  
PN 06-APR-2001; 2001US-00827998.  
PD 26-MAY-2000; 2000US-0207456P.  
XX (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX Gu Y, Shannon ME;  
PI WPI; 2002-697817/75.  
XX New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX Example 2; Page 268; 353pp; English.  
PS This invention describes a novel isolated nucleic acid that encodes one  
XX of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 444 CGGCGCCACAGGCGAGCCAGCAG 466  
DB 1 CGGCCAGCACAGGTAGCCAGCAG 23  
RESULT 2349  
ABS75944  
ID ABS75944 standard; DNA; 25 BP.  
XX ABS75944;  
AC ABS75944;  
XX 27-DEC-2002 (first entry)  
DT Human PAPP-Ea associated 25-mer SEQ ID 1470.  
XX PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX Homo sapiens.  
OS US2002102252-A1.  
PN 01-AUG-2002.  
PD 06-APR-2001; 2001US-00827998.  
XX



PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX  
DR WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX  
PS Example 2; Page 268; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 444 CGCGCCACAGGCCAGCCAGCAG 466  
Db 3 CGGCCAGCACAGGTAGCCAGCAG 25  
RESULT 2350  
ABS75945  
ID ABS75945 standard; DNA; 25 BP.  
XX  
AC ABS75945;  
XX  
DT 27-DEC-2002 (first entry)  
XX  
DE Human PAPP-Ea associated 25-mer SEQ ID 1471.  
XX  
KW PAPP-E; human; pregnancy associated plasma protein E; abortive;  
KW contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;  
KW dysgenetic pregnancy; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002102252-A1.  
XX  
PD 01-AUG-2002.  
XX  
PF 06-APR-2001; 2001US-00827998.  
XX  
PR 26-MAY-2000; 2000US-0207456P.  
XX  
PA (GUY/) GU Y.  
PA (SHAN/) SHANNON M E.  
XX  
PI Gu Y, Shannon ME;  
XX  
DR WPI; 2002-697817/75.  
XX  
PT New isolated nucleic acid encoding an isoform of human pregnancy  
PT associated plasma protein E, for preventing or aborting pregnancy.  
XX

PS Example 2; Page 268; 353pp; English.  
XX  
CC This invention describes a novel isolated nucleic acid that encodes one  
CC of three new isoforms of human pregnancy associated plasma protein E,  
CC hPAPP-E. The products of the invention have abortive and contraceptive  
CC activity and can be used for gene therapy or in a vaccine. The nucleic  
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be  
CC used in pharmaceutical compositions or vaccines for preventing or  
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of  
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess  
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the  
CC antibodies can be used to assess the expression levels of PAPP-E isoform  
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies  
CC antenatally. This sequence represents an oligomer used in scanning the  
CC human PAPP-E genes described in the disclosure of the invention  
XX  
SQ Sequence 25 BP; 7 A; 8 C; 9 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 444 CGCGCCACAGGCCAGCCAGCAG 466  
Db 2 CGGCCAGCACAGGTAGCCAGCAG 24  
RESULT 2351  
ABK90953  
ID ABK90953 standard; DNA; 25 BP.  
XX  
AC ABK90953;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE PCR primer, 25657, used to amplify human C gamma CH1-hinge intron.  
XX  
KW Human; PCR; primer; ss; antiHIV; chimeric protein; HIV-1;  
KW human immunodeficiency virus-1; envelope glycoprotein; env; gp120; CD4;  
KW cellular receptor; immunoglobulin; Ig; V1; V2; variable region;  
KW variable region-like membrane distal domain; antibody; heavy chain; VH;  
KW VH3; gene therapy; HIV infection; virus replication; constant gamma;  
KW C gamma; CH1-hinge; CH1.  
XX  
OS Homo sapiens.  
XX  
PN WO200259258-A2.  
XX  
PD 01-AUG-2002.  
XX  
PF 22-JAN-2002; 2002WO-IL000060.  
XX  
PR 22-JAN-2001; 2001IL-00141023.  
XX  
PA (GAVI-) GAVISH-GALILEE BIO APPL LTD.  
XX  
PI Gross G, Meyuhas R;  
XX  
DR WPI; 2002-608450/65.  
XX  
PT New nucleic acid molecule encoding chimeric proteins with binding  
PT specificity for a site on HIV envelope glycoprotein gp120 and a site on  
PT gp120 protein or on the extracellular portion of human CD4, for  
PT preventing or treating HIV infection.  
XX  
PS Example 1; Page 23; 48pp; English.  
XX  
CC The invention discloses a nucleic acid molecule encoding a functional  
CC chimeric protein with binding specificity for at least two different  
CC sites. At least one site is on the human immunodeficiency virus-1 (HIV-1)  
CC envelope glycoprotein (env), gp120, and the other site is either on the  
CC gp120 protein or on the extracellular portion of human CD4, the major  
CC cellular receptor for HIV. The chimeric protein essentially comprises a



CC first binding region of a soluble extracellular portion of human CD4,  
CC consisting of the immunoglobulin (Ig) variable region-like membrane  
CC distal domains (V1 and V2) and a second binding region of a variable  
CC region of an antibody heavy chain (VH), encoded by the VH3 gene, which is  
CC capable of being attached to an adjacent and non-overlapping site on the  
CC gp120 protein, or to a site on the extracellular portion of human CD4,  
CC and is capable of increasing the capacity of the extracellular portion of  
CC human CD4 to interact with gp120 and to block the interaction of HIV with  
CC membranal CD4. These two binding regions are physically connected by a  
CC linker region. The chimeric protein of the invention is useful for gene  
CC therapy and for preventing and treating an HIV infection and for  
CC neutralising and inhibiting virus replication and infectivity in a  
CC subject, preferably a mammal. The sequence presented is the PCR primer,  
CC 25657, which was used to amplify the human constant (C) gamma heavy chain  
CC domain, CH1, gene of the Ig chain used in the construction of the  
CC chimeric protein

SQ Sequence 25 BP; 5 A; 7 C; 13 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 478 CGGCCGCCAGAGCCAGGAGGAG 500  
||||||| | |||||  
Db 2 CGGCCGCCAGACAGGGAGGAG 24

RESULT 2352  
ABZ83992/c  
ID ABZ83992 standard; DNA; 25 BP.  
XX  
AC ABZ83992;  
XX  
DT 14-MAY-2003 (first entry)  
XX

DE Toxicologically relevant human PCR primer #1151.

XX Toxicologically relevant gene; toxicological response; PCR primer; ss.  
KW  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO2003016500-A2.  
XX  
PD 27-FEB-2003.  
XX

PF 16-AUG-2002; 2002WO-US026514.

PR 16-AUG-2001; 2001US-0313080P.

XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
XX  
XX Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweiser K;  
PI Alen P;  
XX  
DR WPI; 2003-268322/26.

XX Determining a toxicological response to an agent, useful for screening of  
PT drugs, comprises comparing the expression profile of one or more human  
PT toxic response genes to a reference gene expression profile indicative of  
PT toxicity.  
XX  
PS Claim 1; Page 326; 455pp; English.  
XX

CC The present invention describes a method (M1) for determining a  
CC toxicological response to an agent, which comprises comparing the  
CC expression profile of one or more human toxic response genes to a  
CC reference gene expression profile indicative of toxicity, and so  
CC determining the presence of a toxic response to the agent. Also  
CC described: (1) an array comprising one or more polynucleotides selected  
CC from the genes corresponding to the partial sequences given in ABZ82842  
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues

CC ; and (2) determining if a gene putatively identified to be a toxic  
CC response gene plays a role on toxic response pathways by determining the  
CC expression profile of the gene after exposure of cells or a human subject  
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)  
CC exposing cells to an agent or isolating cells from a human subject who  
CC was exposed to an agent; (b) obtaining the test gene expression profile  
CC for a putatively identified toxic response gene after exposure to a known  
CC toxic pharmaceutical or industrial agent; and (c) comparing the test  
CC profile to the expression profile of a gene with a similar function or  
CC comparing the test profile to the expression profile of that gene after  
CC exposure to other known toxic compounds. The methods are useful for  
CC predicting and determining toxicological responses on a cellular, organ  
CC or system level. The arrays comprising the human genes are useful for  
CC toxicological screening of drugs, pharmaceutical compounds and chemicals  
XX  
SQ Sequence 25 BP; 5 A; 2 C; 12 G; 6 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 424 CATCAACCCCTGCACCAGCCGG 446  
||||| | |||||  
Db 23 CATTAACCTCCTCCACCAGCCTG 1

RESULT 2353  
AAD53331  
ID AAD53331 standard; DNA; 25 BP.  
XX  
AC AAD53331;  
XX

DT 28-MAY-2003 (first entry)

DE Probe used in human mucin (MUC4) gene expression studies.

XX Human; mucin; calcium activated chloride channel; CLCA4; CLCA2; asthma;  
KW COPD; chronic obstructive pulmonary disease; cystic fibrosis; therapy;  
KW chronic bronchitis; bronchiectasis; MUC; probe; ss.  
XX

OS Homo sapiens.

XX WO200294876-A2.

PD 28-NOV-2002.

XX 08-MAY-2002; 2002WO-EP005119.

PR 18-MAY-2001; 2001US-00861038.

XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.

XX Szymkowski DE;

PI WPI; 2003-140363/13.

XX New murine calcium activated chloride channel (mCLCA4) for identifying  
PT mCLCA4 expression regulatory factors for treating respiratory mucin  
PT production associated disease conditions, e.g. chronic bronchitis, and  
PT asthma.

XX Example 5; Col 44; 39pp; English.

XX The invention relates to methods and compositions for modulating mucin  
CC secretion by respiratory system cells. The invention also provides murine  
CC calcium activated chloride channel, CLCA4 and human CLCA2 polypeptides  
CC and polynucleotides. CLCA2 sequences are used to diagnose the presence of  
CC mucin secretion respiratory system associated disease conditions in host.  
CC CLCA2 modulators are useful for preparing a composition for the treatment  
CC of respiratory mucin production associated disease conditions such as  
CC asthma, chronic bronchitis, chronic obstructive pulmonary disease (COPD),  
CC cystic fibrosis or bronchiectasis. Sequences of the invention are used in  
CC the identification of mCLCA4 homologues, as a source of new promoter

CC elements, in the identification of mCLCA4 expression regulatory factors,  
CC as probes and primers in hybridisation applications, in identification of  
CC expression patterns in biological specimens and in the preparation of in  
CC vitro models for mCLCA4 function. The present sequence is a probe used in  
CC human mucin gene expression studies  
XX  
SQ Sequence 25 BP; 5 A; 10 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 293 GCGCCACCCCTCTCCACACTGG 315  
||| |||||  
Db 2 GGGCGATACCTCTCCACACTGG 24

RESULT 2354  
AAL61680/c  
ID AAL61680 standard; DNA; 25 BP.  
XX  
AC AAL61680;  
XX  
DT 22-SEP-2003 (first entry)  
XX  
DE Oligonucleotide #37 used in the nucleic acid detection method.  
XX  
KW Nucleic acid detection; fabrication; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003035829-A2.  
XX  
PD 01-MAY-2003.  
XX  
PF 08-OCT-2002; 2002WO-US032088.  
XX  
PR 09-OCT-2001; 2001US-0327864P.  
PR 07-DEC-2001; 2001US-00008978.  
XX  
PA (NANO-) NANOSPHERE INC.  
XX  
PI Park S, Taton TA, Mirkin CA;  
XX  
DR WPI; 2003-430409/40.

CC Detecting nucleic acid having two portions, by providing nanoparticles  
CC having oligonucleotides attached to it, contacting nucleic acid and  
CC nanoparticles to allow hybridization, and observing detectable change.  
XX  
PS Disclosure; Fig 68; 467pp; English.  
XX  
CC The invention relates to a method of detecting a nucleic acid having two  
CC portions. The method involves providing nanoparticles having  
CC oligonucleotides attached to it which has a sequence complementary to  
CC sequence of two portions of nucleic acid, contacting nucleic acid and  
CC nanoparticles to allow hybridisation of oligonucleotides with two or more  
CC portions of nucleic acid and observing a detectable change brought about  
CC by hybridisation. The method and aggregate probes are useful for  
CC detecting two or more nucleic acids (from a biological source) having at  
CC least two portions such as viral RNA, bacterial or fungal DNA, a gene  
CC associated with a disease, synthetic or structurally modified natural or  
CC synthetic RNA or DNA, or a product of a polymerase chain reaction  
CC amplification. The invention is useful for preparing a nanoprobe  
CC conjugate for detecting an analyte and for detecting a nucleic acid bound  
CC to an electrode surface. It is also useful for fabrication and for  
CC separating a selected nucleic acid having two portions from other nucleic  
CC acids. The present sequence is an oligo used to illustrate the method of  
CC the invention  
XX

SQ Sequence 25 BP; 15 A; 3 C; 0 G; 7 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;

Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 1759 TATTCATTAAAGCTTTT TTTT TTTT 1781  
||||| ||| |||||  
Db 23 TATTGATAAGGATTTT TTTT TTTT 1

RESULT 2355  
ACI99045/c  
ID ACI99045 standard; DNA; 25 BP.  
XX  
AC ACI99045;  
XX  
DT 14-OCT-2003 (first entry)  
XX

DE Human microarray DNA oligonucleotide SEQ ID NO 99036.  
XX  
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.  
XX

OS Homo sapiens.  
XX  
PN US2003104410-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 15-MAR-2002; 2002US-00098263.  
XX  
PR 16-MAR-2001; 2001US-0276759P.  
XX  
PA (AFFY-) AFFYMETRIX INC.  
XX  
PI Mittmann MP;  
XX  
DR WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.  
XX  
PS Claim 1; SEQ ID NO 99036; 9pp; English.

XX  
CC The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html  
XX

SQ Sequence 25 BP; 14 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1774 TTTT TTTTGAACCCATTCTTTC 1796  
Db 24 TTCTTTTGTACACGATTCTTTC 2

RESULT 2356  
ACI22395/c  
ID ACI22395 standard; DNA; 25 BP.

XX AC ACI22395;

XX DT 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 22386.

DE EST; ss; probe; expressed sequence tag; microarray; gene expression;  
XX genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX WPI; 2003-567953/53.

DR New array of nucleic acid probes, useful for in situ hybridization, in  
XX Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 22386; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 4 A; 9 C; 4 G; 8 T; 0 U; 0 Other;

QY Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1527 ACGAAGAAAGGTTAGGAGTAG 1549

Db 24 ACGAAGACAGCTTAGCGGAGTAG 2

RESULT 2357  
ACK13084/c

ID ACK13084 standard; DNA; 25 BP.

XX AC ACK13084;

XX DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 113065.

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;  
KW genetic variation; biallelic marker; polymorphism; human;  
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in  
PT Southern, Northern or dot-blot hybridization to identify or detect the  
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 113065; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
CC acid probes including one of 2,018,500 fully defined sequences, or its  
CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
CC Also disclosed is a method of gene expression analysis. The array is used  
CC in monitoring gene expression levels by hybridisation to a DNA library,  
CC in analysis of genetic variation or in hybridisation of tag-labelled  
CC compounds. The nucleic acid probes are specifically designed for analysis  
CC of at least one target sequence. The method of analysis comprises  
CC hybridising at least one or more nucleic acids to at least two or more  
CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
CC probes are attached to a solid support. The analysis comprises monitoring  
CC gene expression levels, identifying biallelic markers or polymorphisms,  
CC or family members of a gene and a cross-species comparison. Each of the  
CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
CC blot hybridisation to identify or detect the sequence or specific  
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
CC primer extensions or in screening cDNA or genomic libraries or subclones  
CC for additional subclones containing segments of DNA that have been  
CC isolated and previously sequenced. The sequence presented is one of the  
CC nucleic acid probes incorporated in the microarray. Note: The sequence  
CC data for this patent can also be obtained in electronic format directly  
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;

QY Query Match 0.6%; Score 16.6; DB 1; Length 25;  
Best Local Similarity 82.6%; Pred. No. 2.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 706 CGACGACCAGCACCTGTGCTGC 728

Db 25 CGACGACACGCACCTTTTCTGC 3









Key	Location/Qualifiers
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2	2
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4	4
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91	91
92	92
93	93
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99	99
100	100



PT New oligomers contg. modified bases - which form a triplex with G-C  
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
PT herpes malignancy and inflammation.  
XX  
PS Claim 12; Page 72; 77pp; English.  
XX  
CC The synthetic oligomer is capable of forming a triplex at physiological  
CC pH with a purine rich target sequence by coupling into the major groove  
CC of the duplex. The specific target sequence of this oligomer is the human  
CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.  
CC a purine rich sequence concd. on one strand of the duplex. The oligomer,  
CC and others like it are useful in diagnosis and therapy of diseases  
CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,  
CC hepatitis B, herpes, malignant tumours and inflammation. The triple  
CC helices form under mild conditions thus assays may be carried out without  
CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501  
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated  
CC on 25-MAR-2003 to correct PD field.)  
XX  
SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0  
  
Qy 2170 TTTTCTTTTCTTTTCTTTT 2187  
Db 1 TTTCTTTTCTTTTCTTTT 18  
  
RESULT 2369  
AAQ25501/c  
ID AAQ25501 standard; DNA; 18 BP.  
XX  
AC AAQ25501;  
XX  
DT 25-MAR-2003 (revised)  
DT 07-DEC-1992 (first entry)  
XX  
DE Purine rich HUMNFR target duplex sequence.  
XX  
KW Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;  
KW hepatitis; malignancy; inflammation; ds.  
XX  
OS Synthetic.  
XX  
PN WO9209705-A1.  
XX  
PD 11-JUN-1992.  
XX  
PF 25-NOV-1991; 91WO-US008811.  
XX  
PR 23-NOV-1990; 90US-00617907.  
PR 18-JAN-1991; 91US-00643382.  
PR 08-APR-1991; 91US-00683420.  
PR 17-APR-1991; 91US-00686544.  
PR 17-APR-1991; 91US-00686546.  
PR 17-APR-1991; 91US-00686547.  
PR 27-SEP-1991; 91US-00766733.  
XX  
PA (GILE-) GILEAD SCI INC.  
XX  
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;  
XX  
DR WPI; 1992-217083/26.  
XX  
PT New oligomers contg. modified bases - which form a triplex with G-C  
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,  
PT herpes malignancy and inflammation.  
XX  
PS Claim 11; Page 64; 77pp; English.  
XX  
CC The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA



sequence beginning at nucleotide 2354. The sequence is a viral duplex sequence contg. a purine-rich region concentrated on one chain of the duplex. The sequence may be prepd. by standard DNA synthesis. The HUMNFR duplex sequence is used as a target for novel oligomers which are capable of forming a triplex at physiological pH by coupling into the major groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of forming a triplex with this sequence. The oligomers are used in the treatment of inflammation. Similar oligomers may be used to target viral DNA duplexes specific for HIV, herpes and other viruses. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)

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PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
XX Claim 12; Page 72; 77pp; English.
PS
XX The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC and others like it are useful in diagnosis and therapy of diseases
CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC hepatitis B, herpes, malignant tumours and inflammation. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
CC and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PD field.)
XX
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2785 GAAAAAAAAAAAAAAAAA 2802
Db 18 GAAAAAAAAAAAAAAAAA 1
|||||
RESULT 2371
AAQ30447/c
ID AAQ30447 standard; DNA; 18 BP.
XX
AC AAQ30447;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
DE Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
XX
KW Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
KW HPV; malignancy; hepatitis; inflammation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 5 /*tag= a
FT /*mod_base= m5c
FT modified_base 18
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "OTHER= N4 N4 ethanocytosine"
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US008811.
XX
XX 23-NOV-1990; 90US-00617907.
XX 18-JAN-1991; 91US-00643382.
XX 08-APR-1991; 91US-00683420.
XX 17-APR-1991; 91US-00686544.
XX 17-APR-1991; 91US-00686546.
XX 17-APR-1991; 91US-00686547.
XX 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
DR

```



XX AAF75597;  
AC 10-MAY-2001 (first entry)  
XX  
DT  
XX  
DE Binary encoded sequence tag method anchored primer #2.  
XX  
XX Binary encoded sequence tag; BEST; nucleic acid analysis;  
KW gene expression; adaptor; PCR primer; ss.  
KW  
KW  
OS Synthetic.  
XX  
XX WO200112855-A2.  
PN  
XX  
XX 22-FEB-2001.  
PD  
XX  
XX 11-AUG-2000; 2000WO-US022164.  
PF  
XX  
XX 13-AUG-1999; 99US-0148870P.  
PR  
PR 06-APR-2000; 2000US-00544713.  
XX  
XX (UYVA ) UNIV YALE.  
PA  
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;  
XX  
XX WPI; 2001-202878/20.  
DR  
XX  
XX Producing binary sequence tags, useful for analyzing nucleic acid  
PT sequence tags, gene expression or gene-expression patterns, involves  
PT generating nucleic acid fragments, which are mixed with offset adaptors  
PT and adaptor-indexers.  
XX  
XX Disclosure; Page 100; 101pp; English.  
PS  
XX The present invention describes a method of producing binary sequence  
CC tags from nucleic acid fragments in a sample, involving incubating the  
CC sample with cleaving reagents, mixing offset adaptors with the sample,  
CC incubating with more cleaving reagents and mixing the sample with adaptor  
CC -indexers where the adaptors are coupled to binary sequence tags. The  
CC method is useful in sequence analysis, including analysis and comparison  
CC of gene expression, nucleic acid samples and genomes  
XX  
XX Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;  
SQ  
Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAAAAAAAAAAAAAAAAA 1  
RESULT 2375  
AAF99943  
ID AAF99943 standard; DNA; 20 BP.  
XX  
AC AAF99943;  
XX  
DT 12-JUL-2001 (first entry)  
XX  
DE Synthetic oligonucleotide #9.  
XX  
XX Oligonucleotide purification; liquid chromatography;  
KW hydrophobic protective group; deprotection; ds.  
XX  
XX Synthetic.  
OS  
XX JP2000342265-A.  
PN  
XX 12-DEC-2000.  
PD  
XX  
XX 02-JUN-1999; 99JP-00154974.  
PF

XX 02-JUN-1999; 99JP-00154974.  
PR  
XX (TOAG ) TOA GOSEI CHEM IND LTD.  
PA  
XX  
DR WPI; 2001-268251/28.  
XX  
PT A process for purification of oligonucleotides using liquid  
PT chromatography.  
XX  
PS Example 1; Page 4; 13pp; Japanese.  
XX  
CC The present sequence is an oligonucleotide provided in a specification  
CC relating to the simplified purification of oligonucleotides by liquid  
CC chromatography. The process comprises: (a) pouring oligonucleotides  
CC protected with a hydrophobic group and oligonucleotide with no protective  
CC group into a liquid chromatography column packed with an acid and alkali  
CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed  
CC developing solvent composed of a buffer made from a volatile salt and a  
CC water soluble organic solvent at a suitable concentration gradient into  
CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into  
CC the column to deprotect the oligonucleotides protected with the  
CC hydrophobic group; (d) pouring a mixed developing solvent composed of a  
CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous  
CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water  
CC soluble organic solvent at a suitable concentration gradient to elute the  
CC deprotected oligonucleotides; and (e) removal of the solvent and the salt  
CC from the eluted oligonucleotides  
XX  
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 2 AAAAAAAAAAGAAAAAAAAA 19  
RESULT 2376  
ABZ91658  
ID ABZ91658 standard; DNA; 20 BP.  
XX  
AC ABZ91658;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
PF  
XX 24-APR-2001; 2001US-0286137P.  
PR  
XX (EPIG-) EPIGENESIS PHARM INC.  
PA  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
DR

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 6900; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA AAAAAAAAAA 2800  
||| ||||| ||||| ||||| |||||  
Db 3 TTAAAAA AAAAAAAAAA 20

RESULT 2377  
ABZ89872  
ID ABZ89872 standard; DNA; 20 BP.  
XX  
AC ABZ89872;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 5114; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of ubiquinone or  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2784 TGA AAAAAAAAAA AAAAAA 2801  
||| ||||| ||||| ||||| |||||  
Db 2 TCA AAAAAAAAAA AAAAAA 19

RESULT 2378  
AAV12302  
ID AAV12302 standard; DNA; 20 BP.  
XX  
AC AAV12302;  
XX  
DT 17-JUN-1998 (first entry)  
XX  
DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.  
XX  
KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;  
KW housekeeping gene; identification; modulator; metastasis; neoplastic;  
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9800532-A2.  
XX  
PD 08-JAN-1998.  
XX  
PF 30-JUN-1997; 97WO-CA000454.  
XX  
PR 01-JUL-1996; 96US-0021152P.  
XX  
PA (WRIG/) WRIGHT J A.  
PA (YOUN/) YOUNG A H.  
XX  
PI Wright JA, Young AH;  
XX  
DR WPI; 1998-086958/08.  
XX  
PT New oligo-nucleotide(s) complementary to untranslated regions of  
housekeeping genes - are useful in, e.g. identifying modulators of tumour







ABA05916/C  
ID ABA05916 standard; DNA; 20 BP.  
XX  
AC ABA05916;  
XX  
DT 05-MAR-2002 (first entry)  
XX  
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.  
XX  
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;  
KW PCR primer; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN EP1152063-A1.  
XX  
PD 07-NOV-2001.  
XX  
PF 03-MAY-2000; 2000EP-00109436.  
XX  
PR 03-MAY-2000; 2000EP-00109436.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Schroeder KH, Koike K;  
XX  
XX WPI; 2002-068256/10.  
DR  
XX  
XX Diagnosing hepatitis B virus (HBV) infection stages and determining the  
PT risk for hepatocellular carcinoma, comprises identifying full length HBV  
PT transcripts and truncated HBV transcripts in a serum sample.  
XX  
PS Example 1; Page 6; 25pp; English.  
XX  
XX The invention relates to diagnosis of hepatitis B virus (HBV) infection  
CC stages comprising identification of full length HBV transcripts (I) and  
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II  
CC is indicative of a particular infection stage. The method is useful for  
CC diagnosing HBV infection stages and determining the risk for developing  
CC hepatocellular carcinoma. The present sequence is that of a HBV  
CC diagnostic PCR primer, useful for the invention  
XX  
SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 1  
DB 18 TTCAAAAA 1  
RESULT 2384  
ABZ87902  
ID ABZ87902 standard; DNA; 20 BP.  
XX  
AC ABZ87902;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human oligonucleotide sequence.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200285308-A2.

XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002WO-US013135.  
XX  
PR 24-APR-2001; 2001US-0286137P.  
XX  
PA (EPIG-) EPIGENESIS PHARM INC.  
XX  
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
DR WPI; 2003-229219/22.  
XX  
PT Pharmaceutical composition for treating ailments associated with impaired  
PT respiration, has oligo(s) antisense to specific gene(s) or its  
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
PT ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 3144; 872pp; English.  
XX  
CC The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels  
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 20 BP; 3 A; 5 C; 10 G; 2 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 551 TCCGGGCTGGAGCGGGC 568  
DB 3 TCCGGGCTGGAGGAGGC 20  
RESULT 2385  
ABX75043  
ID ABX75043 standard; DNA; 20 BP.  
XX  
AC ABX75043;  
XX  
DT 25-MAR-2003 (first entry)  
XX  
DE Human gene 216 polymorphism detection PCR primer #100.  
XX  
KW Human; mouse; ss; primer; gene 216; antiasthmatic; antiinflammatory;  
KW anorectic; chromosome 20p13-p12; single nucleotide polymorphism; SNP;  
KW gene therapy; respiratory disease; asthma; obesity; PCR;  
KW bronchial hyper-responsiveness; chronic obstructive pulmonary disease;  
KW adult respiratory distress syndrome; inflammatory bowel syndrome.  
XX  
OS Homo sapiens.  
XX  
PN WO200283077-A2.







PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
  
RESULT 2390  
AAZ26142/c  
ID AAZ26142 standard; DNA; 21 BP.  
XX  
AC AAZ26142;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 331.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX

CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTATT 1  
  
RESULT 2391  
AAZ26268  
ID AAZ26268 standard; DNA; 21 BP.  
XX  
AC AAZ26268;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 457.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX





CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 1 AAAAAAAAAAAAAAAAAA 18  
RESULT 2394  
AAZ26141/c  
ID AAZ26141 standard; DNA; 21 BP.  
XX  
AC AAZ26141;  
XX  
DT 30-NOV-1999 (first entry)  
XX  
DE Human polymorphic region 330.  
XX  
KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;  
KW cell viability; loss of heterozygosity; precancerous condition; ASI;  
KW allele specific inhibitor; somatic cell; diagnosis; prevention;  
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;  
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;  
KW graft versus host disease; malignant cell removal; bone marrow; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9841648-A2.  
XX  
PD 24-SEP-1998.  
XX  
PF 19-MAR-1998; 98WO-US005419.  
XX  
PR 20-MAR-1997; 97US-0041057P.  
XX  
PA (VARI-) VARIAGENICS INC.  
XX  
PI Housman D, Ledley FD, Stanton VP;  
XX  
DR WPI; 1998-521232/44.  
XX  
PT Identifying target genes for allele-specific drugs - used for diagnosis,  
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,  
PT dysplastic lesions, endometriosis or graft versus host disease.  
XX  
PS Disclosure; Fig 7; 605pp; English.  
XX  
CC This invention describes a novel method for identifying an inhibitor  
CC potentially useful for treatment of cancer, where the inhibitor is active  
CC on a gene vital for cell growth or viability, and where the gene is  
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is  
CC used for preventing the development of cancer in a patient having a  
CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove

CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention  
XX  
SQ Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTTTT 2183  
Db 18 TTTTTTTTTTTTTTTATT 1  
RESULT 2395  
ABK15655  
ID ABK15655 standard; DNA; 21 BP.  
XX  
AC ABK15655;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Anchored oligo-dt reverse primer.  
XX  
KW ss; lipoxigenase; RCI-1; transgenic; plant; plant antifungal;  
KW rice chemically induced cDNA; promoter; transit peptide; plastid;  
KW fungal mycotoxin inhibitor; plant breeding; PCR; primer.  
XX  
OS Synthetic.  
XX  
PN WO200206490-A1.  
XX  
PD 24-JAN-2002.  
XX  
PF 12-JUL-2001; 2001WO-EP008085.  
XX  
PR 13-JUL-2000; 2000GB-00017275.  
PR 15-SEP-2000; 2000GB-00022739.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA (UYZU-) UNIV ZUERICH.  
XX  
PI Dudler R, Schaffrath U, Lawton KA;  
XX  
DR WPI; 2002-188550/24.  
XX  
PT Novel isolated nucleic acid encoding a promoter which is capable of  
PT driving chemically inducible but not wound- or pathogen-inducible  
PT expression of an associated nucleotide sequence.  
XX  
PS Example 3; Page 30; 88pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (a promoter of  
CC rice chemically induced cDNA (RCI-1), which encodes a lipoxigenase)  
CC capable of driving chemically-inducible but not wound- or pathogen-  
CC inducible expression of an associated protein, a 4.5kb genomic clone for the  
CC are the RCI-1 cDNA, its encoded protein, a lipoxigenase transcript  
CC lipoxigenase gene, promoter fragments, the lipoxigenase transit peptide  
CC which directs expressed proteins to the plastid, a vector comprising the  
CC promoter or fragments and a transgenic plant comprising the vector. The  
CC promoter or fragments are useful for expressing a nucleotide sequence of  
CC interest. The transit peptide is useful for targeting an associated  
CC protein of interest to plastids. A nucleic acid which expresses  
CC polypeptide having lipoxigenase activity is useful for inhibiting fungal  
CC mycotoxins when transformed into a plant. The lipoxigenase is useful for  
CC inhibiting fungal mycotoxins. The promoter is useful for regulating  
CC transcription of a chemically inducible but not wound or pathogen  
CC inducible gene, which involves applying a chemical regulator to a plant  
CC or seed containing a chemically regulatable nucleotide sequence.  
CC transgenic plants as described above are useful for breeding improved  
CC plant lines that for example increase the effectiveness of conventional  
CC methods such as herbicide or pesticide treatment or allow to dispense  
CC with the methods due to their modified genetic properties. New crops with



CC improved stress tolerance can be obtained that, due to their optimised  
CC genetic equipment yield harvested product of better quality than products  
CC that were not able to tolerate comparable adverse developmental  
CC conditions. The present sequence is an anchored oligo-dt reverse RT-PCR  
CC primer (reverse transcriptase PCR) used to isolate the cDNA encoding rice  
CC lipoxigenase  
XX  
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 16 T; 0 U; 1 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2163 TCCTTTTTTTTTTTTTTTT 2180  
Db 3 TGCCTTTTTTTTTTTTTTT 20  
  
RESULT 2396  
ABK99283/c  
ID ABK99283 standard; RNA; 21 BP.  
XX  
AC ABK99283;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #13.  
XX  
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.  
XX  
OS Synthetic.  
XX  
PN US2002064771-A1.  
XX  
PD 30-MAY-2002.  
XX  
PF 06-APR-2001; 2001US-00828034.  
XX  
PR 07-APR-2000; 2000US-0195852P.  
XX  
PA (ZHON/) ZHONG W.  
PA (HONG/) HONG Z.  
PA (FERR/) FERRARI E.  
XX  
PI Zhong W, Hong Z, Ferrari E;  
XX  
DR WPI; 2002-582330/62.  
XX  
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3  
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,  
PT and template and primer which do not form a stable duplex in the absence  
PT of HCV NS5B.  
XX  
PS Example; Page 6; 17pp; English.  
XX  
CC The invention relates to a replicase complex comprising a hepatitis C  
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a  
CC complementary nucleic acid primer which is annealed to the 3' terminus of  
CC the template, where the template is at least three nucleotides and the  
CC primer is two or three nucleotides, and the template and primer do not  
CC form a stable duplex in solution in the absence of the HCV NS5B protein.  
CC The complex is useful for detecting HCV replicase activity and permits  
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen  
CC and evaluate antiviral inhibitors and to improve the specificity and  
CC efficacy of the inhibitors. The complex is also useful in the development  
CC of a reliable system for determining kinetic and thermodynamic constants  
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of  
CC mechanistic inhibitors for mis-incorporation or chain termination.  
CC Specifically, the short RNA template and primer pairs are useful in  
CC screening assays which are used for determining kinetic, thermodynamic  
CC and mechanistic properties of NS5B replication and ultimately in the  
CC development of inhibitors of NS5B. Newly identified inhibitors of  
CC replicase activity may be used for developing anti-HCV pharmaceuticals.

CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis  
CC templates  
XX  
SQ Sequence 21 BP; 16 A; 3 C; 1 G; 0 T; 1 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTTTT 2182  
Db 18 CTGTTTTTTTTTTTTTT 1  
  
RESULT 2397  
ADE80960  
ID ADE80960 standard; DNA; 21 BP.  
XX  
AC ADE80960;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human papillomavirus L1 gene type-specific PCR primer SEQ ID NO:10.  
XX  
KW detection; human papillomavirus; HPV; genotype;  
KW HPV genus-specific primer; HPV genus-specific probe; amplification;  
KW hybridisation; genotyping; L1 gene; PCR primer; ss.  
XX  
OS Synthetic.  
OS Human papillomavirus.  
XX  
PN WO2003076667-A1.  
XX  
PD 18-SEP-2003.  
XX  
PF 10-MAR-2003; 2003WO-HU0000020.  
XX  
PR 14-MAR-2002; 2002HU-00000981.  
XX  
PA (JENE/) JENEY C.  
PA (TAKA/) TAKACS T.  
XX  
PI Jeney C, Takacs T;  
XX  
DR WPI; 2003-902774/82.  
XX  
PT Use of amplification primer-mixture and human papillomavirus genus-  
PT specific hybridization probes, for detecting and genotyping human  
PT papillomavirus in biological samples.  
XX  
PS Claim 2; SEQ ID NO 10; 61pp; English.  
XX  
CC The present invention describes a method for detecting many human  
CC papillomavirus (HPV) genotypes from biological samples. The method  
CC comprises amplifying and hybridising the extracted nucleic acid molecules  
CC with HPV genus-specific primers and probes designed from HPV genomic  
CC regions. Amplification primer-mixtures, consensus primers, type-specific  
CC primers, hybridisation probes, and reagent kits of the present invention  
CC can be used for detecting and genotyping HPV. The primer mixture is  
CC useful for the amplification of the 3, 4, 6, 7, 9, 10, 11, 12, 13, 14,  
CC 16, 18, 20, 24, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 40, 41,  
CC 42, 44, 45, 51, 52, 53, 54, 55, 56, 58, 49, 60, 61, 66, 67, 68, 72, 74 or  
CC 77 genotypes of HPV. The HPV genomic regions are useful for designing HPV  
CC genus-specific and HPV genotype-specific hybridisation probes. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 21 BP; 9 A; 2 C; 4 G; 6 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2533 ATACAGGGTATTAGAAT 2550

```
Db          ||||| 3 ATACAGGGTATTAGAA 20
RESULT 2398
AAT28053
ID AAT28053 standard; DNA; 22 BP.
XX
AC AAT28053;
XX
DT 31-DEC-1996 (first entry)
XX
DE 3'-primer K for human fibroblasts.
XX
KW Polymerase chain reaction; PCR; primer; amplify; human; fibroblast; AIDS;
KW enhanced differential display; EDD; mRNA preparation; senescent cell;
KW quiescent cell; dividing cell; senescence-related gene; gene expression;
KW non-senescent cell; age-related lipofuscin; retina; therapy; liver spot;
KW donor tissue; senescent melanocyte; melanin; hypopigmentation; ss.
XX
OS Synthetic.
XX
PN WO9613610-A2.
XX
PD 09-MAY-1996.
XX
PF 24-AUG-1995; 95WO-US011230.
XX
PR 31-OCT-1994; 94US-00332420.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Hirsch KS, Villeponteau B, Feng J, Funk W, West MD;
XX
DR WPI; 1996-251464/25.
XX
PT Identifying, isolating and regulating senescence-related genes - useful
PT to ameliorate problems associated with accumulation of senescent cells,
PT e.g. age-related lipofuscin accumulation in the retina and AIDS.
XX
PS Claim 6; Page 25; 135pp; English.
XX
CC AAT28044-T28075 represent primers for human fibroblasts in enhanced
CC differential display (EDD), which is used in conjuncture with the method
CC of the invention. EDD is an mRNA preparation method. AAT28044-T28055
CC represent T-rich 3'-primers, while AAT28056-T28075 are randomly selected
CC 5'-primers used in EDD of human fibroblasts. The 3'-primers used are
CC complementary to the poly-A tail of the mRNA. In the method of the
CC invention, mRNA is isolated from a senescent cell, and a young quiescent
CC cell, and the mRNAs are amplified in separate reaction mixtures. The
CC amplified sequences are then separated by size or charge, and the
CC products are analysed to identify a gene from young quiescent cells and
CC dividing cells, that is present at a different level from senescent
CC cells. The method can be used for the rapid and efficient identification
CC and isolation of senescence-related genes and gene products, and to
CC detect and distinguish between senescent and non-senescent cells. It can
CC also be used to destroy cells expressing senescence specific (or related)
CC gene products, and to screen for compounds capable of altering gene
CC expression in senescent cells. The method can also be used to ameliorate
CC problems associated with the accumulation of senescent cells such as age-
CC related lipofuscin accumulation in the retina, and in the treatment of
CC AIDS. Also, the method can be used to distinguish young cells from
CC senescent cells in donor tissue, which is useful in removing senescent
CC melanocytes overexpressing melanin which cause hypopigmentation, or liver
CC spots
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTGAA 1784
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```
Db          ||||| 5 AAGCTTTTGTGAA 22
RESULT 2399
AAT58493
ID AAT58493 standard; DNA; 22 BP.
XX
AC AAT58493;
XX
DT 24-MAR-1997 (first entry)
XX
DE First primer #10 for use in enhanced differential display method.
XX
KW Differential Display; Enhanced Differential Display; EDD; screening;
KW gene expression; cell type; different; cell development; gene typing;
KW identification; differentiation; aging; and disease; primer; PCR; ss.
XX
OS Synthetic.
XX
PN US5580726-A.
XX
PD 03-DEC-1996.
XX
PF 29-APR-1994; 94US-00235180.
XX
PR 29-APR-1994; 94US-00235180.
XX
PA (GERO-) GERON CORP.
XX
PI Linskens MHK, Feng J, Villeponteau B, Funk W;
XX
DR WPI; 1997-033564/03.
XX
PT Detection of differentially expressed mRNA mols. - using two-step
PT polymerase chain reaction amplification method.
XX
PS Claim 9; Col 17; 15pp; English.
XX
CC An improved method of Differential Display, named Enhanced Differential
CC Display (EDD) has been designed as a technique for screening differences
CC in gene expression between various cell types or between different stages
CC of cell development. The technique is highly reproducible, leading to
CC precise typing of the expressed genes in any given cell. EDD analysis
CC permits the identification of novel genes involved in differentiation,
CC aging and disease, and enables direct comparisons of different cell types
CC and disease states. By using longer primers, and/or an alteration in the
CC annealing temperatures, the number of false positives can be reduced.
CC First, cDNA is prepared from total cellular RNA using 12 different 22-
CC base oligonucleotides (AAT58484-95) that are targeted to the poly A tail
CC of pol II mRNA transcripts. The last two bases of each primer varies so
CC as to anchor the primer to the 3' end of different sets of mRNAs. A
CC second set of 12 22-base oligo primers (AAT58472-83) is designed to
CC randomly select a subset of cDNAs from each of the twelve 3' primers. PCR
CC amplification of a subset of cDNAs is carried out in a two step process
CC using particular 5' and 3' primers. The amplified gene products can then
CC be directly sequenced or rapidly subcloned for DNA sequencing
XX
SQ Sequence 22 BP; 4 A; 3 C; 3 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTGAA 1784
Db          ||||| 5 AAGCTTTTGTGAA 22
RESULT 2400
AAZ47351
ID AAZ47351 standard; DNA; 22 BP.
XX
```



XX 07-APR-1997; 97JP-00088495.  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX Kato K;  
XX WPI; 1998-523164/45.  
XX Determination of gene expression levels - using combinations of different  
PT cDNA samples tagged with different PCR adaptors.  
XX Example 2; Page 9; 22pp; English.  
XX The present sequence represents a primer which was used to synthesise  
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers  
CC AAV61554 and AAV61556 were added to both mouse liver-derived and mouse  
CC kidney-derived total RNA to generate single-stranded cDNA. These primers  
CC were used in the method of the invention to determine the amount ratio  
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA  
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-  
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to  
CC be quantitatively determined, and because internal standards are not  
CC required to prepare a calibration curve, it is a quicker and less  
CC laborious process  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 22 AAAAAAAAAAAAAAAAAACA 5  
RESULT 2403  
AAX23577  
ID AAX23577 standard; DNA; 23 BP.  
XX  
AC AAX23577;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Deletion sequence oligonucleotide 30.  
XX  
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;  
KW probe; cellular adhesion modulator; cellular proliferation modulator;  
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;  
KW HIV; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9911820-A1.  
XX  
PD 11-MAR-1999.  
XX  
PF 01-SEP-1998; 98WO-US018084.  
XX  
PR 02-SEP-1997; 97US-00923771.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Chen D, Srivatsa GS;  
XX  
DR WPI; 1999-205198/17.  
XX  
PT New compositions comprising sensor arrays made up of unique probe  
PT oligonucleotides - useful for characterizing a sample of target deletion  
PT oligonucleotides.  
XX  
PS Example 9; Page 99; 163pp; English.

XX This invention describes a novel composition comprising a number of  
CC sensor arrays, where each array comprises a unique probe oligonucleotide,  
CC which is the reverse complement of part of a unique target  
CC oligonucleotide present in a mixture of target deletion sequence  
CC oligonucleotides. The compositions form a method for characterizing a  
CC sample of target deletion oligonucleotides which are labelled and  
CC hybridize with the probe oligonucleotides of the sensor arrays. Such  
CC oligonucleotides and their targets are represented in AAX23548-X23709.  
CC Oligonucleotides characterized by the method form pharmaceutical  
CC compositions that are useful for modulating cellular adhesion or  
CC proliferation, and being active against a eukaryotic pathogen, a human  
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human  
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory  
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable  
CC characterization of deletion sequence oligonucleotides having related,  
CC but different nucleobase sequences, and quantification of different  
CC species of deletion sequence ("target") oligonucleotides in a mixture.  
CC Also, if the specificity of the oligonucleotide's nucleobase sequence for  
CC its reverse complement is not modified, the method may be performed using  
CC oligodeoxynucleotides  
XX  
SQ Sequence 23 BP; 4 A; 1 C; 3 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2171 TTTTTTTTTTTTTTTTAA 2188  
Db 1 TTTTTTTTTTTTTTTTGA 18  
RESULT 2404  
AAV35580  
ID AAV35580 standard; DNA; 23 BP.  
XX  
AC AAV35580;  
XX  
DT 04-SEP-1998 (first entry)  
XX  
DE STS probe GV10 generating upper primer.  
XX  
KW Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia;  
KW vesical-ureteral reflux; pelvi-ureteral junction obstruction;  
KW multicystic renal dysplasia; renal agenesis; hydronephrosis; MRD;  
KW Von Mayer-Rokitansky-Kuester disorder; bifid ureter; STS probe;  
KW sequence tagged site; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9815650-A2.  
XX  
PD 16-APR-1998.  
XX  
PF 09-OCT-1997; 97WO-EP005583.  
XX  
PR 09-OCT-1996; 96EP-00202820.  
XX  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
XX  
PI Van De Ven WJM, Frys JGJ, Groenen PMA;  
XX  
PI WPI; 1998-240833/21.  
DR  
XX  
PT Hydronephrosis gene - useful to treat or diagnose renal diseases and  
PT disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction  
PT obstruction, multicystic renal dysplasia or renal agenesis.  
XX  
PS Example 3; Page 46; 73pp; English.  
XX  
CC This primer is used for the generation of sequence tagged sites (STS)



CC probes used for pinpointing chromosome 6 breakpoint. This was used for  
CC isolating the human hydronephrosis (HNG) gene of the invention. A  
CC translocation partner to this HNG gene on chromosome 6 is the chromosome  
CC 19 USF2 gene. The HNG gene can be used as a starting point to design  
CC suitable compounds or techniques for the treatment of renal diseases or  
CC disorders, or nucleotide probes for diagnosing cells involved in renal  
CC diseases or disorders. A protein or a fragment encoded by HNG gene can be  
CC used as a starting point for preparing suitable antibodies for diagnosing  
CC cells involved in renal diseases and disorders. The products and method  
CC can be used to treat or diagnose renal diseases and disorders selected  
CC from vesical-ureteral reflux, uni or bilateral pelvi-ureteral junction  
CC obstruction, multicystic renal dysplasia (MRD), renal agenesis, renal  
CC aplasia, hydronephrosis, Von Mayer-Rokitansky-Kuester disorder and bifid  
CC ureter  
XX  
SQ Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1367 GGCAGCCAGGCATCTGT 1384  
Db 5 GGCAGCCAGGTCATCTGT 22  
  
RESULT 2405  
AAZ87324  
ID AAZ87324 standard; DNA; 23 BP.  
XX  
AC AAZ87324;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Maize cytochrome P450 monooxygenase CYP71C3v2 RT-PCR primer 5' PC-1.  
XX  
KW Cytochrome P450 monooxygenase; CYP71C3v2; herbicide detoxification;  
KW triasulfuron; transgenic plant; herbicide identification;  
KW reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Zea mays.  
XX WO200000585-A2.  
PN 06-JAN-2000.  
XX  
PD 28-JUN-1999; 99WO-US014689.  
XX  
PF 26-JUN-1998; 98US-0090759P.  
XX  
PR (UNII ) UNIV ILLINOIS FOUND.  
PA Schuler MA, Persans MW;  
XX WPI; 2000-170909/15.  
XX  
PT Novel maize cytochrome P450 monooxygenase cDNA used to confer herbicide  
PT resistance to plants.  
XX  
PS Example 1c; Fig 5; 85pp; English.  
XX  
CC The invention relates to maize cytochrome P450 monooxygenase CYP71C3v2  
CC (AA77232) and nucleotides which encode it. CYP71C3v2 cDNA was generated  
CC via reverse transcriptase-PCR (RT-PCR) from poly (A)+ mRNA isolated from  
CC naphthalic anhydride and herbicide (triasulfuron)-treated maize  
CC seedlings. This was used to construct a cDNA library, which was screened  
CC using previously generated cDNA as hybridisation probes. The CYP71C3v2  
CC cDNA clone was extended via 5' RACE (rapid amplification of cDNA ends)  
CC and cloned into pBluescript. Genomic DNA was also screened for clones  
CC encoding CYP71C3v2 - this was found to contain 2 introns (AAZ87321-  
CC Z87322). Cytochrome P450 monooxygenase CYP71C3v2 reductively cleaves  
CC molecular dioxygen to produce functionalised organic substrates.  
CC Nucleotides encoding cytochrome P450 monooxygenase CYP71C3v2 are used to  
CC produce transgenic plants with increased resistance to herbicides, such  
CC as triasulfuron. When such transgenic plants are grown, undesired  
CC vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium  
CC album and quack grass, can easily be controlled. The methods may also be  
CC used to identify those compounds with herbicidal activity. Sequences  
CC AAZ87323-Z87335 represent PCR primers used to isolate, clone and study

CC produce transgenic plants with increased resistance to herbicides, such  
CC as triasulfuron. When such transgenic plants are grown, undesired  
CC vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium  
CC album and quack grass, can easily be controlled. The methods may also be  
CC used to identify those compounds with herbicidal activity. Sequences  
CC AAZ87323-Z87335 represent PCR primers used to isolate, clone and study  
CC maize CYP71C3v2 nucleotide sequences in the exemplifications and the  
CC disclosure of the present invention  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2163 TCCTTTT TTTT TTTT TTTT 2180  
Db 6 TCCTTTT TTTT TTTT TTTT 23  
  
RESULT 2406  
AAZ87324/c  
ID AAZ87324 standard; DNA; 23 BP.  
XX  
AC AAZ87324;  
XX  
DT 22-MAY-2000 (first entry)  
XX  
DE Maize cytochrome P450 monooxygenase CYP71C3v2 RT-PCR primer 5' PC-1.  
XX  
KW Cytochrome P450 monooxygenase; CYP71C3v2; herbicide detoxification;  
KW triasulfuron; transgenic plant; herbicide identification;  
KW reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Zea mays.  
XX WO200000585-A2.  
PN 06-JAN-2000.  
XX  
PD 28-JUN-1999; 99WO-US014689.  
XX  
PF 26-JUN-1998; 98US-0090759P.  
XX  
PR (UNII ) UNIV ILLINOIS FOUND.  
XX  
PI Schuler MA, Persans MW;  
XX WPI; 2000-170909/15.  
XX  
PT Novel maize cytochrome P450 monooxygenase cDNA used to confer herbicide  
PT resistance to plants.  
XX  
PS Example 1c; Fig 5; 85pp; English.  
XX  
CC The invention relates to maize cytochrome P450 monooxygenase CYP71C3v2  
CC (AA77232) and nucleotides which encode it. CYP71C3v2 cDNA was generated  
CC via reverse transcriptase-PCR (RT-PCR) from poly (A)+ mRNA isolated from  
CC naphthalic anhydride and herbicide (triasulfuron)-treated maize  
CC seedlings. This was used to construct a cDNA library, which was screened  
CC using previously generated cDNA as hybridisation probes. The CYP71C3v2  
CC cDNA clone was extended via 5' RACE (rapid amplification of cDNA ends)  
CC and cloned into pBluescript. Genomic DNA was also screened for clones  
CC encoding CYP71C3v2 - this was found to contain 2 introns (AAZ87321-  
CC Z87322). Cytochrome P450 monooxygenase CYP71C3v2 reductively cleaves  
CC molecular dioxygen to produce functionalised organic substrates.  
CC Nucleotides encoding cytochrome P450 monooxygenase CYP71C3v2 are used to  
CC produce transgenic plants with increased resistance to herbicides, such  
CC as triasulfuron. When such transgenic plants are grown, undesired  
CC vegetation such as pigweed, velvet leaf, lambs quarters, Chenopodium  
CC album and quack grass, can easily be controlled. The methods may also be  
CC used to identify those compounds with herbicidal activity. Sequences  
CC AAZ87323-Z87335 represent PCR primers used to isolate, clone and study



RESULT 2409  
AAZ50028/c  
ID AAZ50028 standard; DNA; 23 BP.  
XX  
XX AC  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE  
XX  
XX  
KW Cytochrome p450 monooxygenase; CYP71C3v2; maize; chromosome 4p; weed;  
KW p450 gene; molecular dioxygen; herbicidal; pigweed; transgenic organism;  
KW herbicide resistant; triasulfuron; quack grass; velvet leaf; PCR primer;  
KW labs quarter; Chenopodium album; naphthalic anhydride; ss.  
XX  
OS Zea mays.  
XX  
PN WO200000502-A1.  
XX  
PD 06-JAN-2000.  
XX  
PF 23-JUN-1999; 99WO-US014117.  
XX  
PR 26-JUN-1998; 98US-0090759P.  
XX  
PA (UNII ) UNIV ILLINOIS FOUND.  
XX  
PI Schuler MA, Persans MW;  
XX  
DR WPI; 2000-170902/15.  
XX  
PT Novel maize cytochrome P450 monooxygenase polypeptides and  
PT polynucleotides, used to confer triasulfuron herbicide resistance to  
PT plants.  
XX  
PS Example 1c; Page 52; 77pp; English.  
XX  
CC The present sequence is the oligo (dT) non-degenerate RT-PCR primer, 3'PC  
CC -1, complementary to the poly(A) tract of the CYP71C3v2 mRNA. It is used  
CC to extract and amplify mRNA isolated from naphthalic anhydride-treated  
CC maize seedlings. The CYP71C3v2 gene is mapped to a single locus on the  
CC short arm of maize chromosome 4 (4p). CYP71C3v2 reductively cleaves  
CC molecular dioxygen to produce functionalised organic substrates. It has  
CC herbicidal activity. CYP71C3v2 polynucleotides are used to produce  
CC transgenic organisms, such as yeast, plants and bacteria that are  
CC resistant to herbicides, such as triasulfurons. Undesired vegetation,  
CC e.g. weed, pigweed, velvet leaf, labs quarters, Chenopodium album and  
CC quack grass, can easily be controlled when such transgenic plants are  
CC grown. Transformed organisms can also be used to identify compounds with  
CC herbicidal activity  
XX  
SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 23 AAAAAAAAAAAAAAAAAAGAA 6  
  
RESULT 2410  
ABA01048/c  
ID ABA01048 standard; DNA; 24 BP.  
XX  
XX AC ABA01048;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human sodium pump subunit 12 PCR primer 1.  
XX

KW Human; sodium pump; subunit 12; cytostatic; virucide; immunomodulator;  
KW antiinflammatory; haemostatic; gene therapy; cancer; haemopathy;  
KW human immunodeficiency virus; HIV; infection; immunological disease;  
KW inflammatory disorder; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200177162-A1.  
XX  
PD 18-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-CN000422.  
XX  
PR 27-MAR-2000; 2000CN-00115156.  
XX  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2002-017442/02.  
XX  
PT Human sodium pump subunit 12 of sodium pump and encoded polynucleotide,  
PT used in diagnosis and treatment of malignant tumors, hemopathy, human  
PT immunodeficiency virus infection, immunological diseases and  
PT inflammation.  
XX  
PS Example 2; Page 16; 35pp; Chinese.  
XX  
CC The invention relates to an isolated polypeptide of human sodium pump  
CC subunit 12 comprising a 110 residue amino acid sequence, fully defined in  
CC the specification, or its fragment, analogue or derivative. The  
CC polypeptide is used in the diagnosis and treatment of malignant tumours,  
CC haemopathy, human immunodeficiency virus (HIV) infection, immunological  
CC diseases and various inflammatory disorders. The present sequence is a  
CC primer used to isolate a polynucleotide encoding the polypeptide of the  
CC invention  
XX  
SQ Sequence 24 BP; 0 A; 0 C; 4 G; 20 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 24;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 23 AAAAAAAAAACAAAAAAAAA 6  
  
RESULT 2411  
AAC96428  
ID AAC96428 standard; DNA; 24 BP.  
XX  
XX AC AAC96428;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DQA1 gene PCR primer #30.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.





PA (UYRQ ) UNIV ROCKEFELLER.  
XX Dubertret B, Calame M, Libchaber A;  
PI  
XX WPI; 2002-404569/43.  
DR  
XX  
PS Sensitive detecting proximity changes in a system that utilizes an  
XX interacting fluorophore and quencher, for high sensitivity applications,  
PT involves utilizing a metal surface as quencher.  
PT  
XX  
PS Example 5; Page 33; 62pp; English.  
XX  
CC The present sequence is an oligonucleotide probe that was used in a  
CC molecular beacon in an example from the invention. The probe forms a  
CC hairpin structure in the native state. The 5' end of the probe is  
CC covalently joined via a linker to a disulfide or primary amine. The 3'  
CC end of the probe is covalently joined to an amine-reactive fluorescent  
CC dye such as fluorescein. A gold surface or other metal film surface is  
CC attached to the disulfide or amine group to form the molecular beacon. In  
CC the native state with hybridised termini, the proximity of the  
CC fluorophore and quencher (gold surface) in the molecular beacon is such  
CC that little or no fluorescence is detectable. Upon hybridisation of the  
CC central complementary stretch of the probe to a target sequence (e.g. the  
CC sequence in ABL57070), the hairpin undergoes a conformational change  
CC resulting in an increase in fluorescence, the extent of which is  
CC proportional to the amount of binding partner present. The invention  
CC relates generally to the use of metal surface quenchers such as particles  
CC or films for high sensitivity applications in, for example, detection and  
CC diagnostic systems  
XX  
SQ Sequence 24 BP; 1 A; 3 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 24;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAGAAAAA 2802  
Db 23 GAGAAAAAAGAAAAA 6  
  
RESULT 2414  
ABX92831  
ID ABX92831 standard; DNA; 24 BP.  
XX  
AC ABX92831;  
XX  
DT 16-MAY-2003 (first entry)  
XX  
DE Borrelia burgdorferi KLL10 ZS7 B31 E61 and PKO primer.  
XX  
KW ss; primer; ospC; vaccine; antibacterial; Lyme disease; erythema migrans;  
KW acrodermatitis chronica atrophicans; neuro-borreliosis; arthritis; PCR.  
XX  
OS Borrelia burgdorferi.  
XX  
PN US6486130-B1.  
XX  
PD 26-NOV-2002.  
XX  
PF 27-JUN-1996; 96US-00671548.  
XX  
PR 11-JUL-1991; 91US-00727245.  
PR 22-JAN-1992; 92US-00824161.  
PR 25-JUN-1992; 92US-00903580.  
PR 29-APR-1993; 93US-00053863.  
PR 19-AUG-1994; 94US-00284667.  
XX  
PA (BAXT ) BAXTER VACCINE AG.  
XX  
PI Livey I, Crowe R, Dorner F;  
XX  
DR WPI; 2003-287432/26.

XX Recombinant Borrelia burgdorferi DNA sequence, OspC DNA sequence, useful  
PT for the production of OspC antigen which is useful as a vaccine for  
PT treating Lyme diseases.  
XX  
PS Example 8; Col 29-30; 112pp; English.  
XX  
CC The invention relates to a recombinant Borrelia burgdorferi DNA sequence,  
CC named ospC that encodes an OspC antigen containing amino acid sequence.  
CC The nucleic acid and an expression vector containing it are useful for  
CC the recombinant production of OspC antigen which is useful as a vaccine  
CC for treating Lyme disease and its related disorders e.g. erythema  
CC migrans, acrodermatitis chronica atrophicans, neuro-borreliosis and  
CC arthritis. The present sequence represents a PCR primer used to amplify  
CC Borrelia ospC genes  
XX  
SQ Sequence 24 BP; 6 A; 1 C; 6 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 24;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1760 ATTCATTAAAGCTTTT 1777  
Db 4 ATTCATTAAAGCTTTT 21  
  
RESULT 2415  
ADC51227  
ID ADC51227 standard; DNA; 24 BP.  
XX  
AC ADC51227;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Brassica defensin gene PCR primer #2.  
XX  
KW antimicrobial protein; defensin; transgenic plant;  
KW composite disease resistance; pathogenic bacteria;  
KW rice white leaf blight; brown-stripe disease; glume blight;  
KW seedling damping-off disease; filamentous fungi; rice blight;  
KW sheath blight disease; leaf blight; gene; ss; PCR.  
XX  
OS Unidentified.  
OS Brassica sp.  
XX  
PN JP2003088379-A.  
XX  
PD 25-MAR-2003.  
XX  
PF 18-SEP-2001; 2001JP-00283117.  
XX  
PR 18-SEP-2001; 2001JP-00283117.  
XX  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
XX  
PN WPI; 2003-621123/59.  
XX  
PT Novel protein from Brassica campestris, useful as antimicrobial against  
PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for  
PT treating e.g. rice white leaf blight and sheath blight disease.  
XX  
PS Example 1; SEQ ID NO 7; 34pp; Japanese.  
XX  
CC The invention comprises the amino acid and coding sequences of  
CC antimicrobial (defensin) proteins from Brassica. The DNA and protein  
CC sequences of the invention are useful for producing transformed plants  
CC with composite disease resistance, especially resistant to diseases  
CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-  
CC stripe disease, glume blight, and seedling damping-off disease. As well  
CC as diseases caused by filamentous fungi, such as: rice blight, sheath  
CC blight disease, and leaf blight. The present DNA sequence represents a  
CC PCR primer that was used in the exemplification of the invention.



PR 26-APR-1999; 99EP-00303215.  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
PA Ulfendahl P, Wong K;  
XX WPI; 2000-679677/66.  
DR Identifying extendible primers for use in identification, or  
XX classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX Claim 14; Page 56; 66pp; English.  
PS The present invention provides a method for identifying a set of  
XX extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 1 A; 5 C; 1 G; 18 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2781 AATTGAAAAA 2798  
Db 18 AAGTGA 1  
  
RESULT 2419  
AAC96830/c  
ID AAC96830 standard; DNA; 25 BP.  
XX AAC96830;  
XX 26-FEB-2001 (first entry)  
DT HLA HLA-C gene PCR primer #35.  
XX  
DE DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX Homo sapiens.  
OS WO200065088-A2.  
XX  
PN 02-NOV-2000.  
PD 20-APR-2000; 2000WO-EP003636.  
PF 26-APR-1999; 99EP-00303215.  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
PA Ulfendahl P, Wong K;  
XX WPI; 2000-679677/66.  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX Claim 14; Page 58; 66pp; English.  
PS The present invention provides a method for identifying a set of  
XX extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAA 2799  
Db 18 AGTGA 1  
  
RESULT 2420  
AAC96121/c  
ID AAC96121 standard; DNA; 25 BP.  
XX AAC96121;  
AC 26-FEB-2001 (first entry)  
DT 16s rRNA gene PCR primer #88.  
XX DNA sequence analysis; sequencing; protein sequence; protein structure;  
DE gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
KW Homo sapiens.  
XX WO200065088-A2.  
XX 02-NOV-2000.  
PD 20-APR-2000; 2000WO-EP003636.  
PF 26-APR-1999; 99EP-00303215.  
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
PA Ulfendahl P, Wong K;  
XX WPI; 2000-679677/66.  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX Claim 14; Page 45; 66pp; English.  
PS The present invention provides a method for identifying a set of  
XX extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 4 A; 1 C; 5 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAA 2799  
Db 18 ACTGA 1

```
RESULT 2421
ADB04575/c
ID   ADB04575 standard; DNA; 25 BP.
XX
KW   ADB04575;
AC
XX
DT   20-NOV-2003 (first entry)
XX
DE   Human MDZ7 scanning oligonucleotide SEQ ID 5561.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
XX   EP1281758-A2.
PN
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M, Gu Y, Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 5561; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 25 BP; 4 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   2784 TGAATAAAAAAAAAAAAAA 2801
Db   19 TCAAAAAAAAAAAAAAAAAA 2

RESULT 2422
AAC96251
ID   AAC96251 standard; DNA; 25 BP.
XX
AC   AAC96251;
XX
DT   26-FEB-2001 (first entry)
XX
```

```
DE   HLA DPA1 gene PCR primer #8.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
XX   WO200065088-A2.
PN
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999; 99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P, Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 48; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

Query Match          0.6%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   2170 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db   1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 2423
AAC95851/c
ID   AAC95851 standard; DNA; 25 BP.
XX
AC   AAC95851;
XX
DT   26-FEB-2001 (first entry)
XX
DE   HLA HLA-A gene PCR primer #31.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
XX   WO200065088-A2.
PN
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999; 99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
```



XX Ulfendahl P, Wong K;  
PI WPI; 2000-679677/66.  
XX  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 41; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2782 ATTGAAAAA 2799  
Db 18 ATTGACAAAAA 1  
  
RESULT 2424  
AAC96884  
ID AAC96884 standard; DNA; 25 BP.  
XX  
AC AAC96884;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA HLA-C gene PCR primer #89.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
XX Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 59; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 4 A; 3 C; 2 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2172 TTTT TTTT TTTT TTTT TTTT AAC 2189  
Db 1 TTTT TTTT TTTT TTTT TTTT AAC 18  
  
RESULT 2425  
AAC95722/c  
ID AAC95722 standard; DNA; 25 BP.  
XX  
AC AAC95722;  
XX  
DT 26-FEB-2001 (first entry)  
XX  
DE HLA DQA1 gene PCR primer #19.  
XX  
KW DNA sequence analysis; sequencing; protein sequence; protein structure;  
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;  
KW human leukocyte antigen; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200065088-A2.  
XX  
PD 02-NOV-2000.  
XX  
PF 20-APR-2000; 2000WO-EP003636.  
XX  
PR 26-APR-1999; 99EP-00303215.  
XX  
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.  
XX  
PI Ulfendahl P, Wong K;  
XX  
DR WPI; 2000-679677/66.  
XX  
PT Identifying extendible primers for use in identification, or  
PT classification of a nucleic acid of an organism, allele or gene such as  
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of  
PT specific length.  
XX  
PS Claim 14; Page 39; 66pp; English.  
XX  
CC The present invention provides a method for identifying a set of  
CC extendible primers which can be used in the identification, typing and  
CC classification of genes. This can then be used to predict protein  
CC sequence and structure, in organ donation to match the organ with the  
CC receiver, and to identify bacteria in a sample. The method can be used to  
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in  
CC particular  
XX  
SQ Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2780 GAATTGAAAAA 2797  
Db 18 GAATTGAAAAA 1  
  
RESULT 2426  
AAC96511  
ID AAC96511 standard; DNA; 25 BP.











FT modified\_base 1 sequence in ABL57070"  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "5' disulfide group"  
FT 25  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3' amino group"  
XX  
PN WO200218951-A2.  
XX  
PD 07-MAR-2002.  
XX  
XX 29-AUG-2001; 2001WO-US041941.  
PF 29-AUG-2000; 2000US-0228728P.  
XX 30-MAR-2001; 2001US-0280350P.  
PR  
XX (UYRQ ) UNIV ROCKEFELLER.  
PA  
XX Dubertret B, Calame M, Libchaber A;  
PI WPI; 2002-404569/43.  
XX  
DR Sensitive detecting proximity changes in a system that utilizes an  
XX interacting fluorophore and quencher, for high sensitivity applications,  
PT involves utilizing a metal surface as quencher.  
XX  
PS Example 1; Page 22; 62pp; English.  
XX  
CC The present sequence is an oligonucleotide probe that was used in a  
CC molecular beacon in examples from the invention. The probe has a hairpin  
CC structure in the native state. The disulfide group at the 5' end of the  
CC probe was covalently linked to the 5' phosphate via a (CH2)6 spacer, and  
CC the primary amino group at the 3' was attached to the 3' hydroxyl via a  
CC (CH2)7 spacer. An amino-reactive dye, such as fluorescein, rhodamine 6G  
CC or Texas Red, was covalently linked to the 3'-amino group. A  
CC monomaleimido-gold nanoparticle was then covalently linked to the 5'  
CC sulfhydryl group to form the molecular beacon. In the native state with  
CC hybridised termini, the proximity of the fluorophore and quencher (gold  
CC nanoparticle) in the molecular beacon is such that little or no  
CC fluorescence is detectable. Upon hybridisation of the central  
CC complementary stretch of the probe to a target sequence (e.g. the  
CC sequence in ABL57070 or ABL57071), the hairpin undergoes a conformational  
CC change resulting in an increase in fluorescence, the extent of which is  
CC proportional to the amount of binding partner present. Single mismatch  
CC detection was demonstrated. The invention relates generally to the use of  
CC metal surface quenchers such as particles or films for high sensitivity  
CC applications in, for example, detection and diagnostic systems  
XX  
SQ Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 23 GAGAAA AAAAAAAAAA 6  
  
RESULT 2437  
ABL57077/c  
ID ABL57077 standard; DNA; 25 BP.  
XX  
AC ABL57077;  
XX  
XX 22-JUL-2002 (first entry)  
DT  
XX Molecular beacon oligonucleotide probe.  
DE  
XX Molecular beacon; probe; fluorophore; nanoparticle;  
KW

KW nucleic acid detection; ss.  
XX  
OS Synthetic.  
XX  
FH Location/Qualifiers  
FT stem\_loop 1..22  
FT /\*tag= a  
FT modified\_base 1  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "5' amine"  
FT 6..21  
FT /\*tag= d  
FT /bound moiety= "Target oligonucleotide"  
FT /note= "Forms double-stranded region with bases 1-16 of  
FT sequence in ABL57075"  
FT 25  
FT /\*tag= c  
FT /mod\_base= OTHER  
FT /note= "3' DABCYL"  
XX  
PN WO200218951-A2.  
XX  
PD 07-MAR-2002.  
XX  
XX 29-AUG-2001; 2001WO-US041941.  
PF 29-AUG-2000; 2000US-0228728P.  
XX 30-MAR-2001; 2001US-0280350P.  
PR  
XX (UYRQ ) UNIV ROCKEFELLER.  
PA  
XX Dubertret B, Calame M, Libchaber A;  
PI WPI; 2002-404569/43.  
XX  
DR Sensitive detecting proximity changes in a system that utilizes an  
XX interacting fluorophore and quencher, for high sensitivity applications,  
PT involves utilizing a metal surface as quencher.  
XX  
PS Example 3; Page 30; 62pp; English.  
XX  
CC The present sequence is an oligonucleotide probe that was used in a  
CC molecular beacon in an example from the invention. A rhodamine 6G dye was  
CC attached to the primary amine at the 5' end of the oligonucleotide, which  
CC had DABCYL attached to its 3' end. A rhodamine-DNA-gold conjugate  
CC molecular beacon (see ABL57069) was also used. In the native state with  
CC hybridised termini, the proximity of the fluorophore and quencher (gold  
CC nanoparticle) in the molecular beacon is such that little or no  
CC fluorescence is detectable. Upon hybridisation of the central  
CC complementary stretch of the probe to a target sequence, the hairpin  
CC undergoes a conformational change resulting in an increase in  
CC fluorescence, the extent of which is proportional to the amount of  
CC binding partner present. Single mismatch detection was demonstrated. The  
CC invention relates generally to the use of metal surface quenchers such as  
CC particles or films for high sensitivity applications in, for example,  
CC detection and diagnostic systems  
XX  
SQ Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAA AAAAAAAAAA 2802  
Db 23 GAGAAA AAAAAAAAAA 6  
  
RESULT 2438  
ADE64628/c  
ID ADE64628 standard; DNA; 25 BP.  
XX



PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5552; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2803  
DB 25 AAAAAAAAAAAAAAAAAAAGAA 8  
  
RESULT 2441  
ADB04576  
ID ADB04576 standard; DNA; 25 BP.  
XX  
AC ADB04576;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5562.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5562; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX

CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX  
SQ Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2170 TTTTTTTTTTTTTTTT 2187  
DB 1 TTTTTTTTTTTTTTTTGA 18  
  
RESULT 2442  
ADB04576/C  
ID ADB04576 standard; DNA; 25 BP.  
XX  
AC ADB04576;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 5562.  
XX  
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;  
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
KW developmental disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1281758-A2.  
XX  
PD 05-FEB-2003.  
XX  
PF 30-JUL-2002; 2002EP-00016874.  
XX  
PR 02-AUG-2001; 2001US-00922181.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Shannon M, Gu Y, Nguyen C;  
XX  
DR WPI; 2003-423107/40.  
XX  
PT New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.  
XX  
PS Example 8; SEQ ID NO 5562; 103pp; English.  
XX  
CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX





sensor, where the end of the first inverse repeat arm opposite the complementary probe is bound, directly or indirectly, to a support, a kit for detecting a target nucleotide sequence in a sample comprising the hairpin sensor, and a support, and a hairpin sensor system, in which the particle is conductive or semi-conductive, including at least one of the above hairpin sensor assemblies. The hairpin sensor further comprises a functional group joined to the end of the first inverse repeat arm opposite the complementary probe, or first spacer opposite the first inverse repeat arm, the functional group selected from amino, carboxyl, thiol and hydroxyl. Further, the sensor comprises a ligand positioned between the second inverse repeat arm and the quenchable fluorescing agent, where the ligand is selected from mercapto, hydroxyl, amino, nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The second spacer is positioned between the second inverse repeat arm and the quenchable fluorescing agent which comprises a semiconductor nanocrystal or rhodamine B-labelled dye. Within the microarray the support is capable of accepting a charge. At least one hairpin sensor comprises two or more hairpin sensors. The two or more hairpin sensors include complementary probes that are the same or different and respective quenchable fluorescing agents that are the same or different. The two or more hairpin sensors are arranged in a spatially-defined pattern. The sensor and system are useful for detecting a target nucleotide sequence in a sample. Further, the method involves identifying the target nucleotide sequence by the location of the complementary probe to which the target nucleotide sequence binds. The two or more hairpin sensors include complementary probes or quenchable fluorescing agents, that are different. The sequence presented is the hairpin oligonucleotide, #1, used in an example of the invention.

Query Match	0.6%	Score 16.4;	DB 1;	Length 25;
Best Local Similarity	94.4%;	Pred. No. 2.8e+03;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	2785	GAAGAAAAA	AAAAAAAAA	2802
DG	23	GAGAAAAAA	AAAAAAAAA	6

```

XX (SALA/) SALAFSKY J S.
XX PA
XX XX
XX PI
XX Salafsky JS;
XX WPI; 2003-646172/61.
XX
XX Screening candidate binding partner(s) for binding to test molecule by
XX applying external force field to sample in homogeneous phase,
XX illuminating sample with light beam(s) at fundamental frequencies, and
XX measuring physical properties.
XX Disclosure; Fig 20B; 146pp; English.
XX
XX The present invention relates to a method for detecting interactions
XX between biological components using a nonlinear optical technique. The
XX invention is used for screening candidate binding partner(s) for binding
XX to test molecule. It can also be used to detect changes in orientation or
XX conformation of the probe and/or target. The present sequence is an
XX oligonucleotide used in nonlinear optical technique
XX
XX Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.6%; Score 16.4; DB 1; Length 25;
XX Best Local Similarity 94.4%; Pred. No. 2.8e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2785 GAAAAAAAAAAAAAAAAA 2802
    ||| ||| ||| ||| ||| ||| |||
Db 23 GAGAAAAAAAAAAAAAAAAA 6

```

CC conformation of the probe and/or target. The present sequence is an  
CC oligonucleotide related to the invention  
XX  
SQ Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2165 CTTTTTTTTTTTTTTT 2182  
Db 5 CTTTTTTTTTTTTTCT 22  
  
RESULT 2447  
AAD57848/c  
ID AAD57848 standard; DNA; 25 BP.  
XX  
AC AAD57848;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Oligonucleotide related to the invention.  
XX  
KW Nonlinear optical technique; screening; ss.  
XX  
OS Unidentified.  
XX  
PN WO2003064991-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 17-JUL-2002; 2002WO-US0222681.  
XX  
PR 17-JUL-2001; 2001US-0306040P.  
PR 23-OCT-2001; 2001US-0347821P.  
PR 06-FEB-2002; 2002US-0354668P.  
XX  
PA (SALA/) SALAFSKY J S.  
XX  
PI Salafsky JS;  
XX  
XX WPI; 2003-646172/61.  
DR  
XX  
PT Screening candidate binding partner(s) for binding to test molecule by  
PT applying external force field to sample in homogeneous phase,  
PT illuminating sample with light beam(s) at fundamental frequencies, and  
PT measuring physical properties.  
XX  
PS Disclosure; Page 146; 146pp; English.  
XX  
CC The present invention relates to a method for detecting interactions  
CC between biological components using a nonlinear optical technique. The  
CC invention is used for screening candidate binding partner(s) for binding  
CC to test molecule. It can also be used to detect changes in orientation or  
CC conformation of the probe and/or target. The present sequence is an  
CC oligonucleotide related to the invention  
XX  
SQ Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2802  
Db 23 GAAAAAAAAAAAAAAAAA 6  
  
RESULT 2448  
ACF04465  
ID ACF04465 standard; DNA; 25 BP.  
XX

AC ACF04465;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Real time PCR targeting IL-1ra probe P291.  
XX  
KW Nucleic acid level determination; PCR; primer; probe; DNA quantification;  
KW gene therapy; immunosuppressive; anti-HIV; antiarthritic;  
KW neuroprotective; cytostatic; antiallergic; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "modified by 6FAM"  
FT modified\_base 25  
FT /\*tag= b  
FT /mod\_base= OTHER  
FT /note= "modified by TAMRA-p"  
XX  
PN WO2003060119-A2.  
XX  
PD 24-JUL-2003.  
XX  
PF 20-JAN-2003; 2003WO-EP000493.  
XX  
PR 18-JAN-2002; 2002EP-00447009.  
XX  
PA (ULBR ) UNIV LIBRE BRUXELLES.  
XX  
PI Stordeur P, Goldman M;  
XX  
DR WPI; 2003-598531/56.  
XX  
PT Quantifying in vivo RNA from a biological sample for producing a  
PT medicament for treating immune related disease by determining in vivo  
PT levels of transcripts using nucleic acid/reverse transcription-PCR  
PT reagent mix in an automated setup.  
XX  
PS Disclosure; Page 42; 83pp; English.  
XX  
CC The present invention relates to a method of quantifying in vivo RNA from  
CC a biological sample. This involves collecting the biological sample in a  
CC tube comprising a compound inhibiting RNA degradation and/or gene  
CC induction, forming a precipitate comprising nucleic acids, separating the  
CC precipitate from the supernatant, dissolving the precipitate using a  
CC buffer, forming a suspension, isolating nucleic acids from the suspension  
CC using an automated device, dispersing or distributing a reagent mix for  
CC reverse transcription (RT)-PCR using an automated device, dispersing or  
CC distributing the nucleic acids isolated within the dispersed reagent mix  
CC using an automated device and determining the in vivo levels of  
CC transcripts using the nucleic acid and RT-PCR reagent mix of the previous  
CC step in an automated setup. The method is useful for monitoring or  
CC detecting changes in in vivo nucleic acids levels in a biological agent  
CC present, such as eukaryotic or prokaryotic cells, viruses or phages in a  
CC biological sample or for producing a medicament for treating immune  
CC related disease, e.g., autoimmunity, rheumatoid arthritis, multiple  
CC sclerosis, cancer, immunodeficiencies such as AIDS, allergy, graft  
CC rejection or Graft versus Host Disease. The present sequence is a PCR  
CC primer/probe used in the exemplification of the invention  
XX  
SQ Sequence 25 BP; 6 A; 6 C; 8 G; 5 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1458 GAGACCAGAGTCCAGCTG 1475  
Db 8 GAGACCAGACTCCAGCTG 25





DT 04-APR-2002 (first entry)  
XX Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 7.  
DE  
XX  
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;  
KW infection; allergy; cancer; hypersensitivity; bio-warfare;  
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;  
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;  
KW antiinflammatory; antibacterial; ss.  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..14  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorothioate backbone"  
FT misc\_RNA 1..14  
FT /\*tag= b  
FT misc\_RNA 17..30  
FT /\*tag= c  
XX  
XX WO200193902-A2.  
XX  
XX 13-DEC-2001.  
XX  
XX 07-JUN-2001; 2001WO-US018276.  
XX  
XX 07-JUN-2000; 2000US-0209797P.  
XX  
XX (BIOS-) BIOSYNEXUS INC.  
XX  
XX Mond JJ, Flora M, Klinman DM;  
XX  
XX WPI; 2002-130570/17.  
XX  
XX New immunostimulatory compositions comprising RNA/DNA hybrid  
XX oligonucleotides, useful for enhancing an immune response or inducing  
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or  
XX HIV infection.  
XX  
XX Example 1; Page 30; 68pp; English.  
XX  
XX The present invention relates to an immunostimulatory composition, which  
XX comprises at least one oligonucleotide comprising both an RNA region and  
XX a DNA region. The composition is useful for enhancing an immune response  
XX or inducing cytokines. It can be used as a vaccine adjuvant and in  
XX treating diseases, including pathogenic infection, (non-)malignant  
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or  
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies  
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,  
XX hepatitis, HIV or malaria. The composition is also useful for treating,  
XX preventing or ameliorating the symptoms resulting from exposure to a bio-  
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is  
XX an immunostimulatory oligonucleotide described in the exemplification of  
XX the invention  
XX  
SQ Sequence 30 BP; 28 A; 1 C; 1 G; 0 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 30;  
Best Local Similarity 76.9%; Pred. No. 3.5e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2779 AGAATTGAAAAA 2804  
Db 1 AAAAAAAAAA 26  
RESULT 2452  
AAT93816/c  
ID AAT93816 standard; DNA; 35 BP.  
XX  
AC AAT93816;

XX 25-MAR-2003 (revised)  
DT 24-FEB-1998 (first entry)  
XX  
DE Antitumoural phosphodiester oligonucleotide 6 with cytotoxic activity.  
XX  
KW Phosphodiester; selective binding; cell viability; growth;  
KW tumoural cell line; cytotoxic activity; tumour cell; lymphoma;  
KW lymphoblastic tumour; ss.  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..35  
FT /\*tag= a  
FT /note= "phosphodiester oligonucleotide"  
XX  
XX WO9720924-A1.  
XX  
XX 12-JUN-1997.  
XX  
XX 04-DEC-1996; 96WO-EP005388.  
XX  
XX 04-DEC-1995; 95IT-MI002539.  
XX  
XX (SAIC-) SAICOM SRL.  
XX  
XX Scaggiante B, Quadrifoglio F;  
XX WPI; 1997-319771/29.  
XX  
XX New phosphodiesteric oligonucleotide(s) - which exert a specific and  
XX selective cytotoxic effect on tumour cells, for treating both solid and  
XX liquid tumours.  
XX  
XX Claim 10; Page 5; 38pp; English.  
XX  
XX Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the  
XX generic formula, in the 3'-5' or 5'-3' direction: (Gata')a'-(Gtb')b'--  
XX (Gctc')c'-(Gtd')d'-(Gte')e'-(Gtf')f'-(Gtg')g'--N', where: N and  
XX N' = T or G, equal or different from each other; x = 0-8, equal or  
XX different from each other; a, b, c, d, e, f, and g = 0-10, equal or  
XX different from each other; a', b', c', d', e', f', and g' = 0-30, equal  
XX or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-  
XX 16, equal or different from each other; The oligonucleotides are believed  
XX to selectively bind and sequester some proteins which are essential to  
XX the viability and growth of tumoural cell line. They have specific and  
XX selective cytotoxic activity against tumour cells, and can be used for  
XX treating tumours of the liquid type, in particular of lymphoblastic  
XX origin, and of solid type, in particular lymphomas. The present  
XX phosphodiester oligonucleotide, at a concentration of 15 micromolar,  
XX reduced growth of CCRF-CEM tumoural cells by 83%, which is detectable 48  
XX hours after administration. (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 35 BP; 0 A; 0 C; 5 G; 30 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.4; DB 1; Length 35;  
Best Local Similarity 76.9%; Pred. No. 3.8e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 2779 AGAATTGAAAAA 2804  
Db 32 AAAAAACAAAAAACAAAAACAAAAA 7  
RESULT 2453  
AAX18389  
ID AAX18389 standard; DNA; 18 BP.  
XX  
AC AAX18389;  
XX  
DT 11-MAY-1999 (first entry)  
XX



CC precancerous condition, by administering to the patient a first allele  
CC specific inhibitor (ASI) targeted to an allele of a first essential gene  
CC present in cells of the precancerous condition, where the normal somatic  
CC cells of the patient are heterozygous for the first gene, the inhibitor  
CC is active on at least one but less than all allelic forms of the gene  
CC present in a population and targets only one allelic form present in the  
CC normal somatic cells, and the first gene. The products and methods can be  
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.  
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic  
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and  
CC graft versus host disease. The method can also be used to remove  
CC malignant cells from bone marrow transplants. AAZ25812-Z26825 represent  
CC human polymorphic sites described in the method of the invention

SQ Sequence 21 BP; 13 A; 1 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2776 GTTAGAATTGAAAAAAAAAAAA 2796  
Db 1 GTTAGCTTTAAAAA 21

RESULT 2456

AAZ09196

ID AAZ09196 standard; DNA; 21 BP.

XX

AC AAZ09196;

XX

DT 19-OCT-1999 (first entry)

XX

DE Oligonucleotide 8 for DNA analysis.

XX

KW Primer; DNA analysis; amplification; hybridisation; ss.

XX

OS Synthetic.

XX

PN JP11196874-A.

XX

PD 27-JUL-1999.

XX

PF 14-JAN-1998; 98JP-00005399.

XX

PR 14-JAN-1998; 98JP-00005399.

XX

PA (HITA ) HITACHI LTD.

XX

DR WPI; 1999-496652/42.

XX

PT Analysis of DNA fragment - comprises addition of known common  
PT oligonucleotide, amplification of resultant DNA fragment and analysis and  
PT labelling of amplified DNA.

XX

PS Example 1; Page 12; 17pp; Japanese.

XX

CC This invention describes a novel method for the analysis of a DNA fragment  
CC which comprises: (i) addition of a known common oligonucleotide sequence  
CC to at least one terminal of each DNA fragment, (ii) amplification of the  
CC resultant DNA fragment as a primer using a first common primer containing  
CC a complementary nucleotide sequence to the above mentioned known common  
CC oligonucleotide sequence, a second common primer containing a  
CC complementary nucleotide sequence to the prepared known common  
CC oligonucleotide sequence optionally having been introduced with  
CC complementary nucleotide sequence at a terminal, and a specific primer  
CC capable of hybridisation with a DNA fragment containing whole or part of  
CC the gene having known sequence, to give amplified DNA, (iii) analysis of  
CC the amplified DNA to find the information of the DNA fragment, in which  
CC the specific primers is designed to prepare fragments of the common first  
CC and second primers and to give short fragment of amplified DNA and (iv)  
CC labelling them to make their differentiation. Differentiation of  
CC informations of known and unknown genes readily provides information of

CC unknown gene and simultaneous monitoring of signals derived from minor  
CC genes. Furthermore, labelling of DNAs according to functions of known  
CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers  
CC used to illustrate the method of the invention

XX

SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 2.1e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTTTTTTTTTTTTT 2181

Db 1 TGTGGTTTTTTTTTTTTTTT 21

RESULT 2457

AAZ73804

ID AAZ73804 standard; DNA; 21 BP.

XX

AC AAZ73804;

XX

DT 10-SEP-2001 (first entry)

XX

DE Human biallelic marker downstream amplification primer SEQ ID NO:8160.

XX

KW Human genome; biallelic marker; high density disequilibrium map;

KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;

KW amplification; single nucleotide polymorphism; SNP; PCR primer;

KW diagnosis; ss.

XX

OS Homo sapiens.

XX

PN WO9954500-A2.

XX

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

XX

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST ) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.

XX

PS Claim 8; Page 1970; 2745pp; English.

XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX

SQ Sequence 21 BP; 6 A; 7 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 21;









CC	treatment of muscular dystrophy, genesis dysfunction and cancer. Use of
CC	the protein and polynucleotide can cause muscular and cytostatic
CC	activity. The present sequence represents a PCR primer specific for cDNA
CC	encoding the human transcriptional activator subunit 49 protein
XX	
SQ	Sequence 23 BP; 1 A; 6 C; 4 G; 12 T; 0 U; 0 Other;
	Query Match            0.6%; Score 16.2; DB 1; Length 23;
	Best Local Similarity   85.7%; Pred. No. 2.6e+03;
	Matches   18; Conservative   0; Mismatches   3; Indels   0; Gaps   0;
QY	1502 GAGAAACACAGGAAATAAAAAT 1522 
Dd	23 GAGAAACAGAGGCACAAAAAT 3
<hr/>	
RESULT 2465	
AAL46192	
ID	AAL46192 standard; DNA; 23 BP.
XX	
AC	AAL46192;
XX	
DT	11-JUL-2002 (first entry)
XX	
DE	Human liver cancer expressed protein PP3731 PCR primer #1.
XX	
KW	Human; liver cancer; hepatoma; PP367; PP1597; PP1729; PP3476; PP3731;
KW	PP3856; PP3958; PP3971; PP4519; PP5241; PCR; primer; ss.
XX	
OS	Homo sapiens.
PN	
XX	CN1329064-A.
XX	
PD	02-JAN-2002.
XX	
PF	20-JUN-2000; 2000CN-00116616.
XX	
PR	20-JUN-2000; 2000CN-00116616.
XX	
PA	(SHAN-) SHANGHAI INST TUMOR.
XX	
PI	Gu J, Yang S;
XX	
DR	WPI; 2002-330564/37.
XX	
PT	Novel human protein with expression difference in liver cancer tissue
PT	useful for detecting cancers, such as hepatoma.
XX	
PS	Example 2; Page 14 (Disclosure); 40pp; Chinese.
XX	
CC	The present invention provides the protein and coding sequences of a
CC	number of human protein which are differentially expressed in hepatoma
CC	tissues, and can thus be used to detect liver cancers. These are
CC	designated PP367, PP1597, PP1729, PP3476, PP3731, PP3856, PP3958, PP3971,
CC	PP4519 and PP5241. The present sequence is a PCR primer for a coding
CC	sequence of the invention
XX	
SQ	Sequence 23 BP; 3 A; 12 C; 3 G; 5 T; 0 U; 0 Other;
	Query Match            0.6%; Score 16.2; DB 1; Length 23;
	Best Local Similarity   85.7%; Pred. No. 2.6e+03;
	Matches   18; Conservative   0; Mismatches   3; Indels   0; Gaps   0
QY	302 CTCCTCCCACTGGAGTCGCC 322 
Dd	2 CTCCTCCCACTCCAGTCGCC 22
<hr/>	
RESULT 2466	
ABK91269	
ID	ABK91269 standard; DNA; 24 BP.
XX	
AC	ABK91269;









QY 2781 AATTGAAAAAAAAAAAAAAAAA 2801  
DB 22 ACTTCAAAAAAAAAAAAAAAAAA 2

RESULT 2475  
ABV74353/c  
ID ABV74853 standard; DNA; 24 BP.

XX AC ABV74853;  
XX 05-FEB-2003 (first entry)  
XX Protein 16.17 PCR primer #2.  
XX Protein 16.17; colipase; cancer; HIV infection; cytostatic; anti-HIV;  
KW PCR; primer; ss.

XX Unidentified.  
XX CN1351027-A.  
XX 29-MAY-2002.  
XX 26-OCT-2000; 2000CN-00125840.  
XX 26-OCT-2000; 2000CN-00125840.  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;  
XX WPI; 2002-619851/67.  
XX New polypeptide-protein 16.17 containing colipase characteristics for  
PT treating diseases such as cancer and human immunodeficiency virus  
PT infection.  
XX Example 3; Page 26 (Disclosure); 3lpp; Chinese.

XX The present invention relates to protein 16.17 (see ABB98830), which  
contains colipase characteristics. The protein and its coding sequence  
are useful for treating diseases such as cancer and HIV infection. The  
present sequence is a PCR primer, which was used in an example from the  
invention. Note: The present sequence, SEQ ID 4, shown in the sequence  
listing differs from the SEQ ID 4 shown in the disclosure (see ABV74866)

XX Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.2; DB 1; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.8e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAAAAAA 2804  
DB 24 TGACTACAAAAAAAAAAAAAAAAA 4

RESULT 2476  
ABK67211  
ID ABK67211 standard; DNA; 24 BP.

XX AC ABK67211;  
XX 02-JUL-2002 (first entry)  
XX Human gene specific PCR primer #1299.  
XX Primer; ss; DNA microarray; differential expression analysis; human.  
XX Homo sapiens.

PN US6352829-B1.  
XX 05-MAR-2002.  
XX 05-JAN-1999; 99US-00225928.  
XX 21-MAY-1997; 97US-00859998.  
XX (CLON-) CLONTECH LAB INC.  
XX Chenchik A, Jokhadze G, Bibilashvilli R;  
XX WPI; 2002-314699/35.  
XX Producing sub-population of labeled nucleic acids, useful for analyzing  
PT differences in RNA profiles between several different physiological  
PT sources, using set of distinct gene specific primers.  
XX Example 3; SEQ ID NO 1299; 1lpp; English.

XX The invention relates to producing a sub-population of labeled nucleic  
CC acids (NAs) comprising contacting a NA sample from a physiological  
CC source, with a pool of 50 distinct gene specific primers under suitable  
CC conditions to enzymatically generate sub-population of NAs, where each  
CC gene specific primer has a sequence complementary to a distinct mRNA, and  
CC each labeled NA is generated using a single gene specific primer. The  
CC method is useful for producing a sub-population of labeled NAs which is  
CC useful for analysing the differences in the RNA profiles between several  
CC different physiological sources, where the method comprises producing  
CC subpopulation of labeled NAs for each physiological source, comprising  
CC the population, where the comparison is preferably  
CC performed by hybridising the labeled NAs for each of the distinct  
CC physiological sources to an array of probe NAs stably associated with the  
CC surface of a substrate to produce a hybridisation pattern for each of the  
CC sources, and comparing the patterns for each of the sources, where  
CC differential gene expression assays are utilised in differential  
CC expression analysis of diseased a normal tissue e.g. neoplastic a normal  
CC tissue, or different tissue or sub tissue types. The present sequence is a  
CC human gene specific PCR primer used in the method of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPTO  
CC at <http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1>

XX Sequence 24 BP; 4 A; 10 C; 6 G; 4 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.2; DB 1; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.8e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 266 TCCGCCGGCAGCACCTCTAC 286  
DB 1 TCCGCCGTGCAGCAGTCAAC 21

RESULT 2477  
ABQ77631/c  
ID ABQ77631 standard; DNA; 24 BP.  
XX AC ABQ77631;  
XX 21-OCT-2002 (first entry)  
XX Human Hsmar1 protein 15.95 RT-PCR primer, SEQ ID NO:4.

XX Human; Hsmar1 protein 15.95; mariner1 transposase;  
KW recombinant production; gene therapy; tumour; cancer;  
KW embryonic development disorder; diabetes; menstrual disorder;  
KW peptic ulcer; arrhythmia; anaemia; cytostatic; cardiant;  
KW reverse transcription-PCR; RT-PCR; primer; ss.  
XX Homo sapiens.





```

SQ      Sequence 24 BP; 0 A; 0 C; 6 G; 18 T; 0 U; 0 Other;
      Query Match          0.6%; Score 16.2; DB 1; Length 24;
      Best Local Similarity 85.7%; Pred. No. 2.8e+03;
      Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTTTTTTTT 2186
Db      2 TTTTTTTTGGTTGTTTTTTT 22

RESULT 2481
ABQ77543
ID      ABQ77543 standard; DNA; 24 BP.
XX
AC      ABQ77543;
XX
DT      01-OCT-2002 (first entry)
XX
DE      Human red blood cell cytoplasmic protein 15.29 RT-PCR primer, SEQ ID:3.
XX
KW      Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KW      recombinant production; gene therapy; cerebral anoxia;
KW      respiratory adynamia; arrhythmia; intestinal palsy; anaemia; haemostatic;
KW      cardiant; reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS      Homo sapiens.
XX
PN      CN1339497-A.
XX
PD      13-MAR-2002.
XX
PF      23-AUG-2000; 2000CN-00119732.
XX
PR      23-AUG-2000; 2000CN-00119732.
XX
PA      (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI      Mao Y, Xie Y;
XX
DR      WPI; 2002-472206/51.
XX
PT      New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT      treating anaerobic cerebral disease, respiratory adynamia, arrhythmia,
PT      intestinal palsy, and anemia.
XX
PS      Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC      The invention relates to human red blood cell cytoplasmic protein 15.29
CC      (AAM49384) and nucleic acids encoding it (ABQ77542). The protein has a
CC      molecular weight of 15 kD. The invention also relates to a method for the
CC      recombinant production of the protein, an antagonist of the protein, and
CC      the use of the protein, gene and antagonist in therapeutic applications.
CC      Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC      a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC      arrhythmia, intestinal palsy and anaemia. Sequences ABQ77543- ABQ77544
CC      represent reverse transcription-PCR (RT-PCR) primers used in an
CC      exemplification of the invention to isolate human red blood cell
CC      cytoplasmic protein 15.29 cDNA
XX
SQ      Sequence 24 BP; 3 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

      Query Match          0.6%; Score 16.2; DB 1; Length 24;
      Best Local Similarity 85.7%; Pred. No. 2.8e+03;
      Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2167 TTTTTTTTTTTTTTTTTTTT 2187
Db      4 TTTTTTTTTTTTCCTTTTGA 24

RESULT 2482
ABQ77543/c

```



PS Example 2; Page 18 (disclosure); 33pp; Chinese.

XX The invention relates to human development regulator GTP-binding protein

CC 1 (DRG1) 9.35 polypeptide and its encoding nucleic acid. The

CC polynucleotide, polypeptide and its antagonist are useful for treating

CC e.g. embryo development disorder and cancer. The current sequence

CC represents a human development regulator GTP-binding protein 1 (DRG1)

CC 9.35 related primer

XX Sequence 24 BP; 4 A; 2 C; 4 G; 14 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 2.8e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2777 TTAGAATTGAAAAA 2797

Db 21 TTCCAATGGAAAAA 1

RESULT 2485

ABZ25620

ID ABZ25620 standard; DNA; 24 BP.

XX AC ABZ25620;

XX DT 28-MAR-2003 (first entry)

XX DE Human zinc finger protein 11 PCR primer 1.

XX Human; zinc finger protein 11; tumour; haemopathy; HIV; inflammation;

KW immunological disease; zinc finger; PCR; primer; ss.

XX OS Homo sapiens.

XX CN1364768-A.

XX PD 21-AUG-2002.

XX PF 10-JAN-2001; 2001CN-00105125.

XX PR 10-JAN-2001; 2001CN-00105125.

XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX WPI; 2003-000480/01.

XX New human zinc finger protein 11 and encoding polynucleotide, useful in

PT treating cancer and as an anti-inflammatory.

XX Example 2; Page 16 (Disclosure); 32pp; Chinese.

XX The invention relates to the novel human zinc finger protein 11, and the

CC polynucleotide encoding it. The polypeptide is useful in treating various

CC diseases, such as malignant tumours, haemopathy, HIV infection,

CC immunological diseases and various inflammations. The present sequence

CC represents a PCR primer used to amplify the human zinc finger protein 11

CC cDNA of the invention

XX Sequence 24 BP; 4 A; 5 C; 0 G; 15 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 2.8e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2174 TTTTTCCTTTTACCTTGA 2194

Db 4 TTTTTCCTTTTACCTTAA 24

RESULT 2486

AAL57131/c

ID AAL57131 standard; DNA; 24 BP.

XX AAL57131;

XX DT 04-DEC-2003 (first entry)

XX DE RT-PCR primer 2 related to human zinc finger protein 61-82.

XX KW Human zinc finger protein 61.82; cancer; HIV infection; RT-PCR; PCR;

KW primer; ss.

XX OS Homo sapiens.

XX CN1381486-A.

XX PD 27-NOV-2002.

XX PF 18-APR-2001; 2001CN-00112634.

XX PR 18-APR-2001; 2001CN-00112634.

XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX PI Mao Y, Xie Y;

XX WPI; 2003-258239/26.

XX Polypeptide-human zinc finger protein-61.82 and polynucleotide for coding

PT it.

XX Example 3; Page 20; Opp; Chinese.

XX This invention relates to a novel human zinc finger protein 61.82 and the

CC DNA sequence encoding it. The protein of the invention may be useful for

CC the treatment of diseases such as cancer and HIV infection. The present

CC sequence is that of RT-PCR primer 2 related to the human zinc finger

CC protein 61.82 of the invention and used in example 3 of the specification

XX Sequence 24 BP; 2 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

SQ Query Match 0.6%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 2.8e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2803

Db 24 TGGAAACCAAAAAA 4

RESULT 2487

ADC10360/c

ID ADC10360 standard; DNA; 24 BP.

XX AC ADC10360;

XX DT 18-DEC-2003 (first entry)

XX DE Human NOVX polypeptide gene forward primer SEQ ID NO: 379.

XX ss; primer; cytostatic; antidiabetic; anorectic; cerebroprotective;

KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;

KW thyromimetic; NOVX; pathology; cancer; diabetes; obesity;

KW endocrine disorder; CNS disorder; inflammatory disorder;

XX chromosome mapping; tissue typing; predictive medicine.

XX OS Homo sapiens.

XX WO2003000842-A2.

XX PD 03-JAN-2003.

XX PF 04-JUN-2002; 2002WO-US017443.

XX PR 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 07-JUN-2001; 2001US-0296575P.  
PR 11-JUN-2001; 2001US-0297414P.  
PR 12-JUN-2001; 2001US-0295573P.  
PR 12-JUN-2001; 2001US-0297567P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 15-JUN-2001; 2001US-0298528P.  
PR 18-JUN-2001; 2001US-0299133P.  
PR 19-JUN-2001; 2001US-0299230P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 22-JUN-2001; 2001US-0300177P.  
PR 26-JUN-2001; 2001US-0300883P.  
PR 28-JUN-2001; 2001US-0301530P.  
PR 28-JUN-2001; 2001US-0301550P.  
PR 03-JUL-2001; 2001US-0302951P.  
PR 31-JUL-2001; 2001US-0308890P.  
PR 14-SEP-2001; 2001US-0322297P.  
PR 25-SEP-2001; 2001US-0324669P.  
PR 03-DEC-2001; 2001US-0337477P.  
PR 14-DEC-2001; 2001US-0341562P.  
PR 21-FEB-2002; 2002US-0358656P.  
PR 21-FEB-2002; 2002US-0359122P.  
PR 22-FEB-2002; 2002US-0358978P.  
PR 22-FEB-2002; 2002US-0359034P.  
PR 22-FEB-2002; 2002US-0359035P.  
PR 22-FEB-2002; 2002US-0359121P.  
PR 27-FEB-2002; 2002US-0359964P.  
PR 01-MAR-2002; 2002US-0360858P.  
PR 12-MAR-2002; 2002US-0363430P.  
PR 12-MAR-2002; 2002US-0363676P.  
PR 10-APR-2002; 2002US-0371346P.  
PR 10-MAY-2002; 2002US-0379444P.  
PR 04-JUN-2002; 2002US-00379444.  
XX PA (CURA-) CURAGEN CORP.  
XX PI Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;  
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
PI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
PI Ort T, Padigar M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;  
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;  
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
PI Burgess CE, Lepley DM;  
XX WPI; 2003-210149/20.  
XX PR New isolated NOVX polypeptides and nucleic acid molecules useful for  
PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.  
XX PS Example B; SEQ ID NO 379; 772pp; English.  
XX CC The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to a primer used to  
CC amplify and isolate the coding sequence for one of the polypeptides of  
CC the invention.  
XX SQ Sequence 24 BP; 6 A; 7 C; 3 G; 8 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 2.8e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2214 GAGACTCTTTGAAATGACATG 2234  
||||||| |  
Db 23 GAGACTCTTGAAGATGACATG 3  
RESULT 2488  
AAV57477/c  
ID AAV57477 standard; DNA; 25 BP.  
XX AC AAV57477;  
XX DT 14-DEC-1998 (first entry)  
XX Cytochrome P450ox monoxygenase PCR primer SEQ ID NO:11.  
KW Cytochrome P450 monoxygenase; P450ox; Sorghum bicolor (L.) Moench;  
KW Sinapis alba; biosynthetic conversion; aldoxime; nitrile; cyanohydrin;  
KW cyanogenic glycoside; transgenic plant; resistance; PCR primer; ss.  
XX OS Synthetic.  
OS Sorghum bicolor.  
XX PN WO9840470-A2.  
XX PD 17-SEP-1998.  
XX PF 05-MAR-1998; 98WO-EP001253.  
XX PR 07-MAR-1997; 97EP-00810132.  
XX PR 08-DEC-1997; 97EP-00810954.  
XX PA (NOVS ) NOVARTIS AG.  
PA (UYRO-) UNIV ROYAL VETERINARY & AGRIC.  
XX PI Halkier BA, Bak S, Kahn RA, Moeller BL;  
XX WPI; 1998-520808/44.  
XX PT Cytochrome P450 monoxygenase of the cyanogenic glycoside pathway -  
PT useful for the production of plants with improved nutritive value or pest  
PT resistance.  
XX PS Example 5; Page 29; 32pp; English.  
XX CC The present sequence represents a PCR primer for cytochrome P450  
CC monoxygenase from Sorghum bicolor (L.) Moench, designated P450ox.  
CC Cytochrome P450 monoxygenase catalyses: (i) the conversion of aldoxime  
CC to a nitrile; and (ii) the nitrile to the corresponding cyanohydrin. DNA  
CC encoding cytochrome P450 monoxygenase can be used to obtain transgenic  
CC plants, for the purpose of improving the nutritive value or pest  
CC resistance of the plant. Cytochrome P450 monoxygenase catalyses the  
CC conversion of aldoximes to nitriles to cyanohydrins, which are the  
CC precursors of toxic cyanogenic glycosides, so staple food such as cassava  
CC and lima beans, as well as animal feed such as white clover, can be  
CC rendered less toxic by blocking the cytochrome P450 monoxygenase  
CC activity. Introducing the enzyme to plants or to certain tissues could  
CC help reduce crop damage since the product is also toxic to insects,  
CC acarids and nematodes  
XX SQ Sequence 25 BP; 1 A; 3 C; 3 G; 17 T; 0 U; 1 Other;  
Query Match 0.6%; Score 16.2; DB 1; Length 25;  
Best Local Similarity 94.1%; Pred. No. 3e+03;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAATAAAAAAAAAA 2801  
:|||||||  
Db 25 BAAAAAATAAAAAAAAAA 9



Thu Jun 10 13:10:09 2004

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RESULT 2489
ABAO3917/c
ID ABA03917 standard; DNA; 25 BP.
XX
AC ABA03917;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human connexin 9 PCR primer 2 SEQ ID NO:4.
XX
KW Human; connexin 9; cytostatic; virucidal; immunomodulatory;
KW antiinflammatory; haemostatic; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200181538-A2.
XX
XX 01-NOV-2001.
XX
PF 23-APR-2001; 2001WO-CN000608.
XX
PR 27-APR-2000; 2000CN-00115456.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-034440/04.
XX
PT Human connexin 9 and encoded polynucleotide, applicable in diagnosis and
PT treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and inflammation.
XX
PS Example 2; Page 12; 32pp; Chinese.
XX
CC The present invention describes human connexin 9 (I). (I) has cytostatic,
CC virucidal, immunomodulatory, antiinflammatory and haemostatic activities.
CC (I) and the polynucleotide encoding it (II) are applicable in the
CC diagnosis and treatment of malignant tumour, haemopathy, HIV infection,
CC immunological diseases and various inflammations. The present sequence
CC represents a PCR primer for human connexin 9, which is used in an example
CC from the present invention
XX
SQ Sequence 25 BP; 3 A; 0 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 2784 TGAAAAAATAAAAAAATAAAAAA 2804
Db 25 TAAAAAATAAAAAAATAAAAAA 5

RESULT 2490
AAC96118/c
ID AAC96118 standard; DNA; 25 BP.
XX
AC AAC96118;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16s rRNA gene PCR primer #85.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
```

```

PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.6%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 3e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 3;

QY 2781 AATTGAAAAAATAAAAAA 2801
Db 21 AGTTCCAAAAAATAAAAAA 1

RESULT 2491
AAH38027
ID AAH38027 standard; DNA; 25 BP.
XX
AC AAH38027;
XX
DT 14-AUG-2001 (first entry)
XX
DE SNP specific SNPE primer SEQ ID 823.
XX
KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT
```



**XX** DNA sequence analysis; sequencing; protein sequence; protein structure;  
**KW**

WPI: 1997-372877/34.

XX Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -  
PT and/or predisposition to develop premature atherosclerosis by detecting  
PT increased levels of serum homocysteine.  
XX Disclosure; Page 22; 84pp; English.  
XX Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from  
CC cells exposed to hyperphysiological, normal or subphysiological levels of  
CC homocysteine. PCR products were separated on a sequencing gel and  
CC discrete fractions which were increased or decreased were identified.  
CC This method was used to identify mRNA and the corresponding cDNA which  
CC are increased in the cells of a patient having hyperhomocysteinaemia or a  
CC predisposition to homocysteine mediated atherosclerosis. These  
CC polynucleotides can be used for the diagnosis and treatment of  
CC atherosclerotic diseases and diseases of metabolism of sulphur containing  
CC amino acids (e.g. homocysteinaemia), which are associated with vascular  
CC damage and atherosclerotic disease, specifically unstable angina, acute  
CC myocardial infarction (heart attack), cerebrovascular accidents (stroke),  
CC hypertension, renal artery stenosis, aortic stenosis and deep vein  
CC occlusive disease  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTT TTTT TTTT TTTG 1782  
Db 1 AAGCTTTT TTTT TTTT TTTG 16  
  
RESULT 2497  
AAV36965  
ID AAV36965 standard; cDNA; 16 BP.  
XX  
AC AAV36965;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat pituitary-tumour-transforming-gene anchored primer.  
XX  
KW ss; pituitary-tumour-transforming gene; PTTG; pituitary tumour; PCR;  
KW cancer; oncogene; gene replacement therapy; primer; amplification.  
XX  
OS Synthetic.  
OS Rattus sp.  
XX  
PN WO9822587-A2.  
XX  
PD 28-MAY-1998.  
XX  
PF 21-NOV-1997; 97WO-US021463.  
XX  
PR 21-NOV-1996; 96US-0031338P.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Melmed S, Pei L;  
XX  
DR WPI; 1998-312473/27.  
XX  
PT New pituitary tumour transforming gene and protein - used for diagnosis,  
PT monitoring and treatment of tumours.  
XX  
PS Example 1; Page 23; 44pp; English.  
XX  
CC The primers AAV36965 and AAV36966 were used in the isolation of the  
CC pituitary-tumour transforming gene (PTTG). The PTTG encodes a polypeptide  
CC that is expressed by pituitary tumour cells and binds to anti-PTTG  
CC antibodies (Ab). Recombinant PTTG is useful as an immunogen for raising  
CC Ab, in assays and for therapy. Ab, optionally labelled, are used to

CC detect, e.g. for monitoring treatment or in in vivo imaging, or purify  
CC human PTTG, e.g. for diagnosis of pituitary tumours and for  
CC differentiating between malignant and benign tumours in biopsy samples.  
CC Oligonucleotides and antisense oligonucleotides can also be used  
CC therapeutically to counteract or stimulate biological effects of PTTG.  
CC Many cancers express PTTG, and the nucleic acid sequence can transform  
CC cells without a complementary oncogene; it is responsible for tumour  
CC formation in the pituitary. PTTG is useful in gene replacement therapy  
CC and transgenic animals are used as models for studying pituitary tumours  
XX etc  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTT TTTT TTTT TTTG 1782  
Db 1 AAGCTTTT TTTT TTTT TTTG 16  
  
RESULT 2498  
AAX57361  
ID AAX57361 standard; DNA; 16 BP.  
XX  
AC AAX57361;  
XX  
DT 24-JUL-1999 (first entry)  
XX  
DE P. obesus beacon PCR primer 1.  
XX  
KW Beacon; hypothalamus; obese; lean; agonist; antagonist; treatment;  
KW obesity; anorexia; weight maintenance; energy imbalance; diabetes;  
KW metabolic syndrome; dyslipidemia; hypertension; insulin resistance;  
KW medicament; livestock; diagnosis; PCR primer; ss.  
XX  
OS Synthetic.  
OS Psammomys obesus.  
XX  
PN WO9923217-A1.  
XX  
PD 14-MAY-1999.  
XX  
PF 30-OCT-1998; 98WO-AU000902.  
XX  
PR 31-OCT-1997; 97AU-00000117.  
PR 11-NOV-1997; 97AU-00000323.  
XX  
PA (ITDI-) INT DIABETES INST.  
PA (UYDE-) UNIV DEAKIN.  
XX  
PI Zimmet PZ, Collier G;  
XX  
DR WPI; 1999-337484/28.  
XX  
PT New gene encoding a beacon protein associated with modulation of obesity,  
PT diabetes and metabolic energy levels.  
XX  
PS Example 5; Page 51; 85pp; English.  
XX  
CC This invention describes a novel beacon protein and its encoding nucleic  
CC acid which is expressed in larger amounts in hypothalamus tissue of obese  
CC animals compared to lean animals. Agonists and antagonists of beacon can  
CC be used to treat obesity, anorexia, weight maintenance, energy imbalance,  
CC diabetes, metabolic syndrome, dyslipidemia, hypertension and/or insulin  
CC resistance. The beacon protein, itself is used to manufacture medicaments  
CC for treatment of obesity, anorexia, energy imbalance or diabetes. The  
CC treatment is contemplated for both human and animals, such as those  
CC important to the livestock industry. The antibody and polynucleotides are  
CC useful in diagnosis of conditions as above. This sequence represents a  
CC PCR primer used in the method of the invention  
XX



RESULT 2500

AA  
AC  
XX  
DT

XX RT-PCR primer of the invention SEQ ID 3.  
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.  
KW Synthetic.  
XX JP11032765-A.  
XX OS  
XX 09-FEB-1999.  
XX PD  
XX 18-JUL-1997; 97JP-00208312.  
XX PR  
XX 18-JUL-1997; 97JP-00208312.  
XX PA (TAKI ) TAKARA SHUZO CO LTD.  
XX WPI; 1999-183822/16.  
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.  
XX Disclosure; Page 10; 19pp; Japanese.  
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences  
XX  
SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2784 TGAAGAAAAA 2799  
Db 16 TGAAGAAAAA 1  
RESULT 2502  
AAX07568  
ID AAX07568 standard; cDNA; 16 BP.  
XX AAX07568;  
AC AAX07568;  
XX 21-JUN-1999 (first entry)  
XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.  
XX Secreted protein; fetal kidney; ds.  
OS Homo sapiens.  
XX WO9900405-A1.  
XX 07-JAN-1999.  
XX 29-JUN-1998; 98WO-US013530.  
XX 30-JUN-1997; 97US-00885610.  
XX (GEMY ) GENETICS INST INC.  
XX Jacobs K, McCOY JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
PI

PI Evans C, Agostino MJ;  
XX WPI; 1999-095671/08.  
DR New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential vaccines.  
XX Disclosure; Page 54; 76pp; English.  
XX The sequence is that of the 3' end of a sequence encoding a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. It is also stated to be useful for gene therapy  
XX  
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA 2801  
Db 1 AAAAAA 16  
RESULT 2503  
AAX07568/c  
ID AAX07568 standard; cDNA; 16 BP.  
XX AAX07568;  
AC AAX07568;  
XX 21-JUN-1999 (first entry)  
XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.  
XX Secreted protein; fetal kidney; ds.  
OS Homo sapiens.  
XX WO9900405-A1.  
XX 07-JAN-1999.  
XX 29-JUN-1998; 98WO-US013530.  
XX 30-JUN-1997; 97US-00885610.  
XX (GEMY ) GENETICS INST INC.  
XX Jacobs K, McCOY JM, Lavallie ER, Racie LA, Merberg D, Treacy M;  
PI Evans C, Agostino MJ;  
XX WPI; 1999-095671/08.  
XX New polynucleotides encoding secreted human proteins - are derived from foetal kidney or adult retina cDNA libraries, used as, e.g. potential vaccines.  
XX Disclosure; Page 54; 76pp; English.  
XX The sequence is that of the 3' end of a sequence encoding a secreted protein from a human fetal kidney clone AK296. Such a sequence is predicted to have biological activities which would make them suitable

CC for treating, preventing or ameliorating medical conditions in humans and  
CC animals, although no supporting data is given. Suggested activities  
CC include nutritional activity, cytokine and cell  
CC proliferation/differentiation activity, immune stimulating (e.g. as  
CC vaccines) or suppressing activity, haematopoiesis regulating activity,  
CC tissue growth activity, activin/inhibin activity,  
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,  
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour  
CC invasion suppressor activity, and tumour inhibition activity. It is also  
CC stated to be useful for gene therapy  
XX  
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2181  
Db 16 TTTT TTTT TTTT TTTT TTTT TTTT 1  
  
RESULT 2504  
AAC66068  
ID AAC66068 standard; DNA; 16 BP.  
XX  
AC AAC66068;  
XX  
XX 22-FEB-2001 (first entry)  
XX  
DE DNA chip primer #4.  
XX  
XX DNA chip; primer; nucleoside derivative; photolabile protecting group;  
KW photolithographic nucleic acid chip; ss.  
XX  
XX Synthetic.  
OS  
XX WO2000061594-A2.  
XX  
PN 19-OCT-2000.  
XX  
PD 07-APR-2000; 2000WO-DE001148.  
XX  
PF 08-APR-1999; 99DE-01015867.  
XX  
PR 28-JAN-2000; 2000DE-01003631.  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA  
XX  
XX Beier M, Hoheisel J;  
PI  
XX  
XX WPI; 2000-679457/66.  
XX  
XX New nucleoside derivatives with photolabile protecting groups, useful in  
PT oligonucleotide synthesis, particularly on solid phases, e.g. for  
PT hybridization testing.  
XX  
PS Disclosure; Fig 9; 48pp; German.  
XX  
XX This invention describes nucleoside derivatives (I) with photolabile  
CC protecting groups. (I) are used to synthesize oligonucleotides using the  
CC photolithographic nucleic acid chip method, particularly where these are  
CC intended for performing enzymatic reactions initiated from a free 3'-  
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,  
CC but also reverse transcription, cDNA synthesis etc.), also for  
CC hybridization testing, sequencing and in DNA computing. (I) are produced  
CC with high selectivity by reaction with a mild acylating agent that has  
CC high specificity for the 3'-position, without significant side-reactions  
CC (cf. more reactive acylating agents such as chloroformates)  
XX  
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2181  
Db 16 TTTT TTTT TTTT TTTT TTTT TTTT 1  
  
RESULT 2506  
AAC66068  
ID AAC66068 standard; DNA; 16 BP.  
XX  
AC AAC66068;  
XX  
XX 22-FEB-2001 (first entry)  
XX  
DE DNA chip primer #4.  
XX  
XX DNA chip; primer; nucleoside derivative; photolabile protecting group;  
KW photolithographic nucleic acid chip; ss.  
XX  
XX Synthetic.  
OS  
XX WO2000061594-A2.  
XX  
PN 19-OCT-2000.  
XX  
PD 07-APR-2000; 2000WO-DE001148.  
XX  
PF 08-APR-1999; 99DE-01015867.  
XX  
PR 28-JAN-2000; 2000DE-01003631.  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA  
XX  
XX Beier M, Hoheisel J;  
PI  
XX  
XX WPI; 2000-679457/66.  
XX  
XX New nucleoside derivatives with photolabile protecting groups, useful in  
PT oligonucleotide synthesis, particularly on solid phases, e.g. for  
PT hybridization testing.  
XX  
PS Disclosure; Fig 9; 48pp; German.  
XX  
XX This invention describes nucleoside derivatives (I) with photolabile  
CC protecting groups. (I) are used to synthesize oligonucleotides using the  
CC photolithographic nucleic acid chip method, particularly where these are  
CC intended for performing enzymatic reactions initiated from a free 3'-  
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,  
CC but also reverse transcription, cDNA synthesis etc.), also for  
CC hybridization testing, sequencing and in DNA computing. (I) are produced  
CC with high selectivity by reaction with a mild acylating agent that has  
CC high specificity for the 3'-position, without significant side-reactions  
CC (cf. more reactive acylating agents such as chloroformates)  
XX  
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2801  
Db 1 AAAAAAAAAAAAAAAAAA 16  
  
RESULT 2505  
AAC66068/c  
ID AAC66068 standard; DNA; 16 BP.  
XX  
AC AAC66068;  
XX  
XX 22-FEB-2001 (first entry)  
XX  
DE DNA chip primer #4.  
XX  
XX DNA chip; primer; nucleoside derivative; photolabile protecting group;  
KW photolithographic nucleic acid chip; ss.  
XX  
XX Synthetic.  
OS  
XX WO2000061594-A2.  
XX  
PN 19-OCT-2000.  
XX  
PD 07-APR-2000; 2000WO-DE001148.  
XX  
PF 08-APR-1999; 99DE-01015867.  
XX  
PR 28-JAN-2000; 2000DE-01003631.  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA  
XX  
XX Beier M, Hoheisel J;  
PI  
XX  
XX WPI; 2000-679457/66.  
XX  
XX New nucleoside derivatives with photolabile protecting groups, useful in  
PT oligonucleotide synthesis, particularly on solid phases, e.g. for  
PT hybridization testing.  
XX  
PS Disclosure; Fig 9; 48pp; German.  
XX  
XX This invention describes nucleoside derivatives (I) with photolabile  
CC protecting groups. (I) are used to synthesize oligonucleotides using the  
CC photolithographic nucleic acid chip method, particularly where these are  
CC intended for performing enzymatic reactions initiated from a free 3'-  
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,  
CC but also reverse transcription, cDNA synthesis etc.), also for  
CC hybridization testing, sequencing and in DNA computing. (I) are produced  
CC with high selectivity by reaction with a mild acylating agent that has  
CC high specificity for the 3'-position, without significant side-reactions  
CC (cf. more reactive acylating agents such as chloroformates)  
XX  
SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2181  
Db 16 TTTT TTTT TTTT TTTT TTTT TTTT 1  
  
RESULT 2506  
AAC66068  
ID AAC66068 standard; DNA; 16 BP.  
XX  
AC AAC66068;  
XX  
XX 01-MAR-2001 (first entry)  
XX  
XX

DE MMLV reverse transcriptase PCR primer H-T11G SEQ ID NO:4.  
XX  
KW LIM mineralisation protein; LMP; bone formation; osteopathic;  
KW osteogenic precursor cell; gene therapy; metabolic bone disease;  
XX osteoporosis; bone degenerative disease; PCR primer; ss.  
OS Moloney murine leukemia virus.  
XX  
PN WO200066178-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US011664.  
XX  
PR 30-APR-1999; 99US-0132021P.  
XX  
PA (UYEM-) UNIV EMORY.  
XX  
PI Boden SD, Hair GA;  
XX  
DR WPI; 2000-672828/65.  
XX  
PT New nucleic acid encoding a human LIM mineralization protein for inducing  
PT or inhibiting bone formation, fusing a spine, stimulating production of  
PT an osteogenic cell, or treating bone conditions, such as, osteoporosis.  
XX  
PS Example 9; Page 61; 84pp; English.  
XX  
CC The present invention specifically describes the human LIM mineralisation  
CC proteins (LMP) HLMF-2 and HLMF-3. LMPs have osteopathic activity and can  
CC be used in gene therapy. LMP nucleic acids can be used to induce or  
CC inhibit bone formation, fuse a spine, stimulate production of an  
CC osteogenic cell, or inhibit the expression of HLMF-2 or HLMF-3. They can  
CC be used to treat bone conditions, such as, osteoporosis and other  
CC metabolic bone diseases. Antibodies to the LMP proteins encoded by the  
CC nucleic acids are used in marker assays to identify risk factors in bone  
CC degenerative diseases, such as osteoporosis. The nucleic acids are used  
CC in gene therapy for bone formation which leads to the advantages of: (1)  
CC lower production costs; (2) greater efficacy compared to extracellular  
CC treatment regimens due to the ability to achieve prolonged expression of  
CC the intracellular signal; (3) by-passing the possibility that treatment  
CC with extracellular signals might be hampered due to the presence of  
CC limiting numbers or receptors for those signals; (4) permitting the  
CC delivery of transfected potential osteoprogenitor cells directly to the  
CC site where localised bone formation is required; and (5) permitting  
CC systemic bone formation, which provides a treatment regimen for  
CC osteoporosis and other metabolic bone diseases. The present sequence  
CC represents a reverse transcriptase PCR primer which is used in an example  
CC from the present invention  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTCTTTTGTG 1782  
Db 1 AAGCTTTTCTTTTGTG 16  
  
RESULT 2507  
AAA94101  
ID AAA94101 standard; DNA; 16 BP.  
XX  
AC AAA94101;  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Fruit-associated banana TRX gene PCR primer H-T11G.  
XX  
KW Banana; fruit-associated TRX gene; promoter; GlA; transgenic plant;  
KW fruit ripening; nutrition; PCR primer; ss.

XX Musa acuminata.  
OS  
XX WO200056863-A1.  
PN  
XX 28-SEP-2000.  
PD  
XX 17-MAR-2000; 2000WO-US007293.  
PF  
XX 19-MAR-1999; 99US-0125310P.  
PR  
XX (AGRI-) AGRITOE INC.  
PA  
XX Clendennen SK, Kellogg JA, Phan CB, Mathews HV, Webb NM;  
PI WPI; 2000-628259/60.  
DR  
XX Nucleic acid molecule encoding banana fruit associated promoter and melon  
PT actin promoter, useful for producing transgenic fruit-bearing plants.  
PT  
XX Example 1; Page 35; 72pp; English.  
PS  
XX The present sequence is a PCR primer which was used to isolate and  
CC amplify the promoter of the banana fruit-associated TRX (also known as  
CC the GlA) gene. This was isolated from a banana library using differential  
CC display analysis for banana-specific transcripts. The promoters of the  
CC invention can be used to produce transgenic fruit, with altered or  
CC improved characteristics, in particular their ripening, their nutritional  
CC content and the expression of useful proteins  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTCTTTTGTG 1782  
Db 1 AAGCTTTTCTTTTGTG 16  
  
RESULT 2508  
ABA04585  
ID ABA04585 standard; DNA; 16 BP.  
XX  
AC ABA04585;  
XX  
DT 15-FEB-2002 (first entry)  
XX  
DE Oligonucleotide #5.  
XX  
KW Analytical support; genomic sequencing; mutation detection;  
KW pharmaceutical development; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine  
FT and PO is a phosphate group"  
XX  
PN FR2805348-A1.  
XX  
PD 24-AUG-2001.  
XX  
PF 23-FEB-2000; 2000FR-00002236.  
XX  
PR 23-FEB-2000; 2000FR-00002236.  
XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX



PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;  
XX WPI; 2001-628265/73.  
XX Support for hybridization analysis of nucleic acids for sequencing  
PT techniques, comprises an array of oligonucleotides having a label where  
PT the fluorescence changes follow hybridization.  
XX  
XX  
PS Example 1; Page 12; 33pp; French.  
XX  
CC The present invention relates to an analytical support, to which a number  
CC of oligonucleotides are fixed. The oligonucleotides are labelled with a  
CC fluorescent compound, the fluorescence of which varies when the  
CC oligonucleotide hybridises to its complement. The analytical support is  
CC useful in hybridisation testing for identification of specific nucleic  
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical  
CC development. The present oligonucleotide was used to illustrate the  
CC invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16  
RESULT 2509  
ABA04585/c  
ID ABA04585 standard; DNA; 16 BP.  
XX ABA04585;  
XX 15-FEB-2002 (first entry)  
XX Oligonucleotide #5.  
XX Analytical support; genomic sequencing; mutation detection;  
KW pharmaceutical development; ss.  
XX Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER = Fl(CH2)6-PO-thymine, where Fl is flavine  
FT and PO is a phosphate group"  
XX  
XX FR2805348-A1.  
PN  
XX  
XX 24-AUG-2001.  
PD  
XX  
XX 23-FEB-2000; 2000FR-00002236.  
PF  
XX 23-FEB-2000; 2000FR-00002236.  
PR  
XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
PA  
XX Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;  
PI WPI; 2001-628265/73.  
XX  
XX Support for hybridization analysis of nucleic acids for sequencing  
PT techniques, comprises an array of oligonucleotides having a label where  
PT the fluorescence changes follow hybridization.  
XX  
XX  
PS Example 1; Page 12; 33pp; French.  
XX  
CC The present invention relates to an analytical support, to which a number

CC of oligonucleotides are fixed. The oligonucleotides are labelled with a  
CC fluorescent compound, the fluorescence of which varies when the  
CC oligonucleotide hybridises to its complement. The analytical support is  
CC useful in hybridisation testing for identification of specific nucleic  
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical  
CC development. The present oligonucleotide was used to illustrate the  
CC invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAA 1  
RESULT 2510  
AAF83580  
ID AAF83580 standard; DNA; 16 BP.  
XX  
AC AAF83580;  
XX 23-JUL-2001 (first entry)  
DT  
XX B. gymnorhiza salt-tolerance cDNA amplifying primer H-T11G.  
DE  
XX Salt-stress; genetic modification; salt tolerance; PCR primer; ss.  
KW Bruguiera gymnorhiza.  
XX  
OS WO200130999-A1.  
XX  
PN 03-MAY-2001.  
XX  
PD 28-JUL-2000; 2000WO-JP005102.  
XX  
XX 22-OCT-1999; 99JP-00301621.  
PR 20-DEC-1999; 99JP-00361107.  
PR  
XX (EBAR ) EBARA CORP.  
PA  
XX Karube I, Hanagata N;  
PI  
XX WPI; 2001-308636/32.  
DR  
XX Nucleotide sequences, useful for generating salt-tolerant transgenic  
PT plants, obtained from the leaves of Bruguiera gymnorhiza subjected to  
PT 500 mM NaCl.  
PT  
XX  
PS Example 2; Page 15; 49pp; English.  
PS  
XX The invention provides nucleotide sequences highly expressed in salt-  
CC stressed leaves of Bruguiera gymnorhiza. The invention is useful to  
CC provide salt tolerant plants by genetic modification. Plants transformed  
CC with the DNA sequences have improved salt tolerance. Sequences AAF83580 -  
CC 592 represent PCR primers for amplifying B. gymnorhiza salt tolerance  
CC gene associated cDNA fragments  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1767 AAGCTTTT TTTT TTTT TTTT G 1782  
Db 1 AAGCTTTT TTTT TTTT TTTT G 16  
RESULT 2511

AAS06651  
ID. AAS06651 standard; DNA; 16 BP.  
XX  
AC AAS06651;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cDNA synthesis and differential display primer, HT11G.  
XX  
KW Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;  
KW differential display of reverse transcribed mRNAs by PCR;  
KW testicular cancer; breast cancer; prostate cancer; endometrial cancer;  
KW asthma; hypospadias; cryptorchidism; allergy; hormone replacement therapy;  
KW HRT; endocrine system; HT11G.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200134834-A2.  
XX  
PD 17-MAY-2001.  
XX  
PF 10-NOV-2000; 2000WO-DK000628.  
XX  
PR 11-NOV-1999; 99DK-00001626.  
XX  
PA (RIGS-) RIGSHOSPITALET.  
XX  
PI Leffers H, Jorgensen M, Skakkebaek NE;  
XX  
DR WPI; 2001-335941/35.  
XX  
PT Evaluating a cellular response to an environmental compound, for use in  
PT toxicological analysis, involves determining or comparing the expression  
PT levels of at least one endogenous gene.  
XX  
PS Example 3; Page 27; 77pp; English.  
XX  
CC The sequence represents a downstream PCR primer used in a DDRT-PCR  
CC experiment (and in cDNA synthesis), demonstrating the method of the  
CC invention. The method relates to evaluating a cellular response to an  
CC environmental compound, comprising determining or comparing the  
CC expression levels of at least one endogenous gene e.g by differential  
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be  
CC adapted to identify compounds that act on the level of endogenous gene  
CC expression through activating nuclear receptors. The method is useful in  
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.  
CC testicular, breast, prostate and endometrium), asthma, hypospadias,  
CC cryptorchidism and/or allergy, and for evaluating the efficiency of a  
CC treatment for hormonal deficiency or hormonal replacement therapy, in a  
CC human such as a post-menopausal female. The method is also useful for  
CC identifying environmental chemicals or pharmaceutical compositions that  
CC interact with endocrine systems, and for detecting chemicals that pose a  
CC health threat. Expression levels of endogenous genes are determined  
CC rapidly using a sensitive technique, and the expression of any gene can  
CC be monitored. The assays are far more informative than the currently used  
CC assays, and significantly reduces the number of animals required for the  
CC testing, as it is expected that essentially all the animals in a test  
CC group will respond to the compound  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTT TTTT TTTT TTTT TTTT G 1782  
Db 1 AAGCTTTT TTTT TTTT TTTT TTTT G 16  
  
RESULT 2512  
AAF30895

AAF30895 standard; DNA; 16 BP.  
XX  
AC AAF30895;  
XX  
DT 09-JUL-2001 (first entry)  
XX  
DE Oligonucleotide-minor groove binder complex.  
XX  
KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
KW hybridisation; detection; fluorescence; probe; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /note= "thymine modified by a minor groove binder (2-  
FT dimethylaminonaphthalene-6- sulfonamide"  
XX  
PN WO200131063-A1.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US029786.  
XX  
PR 26-OCT-1999; 99US-00428236.  
XX  
PA (EPOC-) EPOCH BIOSCIENCES INC.  
XX  
PI Dempsy RO, Afonina IA, Vermeulen NMJ;  
XX  
DR WPI; 2001-328656/34.  
XX  
PT Conjugate of oligonucleotide, minor groove binder and latent fluorophore,  
PT useful for detecting specific nucleic acids, e.g. for single-nucleotide  
PT mismatch discrimination.  
XX  
PS Disclosure; Page 101; 105pp; English.  
XX  
CC The present sequence is that of an oligonucleotide (ODN)-minor groove  
CC binder (MGB) complex. MGBs bind in a non-intercalating manner to the  
CC minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF  
CC conjugates of the invention also comprise a latent fluorophore (LF),  
CC which binds similarly to the MGB but in an intercalating manner, or lies  
CC in the minor groove, or is oriented in some other way to the DNA molecule  
CC by MGB, such that it becomes fluorescent (or its fluorescent properties  
CC change detectably). The conjugates are used as hybridisation probes and  
CC amplification primers for fluorescent detection of specifically  
CC hybridising sequences, for analysis or diagnosis, especially (real-time)  
CC PCR, for single-nucleotide mismatch discrimination, target or signal  
CC amplification, array-based assays and sequencing, including detection of  
CC double-stranded DNA by triplex formation  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 16  
  
RESULT 2513  
AAF30895/c  
ID AAF30895 standard; DNA; 16 BP.  
XX  
AC AAF30895;  
XX  
DT 09-JUL-2001 (first entry)  
XX  
DE Oligonucleotide-minor groove binder complex.

XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
KW hybridisation; detection; fluorescence; probe; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH modified\_base 1 /\*tag= a  
FT /note= "thymine modified by a minor groove binder (2-  
FT dimethylaminonaphthalene-6- sulfonamide"  
FT XX  
PN WO200131063-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US029786.  
XX  
XX 26-OCT-1999; 99US-00428236.  
XX  
XX (EPOC-) EPOCH BIOSCIENCES INC.  
XX  
XX Dempcy RO, Afonina IA, Vermeulen NMJ;  
XX WPI; 2001-328656/34.  
XX  
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,  
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide  
XX mismatch discrimination.  
XX  
XX Disclosure; Page 101; 105pp; English.  
XX  
XX The present sequence is that of an oligonucleotide (ODN)-minor groove  
XX binder (MGB) complex. MGBs bind in a non-intercalating manner to the  
XX minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF  
XX conjugates of the invention also comprise a latent fluorophore (LF), lies  
XX which binds similarly to the MGB but in an intercalating manner, or lies  
XX in the minor groove, or is oriented in some other way to the DNA molecule  
XX by MGB, such that it becomes fluorescent (or its fluorescent properties  
XX change detectably). The conjugates are used as hybridisation probes and  
XX amplification primers for fluorescent detection of specifically  
XX hybridising sequences, for analysis or diagnosis, especially (real-time)  
XX PCR, for single-nucleotide mismatch discrimination, target or signal  
XX amplification, array-based assays and sequencing, including detection of  
XX double-stranded DNA by triplex formation  
XX  
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
XX  
XX Query Match 0.6%; Score 16; DB 1; Length 16;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 2786 AAAAAAAAAAAAAA 2801  
XX 16 AAAAAAAAAAAAAA 1  
XX  
XX  
XX RESULT 2514  
XX AAF30880  
XX ID AAF30880 standard; DNA; 16 BP.  
XX  
XX AAF30880;  
XX  
XX 09-JUL-2001 (first entry)  
XX  
XX Oligonucleotide portion of ODN-MGB-LF conjugate.  
XX  
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
KW hybridisation; detection; fluorescence; probe; ss.  
XX Synthetic.  
XX  
XX WO200131063-A1.  
XX  
PN

XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US029786.  
XX  
XX 26-OCT-1999; 99US-00428236.  
XX  
XX (EPOC-) EPOCH BIOSCIENCES INC.  
XX  
XX Dempcy RO, Afonina IA, Vermeulen NMJ;  
XX WPI; 2001-328656/34.  
XX  
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,  
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide  
XX mismatch discrimination.  
XX  
XX Disclosure; Page 58; 105pp; English.  
XX  
XX The present sequence is that of the oligonucleotide (ODN) component of an  
XX ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the  
XX invention. MGBs bind in a non-intercalating manner to the minor groove of  
XX non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly  
XX but in an intercalating manner, or lies in the minor groove, or is  
XX oriented in some other way to the DNA molecule by MGB, such that it  
XX becomes fluorescent (or its fluorescent properties change detectably).  
XX The conjugates are used as hybridisation probes and amplification primers  
XX for fluorescent detection of specifically hybridising sequences, for  
XX analysis or diagnosis, especially (real-time) PCR, for single-nucleotide  
XX mismatch discrimination, target or signal amplification, array-based  
XX assays and sequencing, including detection of double-stranded DNA by  
XX triplex formation. Many different targets can be detected a single  
XX reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate  
XX hybridisation-triggered fluorescence. Upon hybridisation to the  
XX complementary target sequence there was an increase in fluorescence  
XX yield, measured as the ratio of the fluorescence emitted by the hybrid  
XX between the ODN-MGB-LF conjugate and its target sequence to the  
XX fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,  
XX of 8.3  
XX  
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
XX  
XX Query Match 0.6%; Score 16; DB 1; Length 16;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 2166 TTTT TTTT TTTT TTTT TTTT 2181  
XX 1 TTTT TTTT TTTT TTTT TTTT 16  
XX  
XX  
XX RESULT 2515  
XX AAF30880/c  
XX ID AAF30880 standard; DNA; 16 BP.  
XX  
XX AAF30880;  
XX  
XX 09-JUL-2001 (first entry)  
XX  
XX Oligonucleotide portion of ODN-MGB-LF conjugate.  
XX  
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;  
KW hybridisation; detection; fluorescence; probe; ss.  
XX Synthetic.  
XX  
XX WO200131063-A1.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 2000WO-US029786.  
XX  
XX 26-OCT-1999; 99US-00428236.  
XX  
PR

XX (EPOC-) EPOCH BIOSCIENCES INC.  
PA Dempcy RO, Afonina IA, Vermeulen NMJ;  
XX WPI; 2001-328656/34.  
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,  
PT useful for detecting specific nucleic acids, e.g. for single-nucleotide  
PT mismatch discrimination.  
XX Disclosure; Page 58; 105pp; English.  
PS  
XX The present sequence is that of the oligonucleotide (ODN) component of an  
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the  
CC invention. MGBs bind in a non-intercalating manner to the minor groove of  
CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly  
CC but in an intercalating manner, or lies in the minor groove, or is  
CC oriented in some other way to the DNA molecule by MGB, such that it  
CC becomes fluorescent (or its fluorescent properties change detectably).  
CC The conjugates are used as hybridisation probes and amplification primers  
CC for fluorescent detection of specifically hybridising sequences, for  
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide  
CC mismatch discrimination, target or signal amplification, array-based  
CC assays and sequencing, including detection of double-stranded DNA by  
CC triplex formation. Many different targets can be detected a single  
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate  
CC hybridisation-triggered fluorescence. Upon hybridisation to the  
CC complementary target sequence there was an increase in fluorescence  
CC yield, measured as the ratio of the fluorescence emitted by the hybrid  
CC between the ODN-MGB-LF conjugate and its target sequence to the  
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,  
CC of 8.3  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
DB 16 AAAAAAAAAAAAAA 1  
RESULT 2516  
AAH42481  
ID AAH42481 standard; DNA; 16 BP.  
XX AAH42481;  
XX 01-OCT-2001 (first entry)  
DE Oligonucleotide used to produce branched chain compounds.  
XX Branched chain compound; nucleic acid synthesis; primer extension;  
KW reverse transcription; nucleic acid hybridization;  
KW nucleic acid amplification; ss.  
XX Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /note= "COOH attached"  
FT 2. .3  
FT /\*tag= c  
FT /note= "branch present"  
FT 2  
FT /\*tag= b  
FT /note= "COOH attached"  
PN EP1111068-A1.

XX 27-JUN-2001.  
PD  
XX  
PF 21-DEC-1999; 99EP-00125484.  
XX  
PR 21-DEC-1999; 99EP-00125484.  
XX  
PA (LION-) LION BIOSCIENCE AG.  
PA (VBCG-) VBC GENOMICS GMBH.  
XX  
PI Schmidt W, Hiller R, Huber M, Mueller M;  
XX WPI; 2001-466959/51.  
DR  
XX Branched compounds useful in e.g. nucleic acid synthesis reaction  
PT comprises nucleic acid moieties optionally extended by a polymerase.  
XX  
PS Example 1; Page 10; 31pp; English.  
XX The specification describes branched compounds containing nucleic acid  
CC moieties optionally extended by a polymerase. The branched chain  
CC compounds of the invention are used in nucleic acid synthesis reaction,  
CC primer extension reaction, reverse transcription reaction of RNA into  
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a  
CC nucleic acid), and nucleic acid amplification experiment (for analysing  
CC the expression pattern of genes). The compounds are also used in solid-  
CC phase enzymatic reactions. The present sequence was used in the course of  
CC the invention to produce branched chain compounds  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2181  
DB 1 TTTTTTTTTTTTTTTT 16  
RESULT 2517  
AAH42481/C  
ID AAH42481 standard; DNA; 16 BP.  
XX  
AC AAH42481;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Oligonucleotide used to produce branched chain compounds.  
XX Branched chain compound; nucleic acid synthesis; primer extension;  
KW reverse transcription; nucleic acid hybridization;  
KW nucleic acid amplification; ss.  
XX Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1 /\*tag= a  
FT /note= "COOH attached"  
FT 2. .3  
FT /\*tag= c  
FT /note= "branch present"  
FT 2  
FT /\*tag= b  
FT /note= "COOH attached"  
PN EP1111068-A1.  
XX  
PD 27-JUN-2001.  
XX  
PF 21-DEC-1999; 99EP-00125484.  
XX



PR 21-DEC-1999; 99EP-00125484.  
XX (LION-) LION BIOSCIENCE AG.  
PA (VBCG-) VBC GENOMICS GMBH.  
XX Schmidt W, Hiller R, Huber M, Mueller M;  
PI WPI; 2001-466959/51.  
XX Branched compounds useful in e.g. nucleic acid synthesis reaction  
DR comprises nucleic acid moieties optionally extended by a polymerase.  
XX  
XX Example 1; Page 10; 31pp; English.  
PS The specification describes branched compounds containing nucleic acid  
XX moieties optionally extended by a polymerase. The branched chain  
CC compounds of the invention are used in nucleic acid synthesis reaction,  
CC primer extension reaction, reverse transcription reaction of RNA into  
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a  
CC nucleic acid), and nucleic acid amplification experiment (for analysing  
CC the expression pattern of genes). The compounds are also used in solid-  
CC phase enzymatic reactions. The present sequence was used in the course of  
CC the invention to produce branched chain compounds  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAAAAAA 2801  
DB 16 AAAAAAAAAAAAAAAAAA 1  
  
RESULT 2518  
ABA02556  
ID ABA02556 standard; DNA; 16 BP.  
XX ABA02556;  
AC  
XX 18-JUN-2002 (first entry)  
DT  
XX HCCS-1 differential display primer H-T\_11\_A.  
DE  
XX Human cervical cancer suppressor protein; HCCS-1; tumour suppressor;  
KW apoptosis; cancer; cytostatic; proliferation; differential display; ss;  
KW normal exocervical tissue; primer.  
XX  
XX Homo sapiens.  
OS  
XX WO200181387-A1.  
PN  
XX 01-NOV-2001.  
PD  
XX 04-DEC-2000; 2000WO-KR001406.  
PF  
XX 25-APR-2000; 2000KR-00021897.  
PR  
XX (KIMJ/) KIM J W.  
PA  
XX Kim JW;  
PI  
XX WPI; 2002-075106/10.  
DR  
XX Human tumor suppressor protein and the encoding polynucleotide useful for  
XX treating cancer, and vector comprising the polynucleotide useful for  
PT suppressing proliferation of cancer cells.  
PT  
XX Example 1; Page 34; 37pp; English.  
PS  
XX The present sequence is that of a primer used for the differential  
CC display of a human cervical cancer suppressor 1 (HCCS-1) gene fragment  
CC

CC (see ABA02555 and ABA02558) from normal exocervical tissue. The gene  
CC encodes the HCCS-1 protein (see ABB04180). The specification describes a  
CC tumour suppressor protein, HCCS-1, and the polynucleotide that encodes  
CC it. The invention has cytostatic activity. HCCS-1 acts as a tumour  
CC suppressor by inducing apoptosis of the cancer cell. An expression vector  
CC containing the inventive HCCS-1 gene may be used to suppress the  
CC proliferation of cancer cells by inducing apoptosis. The invention also  
CC provides a pharmaceutical composition for treating or preventing cancer  
CC which comprises the inventive tumour suppressor gene  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTTTTTTTTT 1782  
DB 1 AAGCTTTTTTTTTTTT 16  
  
RESULT 2519  
ABK87148  
ID ABK87148 standard; DNA; 16 BP.  
XX  
XX ABK87148;  
AC  
XX 07-OCT-2002 (first entry)  
DT  
XX Scarlet runner bean anchor/reverse RT-PCR primer G.  
DE  
XX Expression cassette; promoter activity; suspensor cell; plant embryo;  
KW modulation of gene transcription; Scarlet runner bean; RT-PCR;  
KW reverse transcriptase-PCR; primer; transgenic; ss.  
XX  
XX Phaseolus coccineus.  
OS  
XX Synthetic.  
OS  
XX WO200244333-A2.  
PN  
XX 06-JUN-2002.  
PD  
XX 28-NOV-2001; 2001WO-US044737.  
PF  
XX 28-NOV-2000; 2000US-00724857.  
PR  
XX 28-NOV-2000; 2000US-0253672P.  
PR  
XX (REGC ) UNIV CALIFORNIA.  
PA (CERE-) CERES INC.  
PA  
XX Weterings K, Apuya NR, Tatarinova T, Goldberg RB;  
PI  
XX WPI; 2002-508506/54.  
DR  
XX Expression cassette comprises promoters with basal promoter activity  
XX operably linked to a heterologous polynucleotide, useful for expression  
PT genes in suspensor cells in plants and/or basal region of plant embryo.  
PT  
XX Example; Page 54; 114pp; English.  
PS  
XX The present invention relates to expression cassettes comprising a  
CC promoter sequence and a promoter polynucleotide with basal promoter  
CC activity, where the promoter sequence is operably linked to a  
CC heterologous polynucleotide, and when the expression cassette is inserted  
CC into a plant, the heterologous polynucleotide is specifically expressed  
CC in a suspensor cell and/or basal region of a plant embryo. The invention  
CC also provides polynucleotide sequences encoding Scarlet runner bean  
CC (Phaseolus coccineus) G564 and C541 proteins for use in the expression  
CC cassettes of the invention. The expression cassettes comprising promoters  
CC and promoter control elements are useful for modulating transcription of  
CC genes in a plant suspensor cell and/or basal region of a plant embryo.  
CC The present sequence represents an anchor/reverse transcriptase  
CC (RT)-PCR primer used in the examples of the present invention  
CC

```
XX SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTG 1782
Db 1 AAGCTTTTGTG 16

RESULT 2520
AAD34285
ID AAD34285 standard; DNA; 16 BP.
XX AC AAD34285;
XX DT 16-JUL-2002 (first entry)
XX DE Mouse E2 cDNA amplifying PCR primer, H-T11-G.
XX KW Mouse; metabolism; E2 gene; insulin resistance syndrome; dyslipidaemia;
XX KW therapy; non-insulin dependent diabetes mellitus; NIDDM; antilipidaemic;
XX KW obesity; atherosclerosis; antiarteriosclerotic; anorectic; PCR; primer;
XX OS Mus sp.
XX PN WO200218421-A2.
XX PD 07-MAR-2002.
XX PF 23-AUG-2001; 2001WO-GB003807.
XX PR 28-AUG-2000; 2000US-0228118P.
XX PA (ASTR ) ASTRAZENECA AB.
XX PI (ASTR ) ASTRAZENECA UK LTD.
XX PI Brodin P, Thelin A;
XX WPI; 2002-329753/36.
XX New E2 genes and proteins, useful for identifying or manufacturing agents
XX PT for controlling insulin resistance syndrome or related disorders, e.g.
XX PT non-insulin dependent diabetes mellitus, dyslipidemia or atherosclerosis.
XX PS Example 3; Page 19; 52pp; English.
XX CC The invention relates to the regulation of metabolism and in particular
XX CC to a gene named E2 involved in insulin resistance syndrome. E2 gene and
XX CC protein are useful for identifying therapeutic agents for controlling
XX CC insulin resistance syndrome and other related disorders. They are
XX CC particularly useful in manufacturing compositions or pharmaceutical for
XX CC controlling the disorders. Particularly, the chemical compound or
XX CC composition is useful for controlling insulin resistance syndrome and
XX CC other related disorders, e.g. non-insulin dependent diabetes mellitus
XX CC (NIDDM), dyslipidaemia, obesity or atherosclerosis. The present sequence
XX CC is a PCR primer used to amplify mouse E2 cDNA
XX SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTGTG 1782
Db 1 AAGCTTTTGTG 16

RESULT 2521
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```
ABLS7075
ID ABL57075 standard; DNA; 16 BP.
XX AC ABL57075;
XX DT 22-JUL-2002 (first entry)
XX DE Molecular beacon target sequence.
XX KW Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT misc_binding 1..16
FT /*tag= a
FT /bound moiety= "Molecular beacon"
FT /note="forms double-stranded region with bases 5-21 of
FT sequence in ABL57069"
XX PN WO200218951-A2.
XX PD 07-MAR-2002.
XX PF 29-AUG-2001; 2001WO-US041941.
XX PR 29-AUG-2000; 2000US-0228728P.
XX PR 30-MAR-2001; 2001US-0280350P.
XX PA (UYRQ ) UNIV ROCKEFELLER.
XX PI Dubertret B, Calame M, Libchaber A;
XX WPI; 2002-404569/43.
XX Sensitively detecting proximity changes in a system that utilizes an
XX PT interacting fluorophore and quencher, for high sensitivity applications,
XX PT involves utilizing a metal surface as quencher.
XX PS Example 3; Page 30; 62pp; English.
XX CC The present sequence is that of a perfectly matched target sequence for a
XX CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
XX CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
XX CC a nanoparticle. In the native state, the probe forms a hairpin
XX CC conformation with hybridised termini. The proximity of the fluorophore
XX CC and quencher (gold nanoparticle) in the molecular beacon results in
XX CC little or no detectable fluorescence. Upon hybridisation of the central
XX CC complementary stretch of the probe to a target sequence, such as the
XX CC present sequence, the hairpin undergoes a conformational change resulting
XX CC in an increase in fluorescence, the extent of which is proportional to
XX CC the amount of target sequence present. Single mismatches can be detected.
XX CC The invention relates generally to the use of metal surface quenchers
XX CC such as particles or films for high sensitivity applications in, for
XX CC example, detection and diagnostic systems
XX SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2800
Db 1 GAAAAAAAAAAAAA 16

RESULT 2522
ABA97402
ID ABA97402 standard; DNA; 16 BP.
XX AC ABA97402;
XX XX
```

DT 18-JUN-2002 (first entry)  
XX Nucleotide sequence of oligomer # 1 used to test thermal stability.  
DE  
XX Protein nucleic acid molecule; PNA; ds.  
KW  
XX Synthetic.  
OS  
XX WO200168673-A1.  
PN  
XX 20-SEP-2001.  
PD  
XX 13-MAR-2001; 2001WO-US008111.  
PF  
XX 14-MAR-2000; 2000US-0189190P.  
PR  
XX 30-NOV-2000; 2000US-0250334P.  
XX  
PA (ACTI-) ACTIVE MOTIF.  
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;  
PI Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;  
PI  
XX WPI; 2002-041177/05.  
DR  
XX Oligonucleotides analogs useful in detection, separation and purification  
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.  
PT  
XX Example 17; Page 118; 197pp; English.  
PS  
XX This invention relates to oligonucleotide analogues comprising a protein  
CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
CC separation of nucleic acid molecules and as probes, primers, linkers,  
CC adapters and antisense agents on solid supports. Modifications enhance  
CC their use as capture and detection probes e.g. by the incorporation of  
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
CC fluorescein and reporter molecules such as alkaline phosphatase. They are  
CC also used for enhancing or inhibiting the activity of an enzyme or  
CC cellular activity. The compounds are stable to nucleases and proteases,  
CC have high affinity, binding specificity and solubility. The polyamide  
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind  
CC nucleic acid molecules with greater affinity than DNA or RNA  
CC concentration. The compounds are relatively simple to synthesize and are  
CC used in a wide variety of applications. This sequence represents a DNA  
CC oligomer which is used to represent the thermal stability of the  
CC oligomers of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTTTT 2181  
Db 1 TTTTTTTTTTTTTTTT 16  
RESULT 2523  
ABA97402/C  
ID ABA97402 standard; DNA; 16 BP.  
XX  
AC ABA97402;  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX Nucleotide sequence of oligomer # 1 used to test thermal stability.  
DE  
XX Protein nucleic acid molecule; PNA; ds.  
KW  
XX Synthetic.  
OS  
XX WO200168673-A1.  
PN  
XX

PD 20-SEP-2001.  
XX  
PF 13-MAR-2001; 2001WO-US008111.  
XX  
PR 14-MAR-2000; 2000US-0189190P.  
PR 30-NOV-2000; 2000US-0250334P.  
XX  
PA (ACTI-) ACTIVE MOTIF.  
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;  
PI Chakhmakhcheau O, Buryakova A, Choob M, Hondorp K;  
PI  
XX WPI; 2002-041177/05.  
DR  
XX Oligonucleotides analogs useful in detection, separation and purification  
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.  
PT  
XX Example 17; Page 118; 197pp; English.  
PS  
XX This invention relates to oligonucleotide analogues comprising a protein  
CC nucleic acid molecule (PNA) monomer. They are used in the detection and  
CC separation of nucleic acid molecules and as probes, primers, linkers,  
CC adapters and antisense agents on solid supports. Modifications enhance  
CC their use as capture and detection probes e.g. by the incorporation of  
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as  
CC fluorescein and reporter molecules such as alkaline phosphatase. They are  
CC also used for enhancing or inhibiting the activity of an enzyme or  
CC cellular activity. The compounds are stable to nucleases and proteases,  
CC have high affinity, binding specificity and solubility. The polyamide  
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind  
CC nucleic acid molecules with greater affinity than DNA or RNA  
CC concentration. The compounds are relatively simple to synthesize and are  
CC used in a wide variety of applications. This sequence represents a DNA  
CC oligomer which is used to represent the thermal stability of the  
CC oligomers of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAAAA 1  
RESULT 2524  
ABK90584  
ID ABK90584 standard; DNA; 16 BP.  
XX  
AC ABK90584;  
XX  
XX 15-NOV-2002 (first entry)  
DT  
XX Target cDNA PCR primer #2.  
DE  
XX Cancer; somatic cell; embryonic cell; cancer; pre-implantation embryo;  
KW germ cell; embryonal carcinoma cell; embryonic stem cell; oocyte; ss;  
KW PCR; primer.  
XX  
OS Unidentified.  
XX WO200264828-A1.  
PN  
XX 22-AUG-2002.  
PD  
XX 09-FEB-2001; 2001WO-GB000538.  
PF  
XX 09-FEB-2001; 2001WO-GB000538.  
PR  
XX (UNLO ) UNIV COLLEGE LONDON.  
PA  
XX

PI Monk M;  
XX WPI; 2002-643493/59.  
DR  
XX  
PT New targets expressed in embryonic cell but not in non-diseased somatic  
PT cell, useful in medicine for diagnosis and/or therapy, and for  
PT identifying an agent capable of inhibiting the action of the target.  
XX  
PS  
XX Example 1; Page 54; 77pp; English.  
CC The invention relates to a new target for use in medicine which is  
CC expressed and/or present at a high level in an embryonic cell, is not  
CC expressed or is expressed and/or present at low level in a non-diseased  
CC somatic cell and is not expressed in or is expressed and/or present at a  
CC low level in a diseased somatic cell. The target is useful in the  
CC preparation of a medicament for treating a disease, particularly cancer.  
CC The human embryonic cells (oocytes, pre-implantation embryos, germ cells,  
CC embryonal carcinoma cells and/or embryonic stem cells) are useful in  
CC identifying targets re-expressed in cancer cells for preventing, treating  
CC or curing cancer. The target may be used in medicine for diagnosis and/or  
CC therapy, and to identify an agent capable of inhibiting the action of the  
CC target. This sequence represents a PCR primer used to amplify target cDNA  
CC of the invention  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1767 AAGCTTTT TTTT TTTG 1782  
|||||  
Db 1 AAGCTTTT TTTT TTTG 16  
  
RESULT 2525  
AAD32157  
ID AAD32157 standard; DNA; 16 BP.  
XX  
AC AAD32157;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE H-T11-G PCR primer, to determine ADAMTS-1 role in IRS and obesity.  
XX  
KW A disintegrin and metalloproteinase with thrombospondin type 1 motif;  
KW ADAMTS-1; non-insulin dependent diabetes mellitus; ADAM; obesity; IRS;  
KW insulin resistance syndrome; NIDDM; atherosclerosis; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
XX WO200216632-A1.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 16-AUG-2001; 2001WO-GB003650.  
PF  
XX  
XX 22-AUG-2000; 2000SE-00002973.  
PR  
XX  
XX (ASTR ) ASTRAZENECA AB.  
PA  
XX (ASTR ) ASTRAZENECA UK LTD.  
PA  
XX  
XX Brodin P, Thelin A;  
PI  
XX WPI; 2002-269365/31.  
DR  
XX  
XX Use of a modulator of ADAMTS-1 ( a disintegrin and metalloproteinase) for  
PT the treatment of obesity, insulin resistance syndrome (IRS), non-insulin  
PT dependent diabetes mellitus (NIDDM) or atherosclerosis.  
XX  
XX Example 1; Page 39; 47pp; English.  
PS  
XX The invention relates to the use of modulators of A Disintegrin And

CC Metalloproteinase (ADAM) with Thrombospondin type 1 motif (ADAMTS-1)  
CC which are used in the preparation of a medicament for the treatment of  
CC obesity, insulin resistance syndrome (IRS), non-insulin dependent  
CC diabetes mellitus (NIDDM) and atherosclerosis. The invention also relates  
CC to methods for screening specific modulators of ADAMTS-1 activity. The  
CC present sequence is a PCR primer used to determine the role of ADAMTS-1  
CC in IRS, obesity, NIDDM and atherosclerosis  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1767 AAGCTTTT TTTT TTTG 1782  
|||||  
Db 1 AAGCTTTT TTTT TTTG 16  
  
RESULT 2526  
ABK12623  
ID ABK12623 standard; DNA; 16 BP.  
XX  
AC ABK12623;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Mouse E4 protein, PCR primer H-T11-G.  
XX  
KW Mouse; E4; insulin resistance syndrome; NIDDM; dyslipidaemia; obesity;  
KW non-insulin dependent diabetes mellitus; atherosclerosis; primer; ss.  
XX  
OS Mus sp.  
OS Synthetic.  
XX  
XX WO200218568-A2.  
PN  
XX 07-MAR-2002.  
PD  
XX  
XX 23-AUG-2001; 2001WO-GB003828.  
PF  
XX  
XX 28-AUG-2000; 2000US-0228117P.  
PR  
XX 10-APR-2001; 2001US-0282496P.  
PR  
XX (ASTR ) ASTRAZENECA AB.  
PA (ASTR ) ASTRAZENECA UK LTD.  
PA  
XX Brodin P, Thelin A;  
PI  
XX WPI; 2002-304254/34.  
DR  
XX  
XX New isolated polynucleotide encoding E4 gene involved in insulin  
PT resistance syndrome, useful for identifying chemical compound useful for  
PT controlling e.g. non-insulin dependent diabetes mellitus.  
XX  
XX Example 3; Page 19; 46pp; English.  
PS  
XX  
XX The invention relates to an isolated polynucleotide (I) molecule  
CC comprising a nucleotide sequence which encodes an E4 polypeptide (II) or  
CC its fragment of at least 10 amino acids. (II) is useful for identifying a  
CC chemical compound capable of modulating the activity of E4 by contacting  
CC the chemical compound with (II) or a transgenic non-human mammal and  
CC measuring any effect of chemical compound on the activity of (II) or  
CC transgenic non-human mammal, where the identifying method is useful for  
CC making a pharmaceutical composition, which comprises mixing the compound  
CC thus identified with a carrier, and the compound is preferably an  
CC antibody that is useful for controlling insulin resistance syndrome and  
CC other related disorders such as non-insulin dependent diabetes mellitus  
CC (NIDDM), dyslipidaemia, obesity, and atherosclerosis. The present  
CC sequence represents a PCR primer used to isolate the coding sequence of  
CC mouse E4 protein  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;



Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTG 1782  
Db 1 AAGCTTTTCTTTTCTTTG 16

RESULT 2527  
AAD30090  
ID AAD30090 standard; DNA; 16 BP.  
AC AAD30090;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE PTTG cDNA isolating anchored PCR primer #1.  
XX  
KW Pituitary tumour transforming gene; PTTG1; vulnery; cytostatic;  
KW ophthalmological; antiangiogenic; antisense gene therapy; angiogenesis;  
KW wound healing; tissue regeneration; scar formation; malignant tumour;  
KW retinopathy; PCR primer; ss.  
XX  
OS Unidentified.  
XX  
PN WO200187935-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 12-MAY-2001; 2001WO-US015437.  
XX  
PR 12-MAY-2000; 2000US-00569956.  
PR 13-OCT-2000; 2000US-00687911.  
PR 04-DEC-2000; 2000US-00730469.  
PR 05-FEB-2001; 2001US-00777422.  
PR 11-MAY-2001; 2001US-00854326.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Heaney AP, Ishikawa H, Yu R, Horwitz GA, Zhang X, Melmed S;  
XX WPI; 2002-188148/24.  
XX  
PT Modulating angiogenesis in a tissue comprising mammalian cells by  
PT modulating pituitary tumor transforming gene (PTTG1) expression and/or  
PT endogenous PTTG1 protein function.  
XX  
PS Example 1; Page 63; 183pp; English.  
XX  
CC The invention relates to a method of modulating angiogenesis in a tissue  
CC comprising mammalian cells by modulating pituitary tumour transforming  
CC gene (PTTG) expression and/or endogenous PTTG1 protein function in at  
CC least one of the cells. The method is useful for enhancing or inhibiting  
CC angiogenesis. Specifically, enhancing wound healing and/or tissue  
CC regeneration and limiting scar formation. The method is also useful in  
CC treating malignant tumours and retinopathy. The present sequence is a PCR  
CC primer used for isolating PTTG1 cDNA  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTG 1782  
Db 1 AAGCTTTTCTTTTCTTTG 16

RESULT 2528  
AAD30914

ID AAD30914 standard; DNA; 16 BP.  
XX  
AC AAD30914;  
XX  
DT 31-MAY-2002 (first entry)  
XX  
DE Rat PTTG1 cDNA amplifying PCR primer #1.  
XX  
KW Rat; pituitary tumour transforming gene 1; cellular transformation;  
KW PTTG1; inhibition; immunogen; neoplastic cellular proliferation;  
KW T-lymphocyte; PCR primer; ss.  
XX  
OS Rattus rattus.  
XX  
PN WO200187934-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 12-MAY-2001; 2001WO-US015254.  
XX  
PR 12-MAY-2000; 2000US-00569956.  
PR 13-OCT-2000; 2000US-00687911.  
PR 04-DEC-2000; 2000US-00730469.  
PR 05-FEB-2001; 2001US-00777422.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Horwitz GA, Zhang X, Heaney AP, Melmed S;  
XX WPI; 2002-226703/28.  
XX  
PT Inhibiting neoplastic cellular proliferation and/or transformation of a  
PT mammalian cell, by using Pituitary tumor transforming gene carboxy-  
PT terminal peptides.  
XX  
PS Example 1; Page 65; 190pp; English.  
XX  
CC The patent discloses pituitary tumour transforming gene (PTTG) carboxy  
CC terminal peptides. The invention also relates to methods for inhibiting  
CC neoplastic cellular proliferation and transformation (NP/T) of mammalian  
CC cells. The method involves delivering a composition comprising a PTTG  
CC carboxy-terminal-related polynucleotide, an expression vector comprising  
CC a polynucleotide encoding PTTG C-terminal (PTTG-C) peptide, PTTG-C  
CC peptide to a mammalian cell that overexpresses PTTG. The compositions  
CC comprising PTTG-C peptides are useful for inhibiting neoplastic cellular  
CC proliferation and/or transformation of a mammalian cell. PTTG-C peptides  
CC are useful in bioassays, as immunogens to produce anti-PTTG-C antibodies  
CC and in therapeutic compositions. PTTG antibodies are also useful for  
CC inhibiting the activation of mammalian T-lymphocytes. Sequences of the  
CC invention are used as vaccines and in gene therapy. The present sequence  
CC is a PCR primer which is used for amplifying rat PTTG1 cDNA  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTCTTTG 1782  
Db 1 AAGCTTTTCTTTTCTTTG 16

RESULT 2529  
ABZ21814  
ID ABZ21814 standard; DNA; 16 BP.

XX ABZ21814;  
AC  
XX DT 03-MAR-2003 (first entry)

XX Anti-cancer drug resistance related oligonucleotide #1.

KW Anti-cancer; drug resistance; lung cancer; head and neck cancer; ss.  
XX Synthetic.  
OS  
PN KR2002031530-A.  
XX  
PD 02-MAY-2002.  
XX  
XX 20-OCT-2000; 2000KR-00062030.  
PF  
XX 20-OCT-2000; 2000KR-00062030.  
PR  
XX (PHAR-) PHARMGENIA CO LTD.  
PA  
XX Jun SH;  
PI  
XX WPI; 2002-737801/80.  
DR  
XX DNA sequences relating to anti-cancer drug resistance and the use  
PT thereof.  
PT  
XX  
XX Disclosure; Page 4; 34pp; Korean.  
PS  
XX The present invention describes DNA sequences relating to anti-cancer  
CC drug resistance. The DNA sequences can be used as a component of a kit or  
CC a DNA chip for detecting the presence of anti-cancer resistance. The  
CC method for identifying and sequencing the DNA sequences comprises  
CC obtaining an anti-cancer sensitive cancer tissue and an anti-cancer drug  
CC resistant cancer tissue from patients suffering from lung cancer and head  
CC and neck cancer, isolating mRNAs from the tissues, preparing cDNAs of the  
CC tissues from mRNAs using reverse transcriptase; finding genes showing the  
CC increase or decrease of gene expression in the cancer tissues before and  
CC after the anti-cancer drug treatment using differential display of  
CC polymerase chain reaction (PCR), subjecting the genes to electrophoresis,  
CC amplifying the cDNAs by using PCR, sub-cloning the amplified cDNAs into  
CC pGEM-Teasy plasmid, and sequencing the cDNA using an auto-sequencing  
CC machine. The present sequence represents an oligonucleotide which is used  
CC in the exemplification of the present invention  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTTTTTTTTTG 1782  
Db 1 AAGCTTTTTTTTTTTTG 16  
  
RESULT 2530  
ABN87395  
ID ABN87395 standard; DNA; 16 BP.  
XX  
AC ABN87395;  
XX  
DT 05-AUG-2002 (first entry)  
XX  
XX PTTG isolation related anchor primer SEQ ID NO:11.  
DE  
XX Pituitary tumour-specific gene; PTTG1; PTTG2; transformation;  
KW pituitary tumour transforming gene; malignant tumour; cytostatic;  
KW neoplastic cellular proliferation inhibition; primer; ss.  
XX Synthetic.  
OS  
XX WO200187039-A2.  
PN  
XX 22-NOV-2001.  
PD  
XX  
XX 12-MAY-2001; 2001WO-US015255.  
PF  
XX  
XX 12-MAY-2000; 2000US-00569956.  
PR

PR 13-OCT-2000; 2000US-00687911.  
PR 04-DEC-2000; 2000US-00730469.  
PR 05-FEB-2001; 2001US-00777422.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
XX Prezant TR, Heaney AP, Melmed S;  
PI  
XX WPI; 2002-195496/25.  
DR  
XX Novel method of inhibiting neoplastic cellular proliferation and/or  
PT transformation of a mammalian cell used for treating e.g. malignant  
PT tumours.  
XX  
XX Example 1; Page 61; 175pp; English.  
PS  
XX The present invention describes a method for inhibiting neoplastic  
CC cellular proliferation and/or transformation of a mammalian cell. The  
CC method comprises delivering to a mammalian cell that endogenously over  
CC expresses pituitary tumour transforming gene (PTTG1), a composition  
CC comprising, an expression vector comprising a promoter and a  
CC polynucleotide, where the polynucleotide comprises a first DNA segment  
CC encoding a mammalian PTTG2 peptide the polynucleotide being operatively  
CC linked to the promoter in a transcriptional unit, where PTTG2 is selected  
CC from: (a) a peptide (I) consisting essentially of a 191 amino acid  
CC sequence (see ABB79058) or a functional fragment comprising at least  
CC amino acid residues 1-180; or (b) a mammalian PTTG2 peptide having at  
CC least 95% sequence homology with (I). The expression vector is complexed  
CC with a cellular uptake-enhancing agent such that the PTTG2 peptide is  
CC expressed in the cell where neoplastic cellular proliferation and/or  
CC transformation of the cell is inhibited. PTTG2 protein regulates  
CC transactivating activity by PTTG1 and that PTTG2 peptide molecules have  
CC the ability to down regulate PTTG1 gene expression and/or PTTG1 protein  
CC function in a negative manner. The method is useful in inhibiting  
CC neoplastic cellular proliferation and/or transformation of mammalian  
CC cells both in vivo and in vitro. The method is also useful in treating  
CC malignant tumours. The present sequence represents an anchor primer used  
CC in the isolation of PTTG cDNA, which is used in an example from the  
CC present invention  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1767 AAGCTTTTTTTTTTTTG 1782  
Db 1 AAGCTTTTTTTTTTTTG 16  
  
RESULT 2531  
ABA98029  
ID ABA98029 standard; cDNA; 16 BP.  
XX  
AC ABA98029;  
XX  
XX 03-MAY-2002 (first entry)  
DT  
XX Human PTTG2 cDNA coding sequence SEQ ID NO 63.  
DE  
XX Human; mouse; rat; gene; cytostatic; immunosuppressive; antiasthmatic;  
KW dermatological; antirheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antipsoriatic; antiatherosclerotic; antiallergic;  
KW T-lymphocyte cell; pituitary tumour transforming gene; PTTG; bFGF;  
KW transcription; cell proliferation; lymphocyte; graft rejection; allergic;  
KW asthmatic; autoimmune disease; rheumatoid arthritis; leukaemia; cancer;  
KW tumour; Hodgkin's disease; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200188116-A2.  
PN  
XX

Thu Jun 10 13:10:09 2004

PD 22-NOV-2001.  
XX  
PF 12-MAY-2001; 2001WO-US015438.  
XX  
PR 12-MAY-2000; 2000US-00569956.  
PR 13-OCT-2000; 2000US-00687911.  
PR 04-DEC-2000; 2000US-00730469.  
PR 05-FEB-2001; 2001US-00777422.  
PR 11-MAY-2001; 2001US-00854326.  
XX  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
XX  
PI Stoika R, Horwitz GA, Zhang X, Melmed S;  
XX  
DR WPI; 2002-188151/24.  
DR P-PSDB; ABB08709.  
XX  
PT Inhibiting the activation of a mammalian T-lymphocyte cell useful for  
PT treating immune-related disorders by inhibiting PTTG1 gene expression.  
XX  
PS Example 21; Page 182; 185pp; English.  
XX  
CC The invention relates to inhibiting the activation of a mammalian T-  
CC lymphocyte cell comprising inhibiting pituitary tumour transforming gene  
CC (PTTG1) expression and/or endogenous PTTG1 protein function in the T-  
CC lymphocyte cell, whereby activation of the T-lymphocyte cell is  
CC inhibited. PTTG upregulates bFGF secretion and transactivates DNA  
CC transcription. Compositions and methods of the invention are useful for  
CC inhibiting neoplastic and non-neoplastic proliferation of mammalian T-  
CC lymphocyte cells, including activated normal lymphocytes and transformed  
CC lymphocytes. The compositions and methods are useful in the prevention or  
CC inhibition of xenograft or allograft rejection and in the treatment of  
CC allergic, asthmatic and/or autoimmune conditions such as systemic lupus  
CC erythematosus (SLE), autoimmune myasthenia gravis, rheumatoid arthritis,  
CC autoimmune encephalomyelitis, psoriasis, atherosclerosis and other  
CC autoimmune diseases. The inventive methods and compositions are also  
CC useful in the treatment of T-cell neoplasias, such as leukaemia, or any  
CC haematologic or lymphopoeietic neoplasm e.g. Hodgkin's disease. The  
CC present sequence is that of a PTTG encoding polynucleotide sequence  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1767 AAGCTTTT TTTT TTTG 1782  
Db 1 AAGCTTTT TTTT TTTG 16  
RESULT 2532  
ACC58340  
ID ACC58340 standard; DNA; 16 BP.  
XX  
AC ACC58340;  
XX  
DT 26-AUG-2003 (first entry)  
XX  
DE MMLV-RT PCR; primer H-T11G.  
XX  
KW MMLV; reverse transcriptase; enzyme; LIM mineralization protein; LMP;  
KW osteopathic; cytokine; gene therapy; PCR; primer; ss.  
XX  
OS Moloney murine leukemia virus.  
XX  
PN WO2003042368-A2.  
XX  
PD 22-MAY-2003.  
XX  
PF 14-NOV-2002; 2002WO-US036465.  
XX  
PR 14-NOV-2001; 2001US-0331321P.

PR 13-NOV-2002; 2002US-00331321.  
XX  
PA (MEDT ) MEDTRONIC SOPAMOR DANEK INC.  
XX  
PI Mckay WF, Boden SD, Yoon ST;  
XX  
DR WPI; 2003-505113/47.  
XX  
PT Expressing LIM mineralization protein in non-osseous mammalian cell for  
PT treating intervertebral disc injury, by transfecting cell with nucleic  
PT acid encoding LIM mineralization protein operably linked to promoter.  
XX  
PS Example 9; Page 74; 94pp; English.  
XX  
CC The present sequence is that of H-T11G, an MMLV-RT primer that was used  
CC in differential display PCR of RNA extracted from glucocorticoid-  
CC stimulated rat osteoblasts. cDNA (see ACC58339) encoding rat LIM  
CC mineralization protein (RLMP), a cytokine involved in mineralization of  
CC the bone matrix and in the differentiation of cells into the osteoblast  
CC lineage was subsequently isolated. The invention provides methods of  
CC expressing LIM mineralization protein in non-osseous mammalian cells,  
CC such as stem cells or intervertebral disc cells. The methods involved  
CC transfecting the cells with a nucleic acid encoding LIM mineralization  
CC protein operably linked to a promoter. Expression of the LIM  
CC mineralization protein can stimulate proteoglycan and/or collagen  
CC production for treatment of disc disease associated with trauma or disc  
CC degeneration, e.g. for enhancement of bone repair in fractures and bone  
CC defects, in bone grafting, and in the treatment of osteoporosis  
XX  
SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1767 AAGCTTTT TTTT TTTG 1782  
Db 1 AAGCTTTT TTTT TTTG 16  
RESULT 2533  
ABX16054  
ID ABX16054 standard; DNA; 16 BP.  
XX  
AC ABX16054;  
XX  
DT 02-APR-2003 (first entry)  
XX  
DE RNA differential display 3' anchor primer.  
XX  
KW PCR; primer; ss; SPAF; spermatogenesis associated factor; cytostatic;  
KW AAA-protein; ATPase associated with diverse cellular activities;  
KW squamous cell carcinoma; cancer; infertility; fertility; contraception;  
KW spermatogonia; primary spermatocyte; early pachytene stage;  
KW chemotherapeutic agent; tumour; carcinogenesis; differentiation; RT-PCR;  
KW reverse transcriptase PCR; RNA differential display.  
XX  
OS Synthetic.  
XX  
PN US2002143169-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 08-MAY-2001; 2001US-00850697.  
XX  
PR 27-SEP-1997; 97US-00938308.  
PR 06-FEB-2001; 2001US-00777753.  
XX  
PA (KULE/) KULESZ-MARTIN M F.  
XX (LIUY/) LIU Y.  
PI Kulesz-Martin MF, Liu Y;  
XX

DR WPI; 2003-174143/17.

XX New spermatogenesis associated factor DNA, useful in diagnosing cancer,

PT in designing selective cancer therapy by targeting this gene product, and

PT in basic research on carcinogenesis and differentiation.

XX Example; Page 3; 42pp; English.

PS

XX The invention relates to a purified spermatogenesis associated factor

CC (SPAF, an AAA-protein family member (ATPase associated with diverse

CC cellular activities)) DNA molecule designated SPAF DNA, which is a gene

CC that is altered and overexpressed in poorly differentiated squamous cell

CC carcinoma as compared with normal parental epidermal cells. The gene is

CC naturally expressed in testes, and expresses a spermatogenesis associated

CC protein by translation of the SPAF DNA molecule. The protein is an SPAF

CC spermatoocyte up to early pachytene stage. Also included are a SPAF cDNA

CC molecule having a DNA sequence which is complementary DNA sequence to the

CC novel SPAF DNA, an anti-SPAF antibody, diagnosing cancer (comprising: (a)

CC contacting a cell with a specific probe comprising SPAF cDNA and

CC detecting a reaction; or (b) contacting a cancer cell with an anti-SPAF

CC antibody, and detecting reaction to the antibody), isolating the SPAF

CC gene by contacting the gene with SPAF cDNA or with anti-SPAF antibody,

CC diagnosing infertility by contacting a testes generated cellular material

CC with an anti-SPAF antibody, a chemotherapeutic agent comprising an

CC antibody to SPAF protein conjugated with a tumour binding inhibiting

CC material and a vector containing a testes specific nucleic acid

CC comprising at least a portion of the novel SPAF DNA. SPAF is useful in

CC diagnosing cancer, in designing selective cancer therapy by targeting

CC this gene product, and in basic research on carcinogenesis and

CC differentiation. The SPAF protein, peptide, mRNA and cDNA may be used in

CC designing drugs for treatment and prevention of abnormal development and

CC tumours, and for fertility and/or infertility/contraception. The present

CC sequence is a reverse transcriptase (RT)-PCR primer used in an RNA

CC differential display experiment for mouse SPAF mRNA

XX

SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782

Db 1 AAGCTTTT TTTT TTTG 16

RESULT 2534

ABZ58394

ID ABZ58394 standard; DNA; 16 BP.

XX

AC ABZ58394;

XX

XX 28-APR-2003 (first entry)

DT

XX H-T11G anchored oligo-dT primer.

DE

XX Human cervical cancer 2; HCC-2; human; cervix cancer; oncogene;

KW diagnosis; cytostatic; gene therapy; PCR; primer; ss.

KW

XX Synthetic.

OS

XX WO2003002744-A1.

PN

XX

XX 09-JAN-2003.

PD

XX 27-JUN-2002; 2002WO-KR001227.

PF

XX 28-JUN-2001; 2001KR-00037589.

PR

XX (KIMJ/) KIM J.

PA

XX Kim J;

PI

XX WPI; 2003-210277/20.

DR

XX Human cervical cancer 2 proto-oncogene for diagnosing cancer.

PT

XX Example 2; Page 24; 26pp; English.

PS

XX The present sequence is that of H-T11G-anchored oligo-dT primer, which

CC was used in an example from the invention in the RT-PCR amplification of

CC RNA obtained from healthy cervical, primary cervical cancer and

CC metastatic common iliac lymph node tissues, and from a human cervical

CC cancer cell line. A partial clone (CG401) was obtained, which was used to

CC identify a full-length cDNA (see ABZ58393) for novel human cervical

CC cancer 2 (HCC-2) proto-oncogene. Differential display RT-PCR using the

CC oligo-dT primer showed that CG401 was expressed in cervical cancer

CC tissue, metastatic lymph node tissues and CUMC-6 cells, but not in normal

CC tissues. HCC-2 proto-oncogene can be used in the diagnosis of various

CC cancers, in the production of transgenic animals useful for drug

CC screening, in the production of HCC-2 protein, and in the construction of

CC an antisense gene (claimed) useful in antisense gene therapy

XX

SQ Sequence 16 BP; 2 A; 1 C; 2 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782

Db 1 AAGCTTTT TTTT TTTG 16

RESULT 2535

AAD56451

ID AAD56451 standard; DNA; 16 BP.

XX

AC AAD56451;

XX

XX 07-AUG-2003 (first entry)

DT

XX 2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.

DE

XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;

KW antisense; ss.

KW

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

FT modified\_base 1..16

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "2'-deoxy-2'-fluoroarabinothymidine"

FT misc\_feature 8..9

FT /\*tag= b

FT /note= "Bases 8 and 9 are linked by two secouridine

FT linkers which is represented as S in page 49 and X in

FT page 57 and Fig 7 and 8 of the specification"

XX

PN WO2003037909-A1.

XX

XX 08-MAY-2003.

PD

XX 29-OCT-2002; 2002WO-CA001628.

PF

XX 29-OCT-2001; 2001US-0330719P.

PR

XX (UYMC-) UNIV MCGILL.

PA

XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

PI WPI; 2003-421516/39.

XX

XX Novel acyclic linker-containing oligonucleotide useful for preventing or

PT



PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.  
XX  
XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16  
RESULT 2536  
AAD56451/c  
ID AAD56451 standard; DNA; 16 BP.  
XX  
AC AAD56451;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE 2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.  
XX  
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;  
KW antisense; ss.  
KW  
XX  
OS Unidentified.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 1..16  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"  
FT 8..9  
FT /\*tag= b  
FT /note= "Bases 8 and 9 are linked by two secouridine  
FT linkers which is represented as S in page 49 and X in  
FT page 57 and Fig 7 and 8 of the specification"  
XX  
PN WO2003037909-A1.  
XX  
XX 08-MAY-2003.  
PD  
XX  
PF 29-OCT-2002; 2002WO-CA001628.  
XX  
XX 29-OCT-2001; 2001US-0330719P.  
PR  
XX (UYMC-) UNIV MCGILL.  
XX  
XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;  
PI  
XX WPI; 2003-421516/39.  
XX  
XX Novel acyclic linker-containing oligonucleotide useful for preventing or  
PT decreasing translation, reverse transcription and/or replication of a  
PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX  
PS Example 2; Fig 7; 104pp; English.  
XX  
XX The invention relates to an acyclic linker-containing oligonucleotide  
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of  
CC the invention are useful for preventing or decreasing translation,  
CC reverse transcription and/or replication of a target RNA in a system.  
CC They are useful for selectively preventing gene expression in a sequence-  
CC specific manner, for hybridising to complementary RNA such as cellular  
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary  
CC RNA. They are also useful therapeutically in formulations or medicaments  
CC to prevent or treat a disease characterised by the expression of a  
CC particular target RNA. The invention is used in gene therapy. The present  
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)  
CC H degradation of target RNA. This sequence is used in the exemplification  
CC of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2801  
Db 16 AAAAAA AAAAAA AAAAAA 1  
RESULT 2537  
AAL54078  
ID AAL54078 standard; DNA; 16 BP.  
XX  
AC AAL54078;  
XX  
DT 06-MAR-2003 (first entry)  
XX  
DE Oligo-homodeoxyribonucleotide sequence, oligo dT.  
XX  
KW Detection; single-stranded sensor; detectable fluorescence emission;  
KW forensic testing; paternity testing; tissue typing; hereditary disorder;  
KW human population genetics; human evolutionary history; cystic fibrosis;  
KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.  
XX  
OS Unidentified.  
XX  
PN WO200284271-A2.  
XX  
XX PD 24-OCT-2002.  
XX  
XX PF 16-APR-2002; 2002WO-US012176.  
XX  
XX PR 16-APR-2001; 2001US-00836579.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA (CHAJ/) CHA J N.  
PA  
XX  
PI Cha JN, Morse DE, Stucky GD;  
XX  
XX WPI; 2003-103378/09.  
DR  
XX  
XX Detecting polynucleotides, for pharmacogenetic testing, comprises  
PT contacting a target polynucleotide with a complementary single-stranded  
PT sensor polynucleotide and an agent that allows the sensor to fluoresce  
PT upon excitation.  
XX  
XX Example 1; Page 25; 41pp; English.  
XX  
XX The invention relates to a novel assay for detecting a polynucleotide in  
CC a sample, which comprises: contacting a sample suspected of containing a  
CC target polynucleotide with a predetermined single-stranded sensor  
CC polynucleotide complementary to the target polynucleotide, in a solution  
CC comprising an agent that is a nonaqueous solvent that allows the sensor  
CC polynucleotide to produce a detectable fluorescence emission; exciting

CC the sensor polynucleotide; and determining fluorescence emission. The  
CC assay is useful for detecting a single or double-stranded target  
CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a  
CC wide variety of different applications including pharmacogenetic testing,  
CC forensic testing to identify the species or individual which was the  
CC source of a forensic specimen, in anthropological setting, paternity  
CC testing, testing for compatibility between prospective tissue or blood  
CC donors and patients and in screening for hereditary disorders. The method  
CC is also useful to study alterations of gene expression in response to a  
CC stimulus, disease, drug or medication, and other applications include  
CC human population genetics, analyses of human evolutionary history and  
CC characterisation of human haplotype diversity. The method is useful for  
CC detecting polynucleotide sequences from contaminants or pathogens  
CC including bacteria, yeast, and viruses to detect single nucleotide  
CC polymorphisms, which may be associated with particular alleles or subsets  
CC of alleles. The method is useful for detection of mutations and to detect  
CC nucleotide sequences associated with increased risk of diseases or  
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.  
CC This polynucleotide sequence represents an oligonucleotide sequence used  
CC in a fluorescence technique of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2538  
AAL54078/c  
ID AAL54078 standard; DNA; 16 BP.  
XX  
AC AAL54078;  
XX  
DT 06-MAR-2003 (first entry)  
XX  
DE Oligo-homodeoxyribonucleotide sequence, oligo dt.

Detection; single-stranded sensor; detectable fluorescence emission;  
forensic testing; paternity testing; tissue typing; hereditary disorder;  
human population genetics; human evolutionary history; cystic fibrosis;  
human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.

Unidentified.  
WO200284271-A2.  
24-OCT-2002.  
16-APR-2002; 2002WO-US012176.  
16-APR-2001; 2001US-00836579.  
(REGC ) UNIV CALIFORNIA.  
(CHAJ/) CHA J N.

Cha JN, Morse DE, Stucky GD;  
WPI; 2003-103378/09.

Detecting polynucleotides, for pharmacogenetic testing, comprises  
contacting a target polynucleotide with a complementary single-stranded  
sensor polynucleotide and an agent that allows the sensor to fluoresce  
upon excitation.

Example 1; Page 25; 41pp; English.  
The invention relates to a novel assay for detecting a polynucleotide in  
a sample, which comprises: contacting a sample suspected of containing a

CC target polynucleotide with a predetermined single-stranded sensor  
CC polynucleotide complementary to the target polynucleotide, in a solution  
CC comprising an agent that is a nonaqueous solvent that allows the sensor  
CC polynucleotide to produce a detectable fluorescence emission; exciting  
CC the sensor polynucleotide; and determining fluorescence emission. The  
CC assay is useful for detecting a single or double-stranded target  
CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a  
CC wide variety of different applications including pharmacogenetic testing,  
CC forensic testing to identify the species or individual which was the  
CC source of a forensic specimen, in anthropological setting, paternity  
CC testing, testing for compatibility between prospective tissue or blood  
CC donors and patients and in screening for hereditary disorders. The method  
CC is also useful to study alterations of gene expression in response to a  
CC stimulus, disease, drug or medication, and other applications include  
CC human population genetics, analyses of human evolutionary history and  
CC characterisation of human haplotype diversity. The method is useful for  
CC detecting polynucleotide sequences from contaminants or pathogens  
CC including bacteria, yeast, and viruses to detect single nucleotide  
CC polymorphisms, which may be associated with particular alleles or subsets  
CC of alleles. The method is useful for detection of mutations and to detect  
CC nucleotide sequences associated with increased risk of diseases or  
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.  
CC This polynucleotide sequence represents an oligonucleotide sequence used  
CC in a fluorescence technique of the invention  
XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA AAAAAA AAAAAA 2801  
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 2539  
AAD57845  
ID AAD57845 standard; DNA; 16 BP.  
XX  
AC AAD57845;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Target oligonucleotide #2 used in nonlinear optical technique.

Nonlinear optical technique; screening; ss.  
Unidentified.  
WO2003064991-A2.  
07-AUG-2003.  
17-JUL-2002; 2002WO-US022681.  
17-JUL-2001; 2001US-0306040P.  
23-OCT-2001; 2001US-0347821P.  
06-FEB-2002; 2002US-0354668P.

(SALA/) SALAFSKY J S.  
Salafsky JS;  
WPI; 2003-646172/61.

Screening candidate binding partner(s) for binding to test molecule by  
applying external force field to sample in homogeneous phase,  
illuminating sample with light beam(s) at fundamental frequencies, and  
measuring physical properties.

Disclosure; Fig 20-B; 146pp; English.

CC The present invention relates to a method for detecting interactions  
CC between biological components using a nonlinear optical technique. The  
CC invention is used for screening candidate binding partner(s) for binding  
CC to test molecule. It can also be used to detect changes in orientation or  
CC conformation of the probe and/or target. The present sequence is a target  
CC oligonucleotide used in nonlinear optical technique

XX  
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAA 2800  
Db 1 GAAAAA AAAAAA AAAAA 16

RESULT 2540  
ADB68519  
ID ADB68519 standard; DNA; 16 BP.

XX  
AC ADB68519;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE DNA hybridisation oligomer SEQ ID 9.

KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;  
KW gene expression; respiration; secretion; signalling;  
KW ion-channel activity; cell motility; developmental phenotype;  
KW tumour regression; hybridisation; ss.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT misc\_difference 1 /\*tag= a  
FT /note= "Optional N-terminal acetyl"

XX  
PN WO2003068798-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003904.  
XX  
PR 09-FEB-2002; 2002US-00072975.  
XX  
PA (ACTI-) ACTIVE MOTIF.

PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;  
XX  
DR WPI; 2003-689653/65.

XX  
PT Method of inhibiting expression of genes or RNA transcripts, useful for  
PT therapy and determining effects of genes, by administering oligomers  
PT containing hydroxyproline nucleic acid.

XX  
PS Example 17; Page 233; 240pp; English.

XX  
CC The invention relates to a novel method of inhibiting the expression of  
CC one or more genes or RNA transcripts by administering at least one  
CC oligonucleotide analogue that includes at least one hydroxyproline  
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The  
CC oligonucleotides of the invention may be used to monitor properties  
CC including gene expression, respiration, secretion, signalling, ion-  
CC channel activity, cell motility, developmental phenotype and tumour  
CC regression. Furthermore, they may be utilised to determine the effects of  
CC particular genes, as antisense or homologous recombination constructs  
CC e.g. for creating animal models of disease and finally, for increasing  
CC the activity of some enzymes, such as polymerases. The current sequence  
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This  
CC sequence may also comprise a peptide nucleic acid (PNA).

XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTT TTTTTT TTTTTT 2181  
Db 1 TTTTTT TTTTTT TTTTTT 16

RESULT 2541  
ADB68519/c  
ID ADB68519 standard; DNA; 16 BP.

XX  
AC ADB68519;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE DNA hybridisation oligomer SEQ ID 9.

KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;  
KW gene expression; respiration; secretion; signalling;  
KW ion-channel activity; cell motility; developmental phenotype;  
KW tumour regression; hybridisation; ss.

XX  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT misc\_difference 1 /\*tag= a  
FT /note= "Optional N-terminal acetyl"

XX  
PN WO2003068798-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003904.  
XX  
PR 09-FEB-2002; 2002US-00072975.  
XX  
PA (ACTI-) ACTIVE MOTIF.

PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;  
XX  
DR WPI; 2003-689653/65.

XX  
PT Method of inhibiting expression of genes or RNA transcripts, useful for  
PT therapy and determining effects of genes, by administering oligomers  
PT containing hydroxyproline nucleic acid.

XX  
PS Example 17; Page 233; 240pp; English.

XX  
CC The invention relates to a novel method of inhibiting the expression of  
CC one or more genes or RNA transcripts by administering at least one  
CC oligonucleotide analogue that includes at least one hydroxyproline  
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The  
CC oligonucleotides of the invention may be used to monitor properties  
CC including gene expression, respiration, secretion, signalling, ion-  
CC channel activity, cell motility, developmental phenotype and tumour  
CC regression. Furthermore, they may be utilised to determine the effects of  
CC particular genes, as antisense or homologous recombination constructs  
CC e.g. for creating animal models of disease and finally, for increasing  
CC the activity of some enzymes, such as polymerases. The current sequence  
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This  
CC sequence may also comprise a peptide nucleic acid (PNA).

XX  
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 2542  
AAx69800/c  
ID AAX69800 standard; RNA; 17 BP.  
XX  
AC AAX69800;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.  
XX  
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX  
WPI; 1997-259017/23.  
XX  
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 79; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
Db 17 AAAAAAAAAAAAAAAAAA 2

RESULT 2543  
AAx69801  
ID AAX69801 standard; RNA; 17 BP.  
XX  
AC AAX69801;

XX 28-JUL-1999 (first entry)  
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.  
DE  
XX  
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
XX  
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
XX  
WPI; 1997-259017/23.  
XX  
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
PS Claim 4; Page 79; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 0.0%; Pred. No. 1.4e+03;  
Matches 0; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 UUUUUUUUUUUUUUUUU 16

RESULT 2544  
ABK13941  
ID ABK13941 standard; DNA; 17 BP.  
XX  
AC ABK13941;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE 5'-PCR primer used to produce single pattern characteristic by FokI.  
XX  
KW Identification of transcribed gene; mRNA profile; gene expression;  
KW cellular process; fingerprinting; susceptibility to external factor;  
KW development; disease; PCR; primer; ss.  
XX  
OS Synthetic.





XX The invention relates to determining the presence of and/or identifying a  
CC polyadenylation site within a sequence of a transcribed gene or variants  
CC present in a sample. The method involves assigning to gene fragments gene  
CC candidates within a database by comparing signals in the dataset with the  
CC database, the database comprising data representing mRNAs with known  
CC polyA sites and/or 'virtual genes' representing a possible  
CC polyadenylation site within an actual gene. The method is useful for  
CC determining the presence of and/or identifying a polyadenylation site or  
CC alternative polyadenylation sites within a sequence of a transcribed gene  
CC or sequences of transcribed gene variants present or potentially present  
CC in a sample, in identifying gene features, particularly in identifying  
CC differences between sequence variants that occur in a population of  
CC nucleic acid molecules, especially in identifying or discovering polyA  
CC site usage or determining polyA site usage in a nucleic acid sample, and  
CC gene variants arising from alternative polyA sites. The present sequence  
CC represents a double stranded product DNA fragment

XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2547  
ACF36370  
ID ACF36370 standard; DNA; 17 BP.  
XX  
AC ACF36370;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Nucleotide sequence of a double stranded product DNA.

XX Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;  
KW electrophoresis; type II restriction enzyme; FokI; ds.  
XX Synthetic.

XX WO2003064691-A2.  
XX  
PD 07-AUG-2003.

XX 28-JAN-2003; 2003WO-IB000843.  
XX  
PR 29-JAN-2002; 2002US-0352215P.

XX (GLOB-) GLOBAL GENOMICS AB.

XX Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;  
PI Montelius A;

XX WPI; 2003-618365/58.

XX Producing a population of double-stranded product DNA molecules, useful  
PT for mRNA profiling, comprises amplification by nested polymerase chain  
PT reaction.

XX Example; Fig 2; 105pp; English.

XX The invention relates to producing a population of double-stranded  
CC product DNA molecules comprising amplification by a nested PCR method.  
CC The method is useful in profiling mRNA transcribed in a system under  
CC investigation. The oligonucleotides are used as size standards in  
CC electrophoresis, and as internal controls allowing for calculation of  
CC relative amounts of material present. The present sequence represents a  
CC double stranded product DNA, which aids in outlining an approach to  
CC production of a single pattern characteristic of a sample, employing a

CC type II restriction enzyme (FokI)  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2548  
AAX69799  
ID AAX69799 standard; RNA; 17 BP.

XX  
AC AAX69799;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.

XX Homo sapiens.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR ) CHIRON CORP.

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.

PS Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention

XX Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 6.2%; Pred. No. 1.4e+03;  
Matches 1; Conservative 15; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTT TTTT TTTT TTTT TTTT 2180

Db 2 CUUUUUUUUUUUUUUUUU 17

RESULT 2549  
AAX69802/c  
ID AAX69802 standard; RNA; 17 BP.  
XX  
AC AAX69802;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1097.  
XX  
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9715662-A2.  
XX  
PD 01-MAY-1997.  
XX  
PF 25-OCT-1996; 96WO-US017480.  
XX  
PR 26-OCT-1995; 95US-0005974P.  
PR 11-JAN-1996; 96US-00584040.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
PA (CHIR ) CHIRON CORP.  
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
PI WPI; 1997-259017/23.  
XX  
DR Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
PT rheumatoid arthritis, etc., in a human patient.  
XX  
XX Claim 4; Page 79; 218pp; English.  
XX  
CC The present invention describes nucleic acid molecules which modulate the  
CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
CC receptors of vascular endothelial growth factor (VEGF). A patient  
CC (preferably human) having a condition associated with the level of the  
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
CC treated by administering the nucleic acid molecule or the expression  
CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
CC of nucleic acid molecules from the present invention  
XX  
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 0 T; 15 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2800  
Db 16 GAAAAAAAAAAAAAAAAA 1  
  
RESULT 2550  
AAV37934/c  
ID AAV37934 standard; cDNA; 17 BP.  
XX  
AC AAV37934;  
XX  
DT 05-OCT-1998 (first entry)  
XX  
DE Primer of the specification.

XX Leukocyte; Iga nephropathy; diagnosis; treatment; PCR primer; ss.  
KW  
XX  
OS Synthetic.  
XX  
PN WO9824815-A1.  
XX  
PD 11-JUN-1998.  
XX  
PF 05-DEC-1997; 97WO-JP004469.  
XX  
PR 05-DEC-1996; 96JP-00325752.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PA (KAZU-) KAZUSA DNA RES INST FOUND.  
XX  
PI Ishiwata T, Sakurada M, Nishimura A, Nakagawa S, Kuga T, Nishi T;  
PI Nomura N, Nagase T, Sawada S, Takei M;  
XX  
DR WPI; 1998-333259/29.  
XX  
XX Protein from leukocytes and DNA encoding it - useful as reagents for  
PT diagnosing and treating Iga nephropathy.  
XX  
PS Example 2; Page 33; 41pp; Japanese.  
XX  
CC PCR primers AAV37933-39 are used in the course of the invention. The  
CC specification describes a novel protein isolated from leukocytes of  
CC patients with Iga nephropathy. Oligonucleotides based on the DNA sequence  
CC encoding this protein are useful as reagents for diagnosing and treating  
CC Iga nephropathy  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAAAAAA 2800  
Db 17 GAAAAAAAAAAAAAAAAA 2  
  
RESULT 2551  
AAV49503  
ID AAV49503 standard; cDNA to mRNA; 17 BP.  
XX  
AC AAV49503;  
XX  
DT 18-NOV-1998 (first entry)  
XX  
DE Human eosinophil cell activator HVC002 primer #1.  
XX  
KW Eosinophil cell activator; treatment; diagnosis; malignant tumour;  
KW parasitic infection; allergic inflammation; eosinophilic pneumonia;  
KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9824817-A1.  
XX  
PD 11-JUN-1998.  
XX  
PF 05-DEC-1997; 97WO-JP004470.  
XX  
PR 05-DEC-1996; 96JP-00325762.  
XX  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
PI Yoshisue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;  
PI Nishi T;  
XX





DE PCR primer GT15C used in pollenosis associated gene identification.  
XX  
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;  
KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200020575-A1.  
XX  
XX 13-APR-2000.  
XX  
PF 06-OCT-1999; 99WO-JP005506.  
XX  
XX 06-OCT-1998; 98JP-00284610.  
PR  
XX (GENO-) GENOX RES INC.  
XX  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Lu N, Ogawa K;  
XX  
XX WPI; 2000-317712/27.  
DR  
XX Gene highly expressed in patients with high cedar pollen-specific IgE  
PT levels, useful for diagnosing pollenosis, and screening candidate  
PT compounds for pollenosis treatment.  
XX  
XX Example 6; Page 38; 44pp; Japanese.  
XX  
XX This sequence represents a PCR primer used in the identification of a  
CC human pollenosis associated gene. The gene is highly expressed in  
CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The  
CC invention relates to the nucleotide sequence encoding the pollenosis  
CC associated protein, diagnosing pollenosis and screening candidate  
CC compounds for treating pollenosis. The gene can be used in diagnosing  
CC pollenosis, particularly cedar pollenosis, and screening candidate  
CC compounds for pollenosis treatment  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAATAAAAAA 2800  
Db 17 GAAAAAATAAAAAA 2  
RESULT 2555  
AAX82722/c  
ID AAX82722 standard; DNA; 17 BP.  
XX  
AC AAX82722;  
XX 10-NOV-2000 (first entry)  
XX Human IgA nephropathy-associated cDNA primer #63.  
DE  
XX IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
KW human; primer; ss.  
XX Homo sapiens.  
OS  
XX WO9963085-A1.  
PN  
XX 09-DEC-1999.  
PD  
XX 28-MAY-1999; 99WO-JP002855.  
PF  
XX 02-JUN-1998; 98JP-00152603.  
PR  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
PI Sawada S, Takei M, Shibata K, Furuya A;  
XX  
XX WPI; 2000-097328/08.  
XX  
PT DNA sequences preferentially expressed in IgA nephropathy patients,  
PT proteins encoded by them, and antibodies to those proteins.  
XX  
XX Claim 3; Page 170; 180pp; Japanese.  
XX  
XX This invention describes novel DNA sequences preferentially expressed in  
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to  
CC them. Independent claims cover diagnostic reagents for IgA nephropathy  
CC incorporating the antisense sequences; the treatment of IgA nephropathy  
CC using the antisense sequences for mRNA inhibition; proteins associated  
CC with IgA nephropathy, containing sequences encoded by the DNA sequences;  
CC antibodies recognizing these proteins; the production of the proteins by  
CC culture of host cells transformed with DNA encoding them; diagnostic  
CC reagents for IgA nephropathy containing the antibodies; and compositions  
CC for the treatment of IgA nephropathy which contain the antibodies. The  
CC products of the invention can be used for the diagnosis and treatment of  
CC IgA nephropathy. This sequence represents a primer used in the isolation  
CC and identification of the human IgA nephropathy-associated proteins  
CC described in the method of the invention  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAATAAAAAA 2800  
Db 17 GAAAAAATAAAAAA 2  
RESULT 2556  
AAX82720  
ID AAX82720 standard; DNA; 17 BP.  
XX  
AC AAX82720;  
XX 10-NOV-2000 (first entry)  
XX Human IgA nephropathy-associated cDNA primer #61.  
DE  
XX IgA nephropathy-associated protein; diagnosis; treatment; antisense;  
KW human; primer; ss.  
XX Homo sapiens.  
OS  
XX WO9963085-A1.  
PN  
XX 09-DEC-1999.  
XX 28-MAY-1999; 99WO-JP002855.  
PF  
XX 02-JUN-1998; 98JP-00152603.  
PR  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;  
PI Sawada S, Takei M, Shibata K, Furuya A;  
XX  
XX WPI; 2000-097328/08.  
XX  
XX DNA sequences preferentially expressed in IgA nephropathy patients,  
PT proteins encoded by them, and antibodies to those proteins.  
XX  
XX Claim 3; Page 169; 180pp; Japanese.  
XX  
XX This invention describes novel DNA sequences preferentially expressed in  
CC IgA nephropathy patients, and DNA sequences stringently hybridizing to



CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present  
CC invention  
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2801  
Db 17 AAAAAAAAAAAAAA 2  
RESULT 2560  
AAA25451  
ID AAA25451 standard; DNA; 17 BP.  
XX  
AC AAA25451;  
XX  
DT 19-JUL-2000 (first entry)  
XX  
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.  
XX  
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX Homo sapiens.  
OS  
XX WO9954459-A2.  
PN  
XX  
PD 28-OCT-1999.  
XX  
PF 19-APR-1999; 99WO-US008547.  
XX  
PR 20-APR-1998; 98US-0082404P.  
PR 23-JUN-1998; 98US-00103636.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
PI Matulic-Adamic J;  
XX  
DR WPI; 2000-013248/01.  
XX  
PT New nucleic acids that interact, and optionally cleave, target sequences,  
used to treat cancer.  
XX  
PS Claim 77; Page 79; 148pp; English.  
XX  
CC The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphoro(di)thioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A') that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium), or  
CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
CC for other conditions associated with levels of oestrogen receptor.  
CC Because of the high selectivity for targeted RNA, (A) can also be used to  
CC correlate inhibition of gene expression with alterations in phenotype,  
CC particularly for identification of therapeutic targets, and as research  
CC reagents (for RNA, in the same way that restriction endonucleases are  
CC used with DNA). The combination of modifications in (A) improves  
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
CC AAA24748 to AAA25992 represent their corresponding target sequences.  
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present

CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present  
CC invention  
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
SQ Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTTTTTTTTTTTT 2181  
Db 2 TTTTTTTTTTTTTT 17  
RESULT 2559  
AAA25449/C  
ID AAA25449 standard; DNA; 17 BP.  
XX  
AC AAA25449;  
XX  
DT 19-JUL-2000 (first entry)  
XX  
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.  
XX  
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX Homo sapiens.  
OS  
XX WO9954459-A2.  
PN  
XX  
PD 28-OCT-1999.  
XX  
PF 19-APR-1999; 99WO-US008547.  
XX  
PR 20-APR-1998; 98US-0082404P.  
PR 23-JUN-1998; 98US-00103636.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;  
PI Matulic-Adamic J;  
XX  
DR WPI; 2000-013248/01.  
XX  
PT New nucleic acids that interact, and optionally cleave, target sequences,  
used to treat cancer.  
XX  
PS Claim 77; Page 79; 148pp; English.  
XX  
CC The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphoro(di)thioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A') that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium), or  
CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
CC for other conditions associated with levels of oestrogen receptor.  
CC Because of the high selectivity for targeted RNA, (A) can also be used to  
CC correlate inhibition of gene expression with alterations in phenotype,  
CC particularly for identification of therapeutic targets, and as research  
CC reagents (for RNA, in the same way that restriction endonucleases are  
CC used with DNA). The combination of modifications in (A) improves  
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
CC AAA24748 to AAA25992 represent their corresponding target sequences.  
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences.



CC invention  
XX  
SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16  
RESULT 2561  
ID AAA25451/C  
XX AAA25451 standard; DNA; 17 BP.  
AC AAA25451;  
XX  
DT 19-JUL-2000 (first entry)  
XX  
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1949.  
XX  
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;  
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
KW gene expression modification; cancer; phosphorothioate; endonuclease;  
KW anticancer; breast cancer; endometrium cancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954459-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 19-APR-1999; 99WO-US008547.  
XX  
PR 20-APR-1998; 98US-0082404P.  
PR 23-JUN-1998; 98US-00103636.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;  
PI Matulic-Adamic J;  
XX  
DR WPI; 2000-013248/01.  
XX  
PT New nucleic acids that interact, and optionally cleave, target sequences,  
PT used to treat cancer.  
XX  
PS Claim 77; Page 79; 148pp; English.  
XX  
CC The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphoro(dithioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A') that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium),  
CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
CC for other conditions associated with levels of oestrogen receptor.  
CC Because of the high selectivity for targeted RNA, (A) can also be used to  
CC correlate inhibition of gene expression with alterations in phenotype,  
CC particularly for identification of therapeutic targets, and as research  
CC reagents (for RNA, in the same way that restriction endonucleases are  
CC used with DNA). The combination of modifications in (A) improves  
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
CC AAA24748 to AAA25992 represent their corresponding target sequences.  
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
CC antisense oligonucleotides used in the exemplification of the present  
CC invention

SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2801  
Db 16 AAAAAA AAAAAA AAAAAA 1  
RESULT 2562  
ID AAC64202 standard; DNA; 17 BP.  
XX  
AC AAC64202;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.  
XX  
KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200065046-A1.  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002730.  
XX  
PR 27-APR-1999; 99JP-00120489.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687339/67.  
XX  
PT Pollinosis-associated gene 373 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful  
PT in diagnosis of allergic diseases and screening drug candidates.  
XX  
PS Example 6; Page 69; 80pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 373 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis gene 373; expression constructs and  
CC host cells comprising pollinosis-associated gene 373 nucleic acids;  
CC pollinosis-associated gene 373 primers and probes; antibodies against the  
CC protein encoded by the gene; methods of detection of pollinosis-  
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic  
CC diseases via the detection of pollinosis-associated gene 373 nucleic  
CC acids. The invention additionally encompasses methods of screening drug  
CC candidates for the treatment of allergic disease by measuring the  
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated  
CC T-cells in the presence of a test compound relative to a control.  
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic  
CC diseases and in the screening of drug candidates for the treatment of  
CC such diseases. The present sequence represents a PCR primer used in the  
CC isolation of human pollinosis-associated gene 373 cDNA  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







OS Synthetic.  
XX WO200065049-A1.  
PN  
XX  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002733.  
XX  
PR 27-APR-1999; 99JP-00120491.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
XX  
DR WPI; 2000-687342/67.  
XX  
PT Pollinosis-associated gene 513 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
PS Example 6; Page 38; 46pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 513 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates to methods of  
CC detection of pollinosis-associated gene 513 nucleic acids; a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 513 nucleic acids; and methods of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 513  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 513 cDNA  
XX  
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2785 GAAAAAAAAAAAAA 2800  
Db | | | | | | | | | | | | | | | | | | | |  
17 GAAAAAAAAAAAAA 2  
  
RESULT 2568  
AAC64161  
ID AAC64161 standard; DNA; 17 BP.  
XX  
AC AAC64161;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.  
XX  
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO200065048-A1.  
PN  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002732.  
XX  
PR 27-APR-1999; 99JP-00120492.  
XX

XX (GENO-) GENOX RES INC.  
PA Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
XX Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;  
PI  
XX  
DR WPI; 2000-687341/67.  
XX  
PT Pollenosis-associated gene 581 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.  
XX  
PS Example 6; Page 39; 69pp; Japanese.  
XX  
CC The invention relates to the human pollinosis-associated gene 581 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. The invention also relates also relates  
CC to the protein encoded by pollinosis-associated gene 581; to expression  
CC constructs and host cells comprising pollinosis-associated gene 581  
CC nucleic acids; pollinosis-associated gene 581 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 581 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 581 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by  
CC measuring the expression of pollinosis-associated gene 581 in pollen  
CC antigen-stimulated T-cells in the presence of a test compound relative to  
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of  
CC allergic diseases and in the screening of drug candidates for the  
CC treatment of such diseases. The present sequence represents a PCR primer  
CC used in the isolation of human pollinosis-associated gene 581 cDNA  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2172 TTTTTTTTTTTTTTTA 2187  
Db | | | | | | | | | | | | | | | | | | | |  
2 TTTTTTTTTTTTTTTA 17  
  
RESULT 2569  
AAC64162/C  
ID AAC64162 standard; DNA; 17 BP.  
XX  
AC AAC64162;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.  
XX  
KW Human; pollinosis-associated gene 581; IgE; immunoglobulin E;  
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;  
KW drug screening; allergic disease; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO200065048-A1.  
PN  
XX  
PD 02-NOV-2000.  
XX  
PF 26-APR-2000; 2000WO-JP002732.  
XX  
PR 27-APR-1999; 99JP-00120492.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;



XX WPI; 2000-687341/67.

DR

XX Pollenosis-associated gene 581 undergoing significantly low expression in

PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis

PT of allergic diseases and screening drug candidates.

XX

PS Example 6; Page 40; 69pp; Japanese.

XX

CC The invention relates to the human pollinosis-associated gene 581 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates to methods

CC to the protein encoded by pollinosis-associated gene 581; to expression

CC constructs and host cells comprising pollinosis-associated gene 581

CC nucleic acids; pollinosis-associated gene. 581 primers and probes;

CC antibodies against the protein encoded by the gene; methods of detection

CC of pollinosis-associated gene 581 nucleic acids; and a method of

CC diagnosis of allergic diseases via the detection of pollinosis-associated

CC gene 581 nucleic acids. The invention additionally encompasses methods of

CC screening drug candidates for the treatment of allergic disease by

CC measuring the expression of pollinosis-associated gene 581 in pollen

CC antigen-stimulated T-cells in the presence of a test compound relative to

CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of

CC allergic diseases and in the screening of drug candidates for the

CC treatment of such diseases. The present sequence represents a PCR primer

CC used in the isolation of human pollinosis-associated gene 581 cDNA

XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2800

Db ||||||||||||||||

17 GAAAAAAAAAAAAAAAAA 2

RESULT 2570

AAC64213

ID AAC64213 standard; DNA; 17 BP.

XX

AC AAC64213;

XX

DT 21-FEB-2001 (first entry)

XX

DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.

XX

KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;

KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;

KW drug screening; allergic disease; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO200065051-A1.

XX

PD 02-NOV-2000.

XX

PF 26-APR-2000; 2000WO-JP002735.

XX

PR 27-APR-1999; 99JP-00120493.

XX

PA (GENO-) GENOX RES INC.

XX

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX

DR WPI; 2000-687344/67.

XX

PT Pollinosis-associated gene 627 undergoing significantly low expression in

PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis

PT of allergic diseases and screening drug candidates.

XX

PS Example 6; Page 41; 51pp; Japanese.

XX

CC The invention relates to the human pollinosis-associated gene 627 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates to methods of

CC detection of pollinosis-associated gene 627 nucleic acids; a method of

CC diagnosis of allergic diseases via the detection of pollinosis-associated

CC gene 627 nucleic acids; and a method of screening drug candidates for the

CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 627 in pollen antigen-stimulated T-cells in the presence

CC of a test compound relative to a control. Pollinosis-associated gene 627

CC is useful in the diagnosis of allergic diseases and in the screening of

CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-

CC associated gene 627 cDNA

XX

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTTTTTTTTTTTTTA 2187

Db ||||||||||||||||

2 TTTTTTTTTTTTTTTA 17

RESULT 2571

AAC64214/c

ID AAC64214 standard; DNA; 17 BP.

XX

AC AAC64214;

XX

DT 21-FEB-2001 (first entry)

XX

DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.

XX

KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;

KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;

KW drug screening; allergic disease; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO200065051-A1.

XX

PD 02-NOV-2000.

XX

PF 26-APR-2000; 2000WO-JP002735.

XX

PR 27-APR-1999; 99JP-00120493.

XX

PA (GENO-) GENOX RES INC.

XX

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;

XX

DR WPI; 2000-687344/67.

XX

PT Pollinosis-associated gene 627 undergoing significantly low expression in

PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis

PT of allergic diseases and screening drug candidates.

XX

PS Example 6; Page 42; 51pp; Japanese.

XX

CC The invention relates to the human pollinosis-associated gene 627 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using

CC the differential display method. The invention also relates to methods of



CC detection of pollinosis-associated gene 627 nucleic acids; a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 627 nucleic acids; and a method of screening drug candidates for the  
CC treatment of allergic disease by measuring the expression of pollinosis-  
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence  
CC of a test compound relative to a control. Pollinosis-associated gene 627  
CC is useful in the diagnosis of allergic diseases and in the screening of  
CC drug candidates for the treatment of such diseases. The present sequence  
CC represents a PCR primer used in the isolation of human pollinosis-  
CC associated gene 627 cDNA

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAA 2800  
| | | | | | | | | | | | | | | | | |  
Db 17 GAAAAAAAAAAAAA 2

RESULT 2572  
AAC64231/c  
ID AAC64231 standard; DNA; 17 BP.

XX AAC64231;

DT 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.

XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

XX WO200065050-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP002734.

XX 27-APR-1999; 99JP-00120494.

XX (GENO-) GENOX RES INC.  
XX (EISA ) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;

XX WPI; 2000-687343/67.

XX Pollinosis-associated gene 795 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.

PS Page 45; Example 6; 73pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 795 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. Pollinosis-associated gene 795 has  
CC homology with the human vimentin gene. The invention also relates also  
CC relates to the protein encoded by pollinosis gene 795; to expression  
CC constructs and host cells comprising pollinosis-associated gene 795  
CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 795 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated

CC gene 795 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by  
CC measuring the expression of pollinosis-associated gene 795 in pollen  
CC antigen-stimulated T-cells in the presence of a test compound relative to  
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of  
CC allergic diseases and in the screening of drug candidates for the  
CC treatment of such diseases. The present sequence represents a PCR primer  
CC used in the isolation of human pollinosis-associated gene 795 cDNA

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAA 2800  
| | | | | | | | | | | | | | | | | |  
Db 17 GAAAAAAAAAAAAA 2

RESULT 2573  
AAC64230  
ID AAC64230 standard; DNA; 17 BP.

XX AAC64230;

DT 21-FEB-2001 (first entry)

DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.

XX Human; pollinosis-associated gene 795; vimentin homologue; IgE;  
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;  
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.

XX Synthetic.

XX WO200065050-A1.

XX 02-NOV-2000.

XX 26-APR-2000; 2000WO-JP002734.

XX 27-APR-1999; 99JP-00120494.

XX (GENO-) GENOX RES INC.  
XX (EISA ) EISAI CO LTD.

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;  
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;  
PI Yokoi A;

XX WPI; 2000-687343/67.

XX Pollinosis-associated gene 795 undergoing significantly low expression in  
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis  
PT of allergic diseases and screening drug candidates.

PS Page 45; Example 6; 73pp; Japanese.

XX The invention relates to the human pollinosis-associated gene 795 which  
CC exhibits significantly reduced expression in the T-cells of individuals  
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene  
CC was isolated from T-cells from individuals allergic to cedar pollen using  
CC the differential display method. Pollinosis-associated gene 795 has  
CC homology with the human vimentin gene. The invention also relates also  
CC relates to the protein encoded by pollinosis gene 795; to expression  
CC constructs and host cells comprising pollinosis-associated gene 795  
CC nucleic acids; pollinosis-associated gene 795 primers and probes;  
CC antibodies against the protein encoded by the gene; methods of detection  
CC of pollinosis-associated gene 795 nucleic acids; and a method of  
CC diagnosis of allergic diseases via the detection of pollinosis-associated  
CC gene 795 nucleic acids. The invention additionally encompasses methods of  
CC screening drug candidates for the treatment of allergic disease by



DT 12-SEP-2001 (first entry)

XX Human cDNA synthesis and differential display primer, HT11GG.

DE

XX

XX Human; Estrogen response element; ERE; DDRT-PCR; ss; PCR primer;

KW differential display of reverse transcribed mRNAs by PCR;

KW testicular cancer; breast cancer; prostate cancer; endometrial cancer;

KW asthma; hypospadia; cryptorchism; allergy; hormone replacement therapy;

KW HRT; endocrine system; HT11GG.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX WO200134834-A2.

PN

PD 17-MAY-2001.

XX

XX 10-NOV-2000; 2000WO-DK000628.

PF

XX 11-NOV-1999; 99DK-00001626.

PR

XX (RIGS-) RIGSHOSPITALET.

PA

XX Leffers H, Jorgensen M, Skakkebaek NE;

PI

XX WPI; 2001-335941/35.

DR

XX Evaluating a cellular response to an environmental compound, for use in

XX toxicological analysis, involves determining or comparing the expression

PT levels of at least one endogenous gene.

PT

XX

XX Example 3; Page 27; 77pp; English.

PS

XX The sequence represents a downstream PCR primer used in a DDRT-PCR

CC experiment (and in cDNA synthesis), demonstrating the method of the

CC invention. The method relates to evaluating a cellular response to an

CC environmental compound, comprising determining or comparing the

CC expression levels of at least one endogenous gene e.g by differential

CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be

CC adapted to identify compounds that act on the level of endogenous gene

CC expression through activating nuclear receptors. The method is useful in

CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.

CC testicular, breast, prostate and endometrium), asthma, hypospadia,

CC cryptorchism and/or allergy, and for evaluating the efficiency of a

CC treatment for hormonal deficiency or hormonal replacement therapy, in a

CC human such as a post-menopausal female. The method is also useful for

CC identifying environmental chemicals or pharmaceutical compositions that

CC interact with endocrine systems, and for detecting chemicals that pose a

CC health threat. Expression levels of endogenous genes are determined

CC rapidly using a sensitive technique, and the expression of any gene can

CC be monitored. The assays are far more informative than the currently used

CC assays, and significantly reduces the number of animals required for the

CC testing, as it is expected that essentially all the animals in a test

CC group will respond to the compound

XX

SQ Sequence 17 BP; 2 A; 1 C; 3 G; 11 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1767 AAGCTTTT TTTT TTTG 1782

DB 1 AAGCTTTT TTTT TTTG 16

RESULT 2577

AAC91720/c

ID AAC91720 standard; DNA; 17 BP.

XX

AC AAC91720;

XX

DT 27-MAR-2001 (first entry)

XX PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.

DE

XX

XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;

KW reduced expression; detection; diagnosis; drug screening;

KW allergic disease; PCR primer; ss.

XX

OS Synthetic.

XX WO200073440-A1.

PN

PD 07-DEC-2000.

XX

XX 18-MAY-2000; 2000WO-JP003192.

PF

XX 27-MAY-1999; 99JP-00148785.

PR

XX (GENO-) GENOX RES INC.

PA (EISA ) EISAI CO LTD.

XX

XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;

PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;

PI Yokoi A;

XX

DR WPI; 2001-032159/04.

XX

XX Pollinosis-associated gene 787 undergoing significantly low expression in

PT subjects after pollen scattering, useful in diagnosis of allergic

PT diseases and screening candidate compounds to regulate response of T

PT cells to antigen stimulus.

XX

PS Example 6; Page 40; 54pp; Japanese.

XX

CC The invention relates to the human pollinosis-associated gene 787 which

CC exhibits significantly reduced expression in the T-cells of individuals

CC after the pollen-scattering season, relative to expression levels in T-

CC cells before the pollen-scattering season. The gene was isolated from T-

CC cells from individuals allergic to pollen using the differential display

CC method. The invention also relates to pollinosis-associated gene 787

CC primers and probes; methods of detection of pollinosis-associated gene

CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the

CC detection of pollinosis-associated gene 787 nucleic acids. The invention

CC additionally encompasses a method of screening drug candidates for the

CC treatment of allergic disease by measuring the expression of pollinosis-

CC associated gene 787 in pollen antigen-stimulated T-cells in the presence

CC of a test compound relative to a control. Pollinosis-associated gene 787

CC is useful in the diagnosis of allergic diseases and in the screening of

CC drug candidates for the treatment of such diseases. The present sequence

CC represents a PCR primer used in the isolation of human pollinosis-

CC associated gene 787 cDNA

XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2800

DB 17 GAAAAAAAAAAAAA 2

RESULT 2578

AAC91719

ID AAC91719 standard; DNA; 17 BP.

XX

AC AAC91719;

XX

DT 27-MAR-2001 (first entry)

XX

DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.

XX

KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;





```
AAH47126
ID AAH47126 standard; DNA; 17 BP.
XX
XX AAH47126;
AC
XX
XX 30-NOV-2001 (first entry)
DT
XX
DE Nucleotide sequence of primer GT15A.
XX
XX B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW PCR primer; ss.
KW
XX Homo sapiens.
OS
XX WO200165259-A1.
XX
XX 07-SEP-2001.
PF
XX 23-FEB-2001; 2001WO-JP001372.
XX
XX 02-MAR-2000; 2000JP-00061832.
PR
XX (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA
XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
PI WPI; 2001-557789/62.
XX
DR Diagnosis of allergies including atopic dermatitis.
XX
XX Example 6; Page 65; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 2172 TTTT TTTT TTTT TTTT TTA 2187
Db ||||| ||||| ||||| |||||
2 TTTT TTTT TTTT TTTT TTA 17
RESULT 2583
ABK49634
ID ABK49634 standard; DNA; 17 BP.
XX
AC ABK49634;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
OS Homo sapiens.
XX
PN WO200224903-A1.
XX
PD 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-JP008246.
PF
XX 25-SEP-2000; 2000JP-00291318.
PR
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XX (GENO-) GENOX RES INC.  
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
PA (EISA ) EISAI CO LTD.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;  
PI Takahashi E;  
XX WPI; 2002-315738/35.  
DR  
XX  
XX Examining allergic diseases by differential display of gene showing  
PT different expression particularly increased expression in remission stage  
PT in eosinophils of patients, also applicable in screening candidate  
PT compounds for remedies.  
XX  
PS Example 1; Page 56; 72pp; Japanese.  
XX  
CC The invention relates to a method for examining allergic diseases  
CC comprises determining the expression level of a gene containing, the  
CC human cDNA appearing as ABK49633 which has homology with  
CC acetyltransferases in the eosinophils of a patient and comparing the  
CC expression level with that in the eosinophils of a healthy individual  
CC (i.e. differential display). Also included are methods of screening for  
CC candidate compounds which affect the expression level of the gene or the  
CC activity of the protein encoded by the gene (including related proteins  
CC and mutants), the use of probes based on the gene sequence in the  
CC examination of allergic diseases, the use of reporter constructs in the  
CC screening of candidate compounds, a vector containing a the transcription  
CC -controlling region of the gene, cells transformed with the vector, an  
CC antibody against the protein and a model animal for allergic diseases  
CC which is a transgenic non-human vertebrate with lowering of expression  
CC intensity of the gene in eosinophils. The method is examining allergic  
CC diseases particularly atopic dermatitis which is also applicable in  
CC screening candidate compounds for remedies. Such method can be performed  
CC in high throughput, at low cost. The present sequence is a differential  
CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
CC protein 20-90-05  
XX  
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2172 TTTTTTTTTTTTTTTT 2187  
Db |||||||  
2 TTTTTTTTTTTTTTTT 17  
RESULT 2584  
ABK49635/c  
ID ABK49635 standard; DNA; 17 BP.  
XX  
AC ABK49635;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.  
XX  
KW Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;  
KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.  
XX  
OS Homo sapiens.  
XX WO200224903-A1.  
PN  
XX  
PD 28-MAR-2002.  
XX  
PF 21-SEP-2001; 2001WO-JP008246.  
XX  
PR 25-SEP-2000; 2000JP-00291318.  
XX  
PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.  
PA (EISA ) EISAI CO LTD.  
XX  
PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;  
PI Takahashi E;  
XX WPI; 2002-315738/35.  
DR  
XX  
XX Examining allergic diseases by differential display of gene showing  
PT different expression particularly increased expression in remission stage  
PT in eosinophils of patients, also applicable in screening candidate  
PT compounds for remedies.  
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PS Example 1; Page 56; 72pp; Japanese.  
XX  
CC The invention relates to a method for examining allergic diseases  
CC comprises determining the expression level of a gene containing, the  
CC human cDNA appearing as ABK49633 which has homology with  
CC acetyltransferases in the eosinophils of a patient and comparing the  
CC expression level with that in the eosinophils of a healthy individual  
CC (i.e. differential display). Also included are methods of screening for  
CC candidate compounds which affect the expression level of the gene or the  
CC activity of the protein encoded by the gene (including related proteins  
CC and mutants), the use of probes based on the gene sequence in the  
CC examination of allergic diseases, the use of reporter constructs in the  
CC screening of candidate compounds, a vector containing a the transcription  
CC -controlling region of the gene, cells transformed with the vector, an  
CC antibody against the protein and a model animal for allergic diseases  
CC which is a transgenic non-human vertebrate with lowering of expression  
CC intensity of the gene in eosinophils. The method is examining allergic  
CC diseases particularly atopic dermatitis which is also applicable in  
CC screening candidate compounds for remedies. Such method can be performed  
CC in high throughput, at low cost. The present sequence is a differential  
CC display PCR primer for the cDNA encoding the human acetyltransferase-like  
CC protein 20-90-05  
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SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;  
Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2785 GAAAAAAAAAAAAA 2800  
Db |||||||  
17 GAAAAAAAAAAAAA 2  
RESULT 2585  
ABL59038  
ID ABL59038 standard; DNA; 17 BP.  
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AC ABL59038;  
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DT 20-AUG-2002 (first entry)  
XX  
DE Nucleotide sequence of PCR primer GT15A.  
XX  
KW Human; allergosis; eosinophil; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX JP2002095500-A.  
PN  
XX  
PD 02-APR-2002.  
XX  
PF 25-SEP-2000; 2000JP-00291316.  
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PR 25-SEP-2000; 2000JP-00291316.  
XX  
PA (GENO-) GENOX SOYAKU KENKYUSHO KK.  
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.  
XX  
DR WPI; 2002-439993/47.

